

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
 Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: <u>02-06-03</u>	Search Site: _____	Vendors
Searcher: <u>Beverly C 4994</u>	_____ STIC	_____ IG Suite
Terminal time: <u>20</u>	_____ CM-1	_____ STN
Elapsed time: _____	_____ Pre-S	_____ Dialog
CPU time: _____	Type of Search	_____ APS
Total time: <u>25</u>	_____ N.A. Sequence	_____ Geninfo
Number of Searches: _____	_____ A.A. Sequence	_____ SDC
Number of Databases: <u>1</u>	_____ Structure	_____ DARC/Questel
	_____ Bibliographic	✓ Other <u>CGN</u>

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:17:31 ; Search time 0.90249 Seconds
(without alignments)
1597.820 Million cell updates/sec

Title: US-09-689-159a-2_COPY_346_360

Perfect score: 15

Sequence: 1 SHLCPHRSPESSRAA 15

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	463	2	presenilin 1-463 -
2	15	100.0	467	2	presenilin 1, sp1
3	15	100.0	467	2	S182 protein - mou
4	8	53.3	347	2	hypothetical prote
5	7	46.7	327	2	hypothetical prote
6	7	46.7	343	2	hypothetical prote
7	7	46.7	463	2	probable transcrip
8	7	46.7	467	2	presenilin 1 prote
9	7	46.7	512	2	methionine-tRNA II
10	6	40.0	87	2	probable regulator
11	6	40.0	87	2	hypothetical prote
12	6	40.0	138	2	hypothetical prote
13	6	40.0	139	2	hypothetical prote
14	6	40.0	168	2	hypothetical prote
15	6	40.0	240	2	molibdenum cofacto
16	6	40.0	241	2	probable regulator
17	6	40.0	257	2	PK-tax-ort II (alt
18	6	40.0	262	2	probable exodeoxyr
19	6	40.0	262	2	exodeoxyribonuclea
20	6	40.0	301	2	hypothetical prote
21	6	40.0	364	2	DNA replication an
22	6	40.0	382	2	opsin rh3 - fruit
23	6	40.0	401	2	multidrug-efflux t
24	6	40.0	407	2	hypothetical prote
25	6	40.0	408	2	conserved hypothet
26	6	40.0	429	2	histidyl-tRNA synt
27	6	40.0	433	2	histidine-tRNA lig
28	6	40.0	475	2	presenilin-alpha -
29	6	40.0	617	2	dropt9 protein - hu
30	6	40.0	617	2	hypothetical prote

30	6	40.0	640	2	AE1895	hypothetical prote
31	6	40.0	806	2	I64207	preprolactin translo
32	6	40.0	817	1	RVGCT	RNA-directed RNA p
33	6	40.0	818	1	RVGCR	RNA-directed RNA p
34	6	40.0	851	2	S52717	RNA-directed RNA p
35	6	40.0	865	1	VGBERB	glycoprotein B pre
36	6	40.0	889	2	T30715	probable-major cor
37	6	40.0	981	2	B88794	protein K0755.12a
38	6	40.0	1048	2	T30815	platelet-derived g
39	6	40.0	1098	1	PFMSRB	platelet-derived g
40	6	40.0	1106	1	PFHUGB	platelet-derived g
41	6	40.0	1680	2	T01367	hypothetical prote
42	6	40.0	1711	1	A47392	hypothetical prote
43	6	40.0	2664	2	T28626	chromodomain-helic
44	6	33.3	18	2	S58277	variant-specific s
45	5	33.3	26	2	T04371	insulin-like growt
46	5	33.3	39	2	I37554	thymosin-like pro
47	5	33.3	51	2	F86491	homeobox - human (
48	5	33.3	51	2	C72131	hypothetical prote
49	5	33.3	56	2	G72355	hypothetical prote
50	5	33.3	69	1	O0ECP7	ybea protein - Esc
51	5	33.3	69	2	C80713	hypothetical prote
52	5	33.3	69	2	G85563	hypothetical prote
53	5	33.3	76	2	D72667	hypothetical prote
54	5	33.3	82	2	S28280	hypothetical prote
55	5	33.3	87	2	AD3436	cytochrome c (vali
56	5	33.3	102	1	CCEG	conserved hypotnet
57	5	33.3	105	2	AB0318	kora protein - Amy
58	5	33.3	118	2	S70089	hypothetical prote
59	5	33.3	122	2	A05114	MDH2 dehydrogenas
60	5	33.3	124	2	S43840	MDH2 dehydrogenas
61	6	33.3	127	2	AH3491	hypothetical cytos
62	6	33.3	134	2	S23003	trak protein - Esc
63	6	33.3	135	2	C62821	MDH2 dehydrogenas
64	5	33.3	136	2	B84990	50S ribosomal prot
65	5	33.3	145	2	AD2345	hypothetical prote
66	5	33.3	150	2	T08734	hypothetical prote
67	5	33.3	157	2	A97573	nitrogen regulator
68	5	33.3	160	2	A71062	hypothetical prote
69	5	33.3	163	2	B64172	hypothetical prote
70	5	33.3	165	2	D87241	glucokinase - rat
71	5	33.3	165	2	T16984	transcription fact
72	5	33.3	166	2	I49694	glucokinase - mus
73	5	33.3	166	2	I84740	succinate dehydrog
74	5	33.3	168	2	S68480	conserved hypotnet
75	5	33.3	173	2	F75274	splicingmyelin phos
76	5	33.3	177	2	S14747	probable pantocate-
77	5	33.3	176	2	T36394	hypothetical prote
78	5	33.3	183	2	A11820	hypothetical prote
79	5	33.3	185	2	T01887	hypothetical prote
80	5	33.3	189	2	G90855	hypothetical prote
81	5	33.3	189	2	A86369	hypothetical prote
82	5	33.3	191	2	A26213	conserved hypotnet
83	5	33.3	191	2	T28682	hypothetical prote
84	5	33.3	197	2	B72471	hypothetical prote
85	5	33.3	198	2	A45067	lamlnin B1 chain v
86	5	33.3	201	2	AT2631	hypothetical prote
87	5	33.3	201	2	B86488	hypothetical prote
88	5	33.3	206	2	T07771	probable heme tran
89	5	33.3	206	2	T09503	probable heme tran
90	5	33.3	206	2	AF0498	hypothetical prote
91	5	33.3	207	2	T17623	hypothetical prote
92	5	33.3	208	2	A48567	calmodulin-ubiquit
93	5	33.3	214	2	A82157	hypothetical prote
94	5	33.3	214	2	F82627	phosphoglycerate m
95	5	33.3	215	2	T16393	hypothetical prote
96	5	33.3	218	2	H83475	probable transcrip
97	5	33.3	219	2	T42605	envelope protein -
98	5	33.3	224	2	A87094	ATP-dependent Clp
99	5	33.3	227	2	D85018	probable hypotnet
100	5	33.3	228	2	D95865	probable pentose-5
101	5	33.3	230	2	S41043	rum1 protein - fis
102	5	33.3	230	2	T40233	Rumlp - fission ye

103	5	33.3	230	2	A54501	sporulated oocyst
104	5	33.3	238	2	C72576	probable glutamine
105	5	33.3	244	2	B88115	protein F53C3.4 [i
106	5	33.3	244	2	AG2071	hypothetical prote
107	5	33.3	247	2	T33469	hypothetical prote
108	5	33.3	247	2	H69030	coenzyme PQQ synth
109	5	33.3	247	2	T17311	hypothetical prote
110	5	33.3	247	2	B97669	hypothetical prote
111	5	33.3	247	2	AG2893	conserved hypotet
112	5	33.3	249	2	A70745	probable transcrip
113	5	33.3	249	2	T16924	hypothetical prote
114	5	33.3	252	2	B48725	MDV specific prote
115	5	33.3	263	3	AG2910	hypothetical prote
116	5	33.3	265	2	A87345	transcription regu
117	5	33.3	266	2	A12762	conserved hypotet
118	5	33.3	267	2	B97685	monofunctional bio
119	5	33.3	268	2	AD0898	PTS-transport faml
120	5	33.3	270	2	G75411	probable transpos
121	5	33.3	271	2	C96010	conserved hypotet
122	5	33.3	271	2	H97543	hypothetical prote
123	5	33.3	272	2	AG2215	hypothetical prote
124	5	33.3	274	2	T22993	hypothetical prote
125	5	33.3	275	1	G69963	lipoprotein SpoIII
126	5	33.3	278	1	B69025	conserved hypotet
127	5	33.3	279	2	B83456	hypothetical prote
128	5	33.3	280	2	C70642	probable ribosomal
129	5	33.3	281	2	T28857	hypothetical prote
130	5	33.3	284	2	T13621	hypothetical prote
131	5	33.3	286	2	B84807	probable RNA-bindi
132	5	33.3	287	2	T15779	hypothetical prote
133	5	33.3	291	2	G70605	hypothetical prote
134	5	33.3	292	2	T00996	En/Spm-like transp
135	5	33.3	295	2	A43663	host-inducible pro
136	5	33.3	295	2	AF0098	probable exported
137	5	33.3	297	2	T13317	hypothetical prote
138	5	33.3	299	2	F90741	hypothetical prote
139	5	33.3	299	2	A85592	hypothetical prote
140	5	33.3	299	2	AH0602	probable formate a
141	5	33.3	301	1	A54687	transcription fact
142	5	33.3	301	1	A48880	transcription fact
143	5	33.3	301	2	B84282	8-oxoguanine DNA g
144	5	33.3	302	2	T13457	hypothetical prote
145	5	33.3	302	2	F84329	hypothetical prote
146	5	33.3	302	2	S75481	polysialic acid tr
147	5	33.3	303	2	G64405	tetrahydromethanop
148	5	33.3	306	2	B70835	hypothetical prote
149	5	33.3	308	1	H64819	formate acetyltran
150	5	33.3	309	2	T41889	PE38 ori153 - Bomb
151	5	33.3	314	2	T26531	hypothetical prote
152	5	33.3	316	2	F87260	MeCB/TaqA/Cpsf fam
153	5	33.3	317	2	F82672	ATP sulfurylase, s
154	5	33.3	320	2	AB0330	phospholipase A [i
155	5	33.3	321	1	A43681	immediate-early pr
156	5	33.3	321	2	C72869	hypothetical prote
157	5	33.3	321	2	S55640	hypothetical prote
158	5	33.3	323	2	T13005	hypothetical prote
159	5	33.3	326	2	F96522	hypothetical prote
160	5	33.3	328	2	A84291	ornithine cyclodea
161	5	33.3	330	2	A40855	homeotic protein H
162	5	33.3	332	2	S44743	CO2D5.1 protein -
163	5	33.3	332	2	A70388	hydrogenase expres
164	5	33.3	332	2	I57032	gene Tlx-1 protein
165	5	33.3	332	2	AG0809	probable membrane
166	5	33.3	334	2	C22735	hypothetical nox2
167	5	33.3	334	2	A83342	conserved hypotet
168	5	33.3	335	2	B86429	F26G16.5 protein -
169	5	33.3	336	2	T44988	oxidoreductase [im
170	5	33.3	338	2	F83059	ketol-acid reducto
171	5	33.3	338	2	A83835	NADH oxidase BH148
172	5	33.3	338	2	C98842	hypothetical prote
173	5	33.3	338	2	A13043	oxidoreductase Atu
174	5	33.3	342	2	B85757	partial probable o
175	5	33.3	342	2	AB3116	transcription regu
176	5	33.3	346	2	C75139	bifunctional short
177	5	33.3	346	2	T47411	hypothetical prote
178	5	33.3	348	2	G85638	hypothetical prote
179	5	33.3	349	2	T24015	hypothetical prote
180	5	33.3	351	2	D96761	unknown protein [i
181	5	33.3	353	2	F83190	probable UDP-3-O-l
182	5	33.3	356	2	H70882	hypothetical prote
183	5	33.3	356	2	C98171	hypothetical prote
184	5	33.3	358	2	T38920	prostaglandin E2 r
185	5	33.3	358	2	S51312	EP2 prostaglandin
186	5	33.3	361	2	G87706	hypothetical prote
187	5	33.3	363	2	S33702	homeotic protein D
188	5	33.3	364	2	AD3557	acriflavin resista
189	5	33.3	365	2	A34424	CD44 membrane gly
190	5	33.3	366	2	S51363	actin modulator pr
191	5	33.3	368	2	G83180	probable FMN oxido
192	5	33.3	371	2	AB0407	probable zinc-bind
193	5	33.3	371	2	T27643	hypothetical prote
194	5	33.3	374	2	AD0719	probable bacteriop
195	5	33.3	375	2	T23705	hypothetical prote
196	5	33.3	377	2	S21302	succinate dehydrog
197	5	33.3	377	2	H71081	hypothetical prote
198	5	33.3	377	2	UC7535	chitinase (EC 3.2.
199	5	33.3	379	2	S46711	hypothetical prote
200	5	33.3	380	1	TVMSF	transforming prote
201	5	33.3	380	2	T04284	transforming prote
202	5	33.3	381	1	TVMW7	transforming prote
203	5	33.3	384	1	T22434	phosphoprotein pho
204	5	33.3	384	2	AF0636	glucans biosynthes
205	5	33.3	387	2	S65959	cytochrome-c perox
206	5	33.3	388	1	WMVZM1	major envelope ant
207	5	33.3	388	1	WMVZU2	major envelope ant
208	5	33.3	388	2	T30623	major envelope ant
209	5	33.3	388	2	G95375	probable drug resi
210	5	33.3	394	2	A53045	probable 3-hydroxy
211	5	33.3	398	1	S47520	vitamin D-3 25-hyd
212	5	33.3	399	2	F87356	hypothetical prote
213	5	33.3	401	2	T36661	probable DNA polym
214	5	33.3	403	2	B35401	cytochrome P450 10
215	5	33.3	403	2	B70961	probable esterase
216	5	33.3	403	2	T39697	DNAJ protein - fls
217	5	33.3	404	2	S75529	beta ketoacyl-acyl
218	5	33.3	404	2	C96640	hypothetical prote
219	5	33.3	405	4	A61181	homeotic protein H
220	5	33.3	411	2	C87586	metal ion efflux m
221	5	33.3	413	1	A34888	transcription fact
222	5	33.3	413	2	S41114	Gal beta 1,4 GlcNA
223	5	33.3	414	2	A12544	hypothetical prote
224	5	33.3	416	2	E82231	Nifs-related prote
225	5	33.3	417	2	T34561	hypothetical prote
226	5	33.3	418	2	T36358	hypothetical prote
227	5	33.3	422	2	T33562	hypothetical prote
228	5	33.3	425	1	JH0710	transcription fact
229	5	33.3	425	2	AF2246	phosphoribosylform
230	5	33.3	430	1	UYPVE1	nonstructural prot
231	5	33.3	430	2	T21060	hypothetical prote
232	5	33.3	434	2	S50865	avermectin-sensitl
233	5	33.3	435	2	A45231	helix-loop-helix p
234	5	33.3	437	2	T42653	hypothetical prote
235	5	33.3	438	2	A46259	recombination prot
236	5	33.3	439	2	T01050	hypothetical prote
237	5	33.3	439	2	E87638	omega-amino acid-p
238	5	33.3	439	2	F82997	two-component sens
239	5	33.3	442	2	T30157	hypothetical prote
240	5	33.3	442	2	T20788	hypothetical prote
241	5	33.3	445	2	B82954	probable dihydooor
242	5	33.3	447	2	T50705	gamma-aminobutyrat
243	5	33.3	448	2	B85077	hypothetical prote
244	5	33.3	451	2	T36217	plasmid transfer p
245	5	33.3	451	2	G69070	coenzyme F390 synt
246	5	33.3	454	2	T18765	hypothetical prote
247	5	33.3	457	2	S44269	platelet-derived g
248	5	33.3	457	2	A38567	GTP-binding protei

249	5	33.3	457	2	A99862	probable outer mem	322	5	33.3	596	2	JC4697	trehalose trehaloh
250	5	33.3	459	2	AC0075	probable membrane	323	5	33.3	599	2	S75048	aspartate-tRNA lig
251	5	33.3	459	2	T39473	probable geranylge	324	5	33.3	601	2	C89451	aspartate-tRNA lig
252	5	33.3	462	2	T11637	hypothetical prote	325	5	33.3	602	2	G81195	aspartyl-tRNA synt
253	5	33.3	464	2	C46157	hexokinase (EC 2.7	326	5	33.3	602	2	F81831	aspartate-tRNA lig
254	5	33.3	465	2	A46157	hexokinase (EC 2.7	327	5	33.3	604	2	T24456	hypothetical prote
255	5	33.3	465	2	A31810	hexokinase (EC 2.7	328	5	33.3	605	2	T43974	hypothetical prote
256	5	33.3	465	2	I49693	glucokinase (EC 2.	329	5	33.3	610	2	S76234	hypothetical prote
257	5	33.3	466	2	D46157	hexokinase (EC 2.7	330	5	33.3	610	2	S50539	hypothetical prote
258	5	33.3	467	2	D86672	efflux pump antidi	331	5	33.3	611	1	S12566	translation initia
259	5	33.3	468	2	C82722	UDP-N-acetylmuramo	332	5	33.3	611	1	S52229	hypothetical prote
260	5	33.3	471	1	SYECET	glutamate-tRNA lig	333	5	33.3	612	2	AC2396	threonyl-tRNA synt
261	5	33.3	471	1	F91038	glutamate-tRNA syn	334	5	33.3	613	2	T00077	gag-like protein -
262	5	33.3	471	2	H85882	glutamate tRNA syn	335	5	33.3	613	2	T21325	hypothetical prote
263	5	33.3	471	2	T46860	probable glutamate	336	5	33.3	613	2	T34011	hypothetical prote
264	5	33.3	471	2	B83127	probable secretion	337	5	33.3	617	2	T51708	methylytransferase
265	5	33.3	471	2	S46739	hypothetical prote	338	5	33.3	627	2	D84531	probable salt-indu
266	5	33.3	474	2	A10808	glutamate-tRNA lig	339	5	33.3	628	2	S01955	hypothetical prote
267	5	33.3	476	2	T43464	hypothetical prote	340	5	33.3	628	2	S19150	hypothetical prote
268	5	33.3	480	2	B64059	glutamate-tRNA lig	341	5	33.3	629	2	F84428	probable myosin he
269	5	33.3	483	2	T16443	hypothetical prote	342	5	33.3	629	2	T48940	hypothetical prote
270	5	33.3	484	1	SYRZET	glutamate-tRNA lig	343	5	33.3	630	1	F63073	hypothetical prote
271	5	33.3	484	1	T36427	probable rhamnose	344	5	33.3	632	2	B69310	hypothetical prote
272	5	33.3	484	2	T50909	hypothetical prote	345	5	33.3	634	2	T49415	hypothetical prote
273	5	33.3	484	2	D84725	probable acetylact	346	5	33.3	638	2	S67605	hypothetical prote
274	5	33.3	497	2	T51195	hypothetical prote	347	5	33.3	638	2	JC7753	ring finger B-box
275	5	33.3	498	1	A56564	transcription fact	348	5	33.3	641	2	A45054	probable intercell
276	5	33.3	502	2	T02306	probable protein k	349	5	33.3	644	2	T10403	p74 protein - Orgy
277	5	33.3	505	2	S15194	sucrose porin scry	350	5	33.3	645	2	H96011	asparagine synthas
278	5	33.3	506	2	E82721	lysyl-tRNA synthet	351	5	33.3	647	2	C69102	DNA mismatch recog
279	5	33.3	508	2	T41623	probable protein k	352	5	33.3	651	2	B41288	vascular cell adhe
280	5	33.3	508	2	A70125	UDP-N-acetylmuramo	353	5	33.3	651	2	D86977	probable primosoma
281	5	33.3	508	2	AD0076	probable membrane	354	5	33.3	658	2	C81860	DNA mismatch repai
282	5	33.3	509	2	S74935	hypothetical prote	355	5	33.3	662	2	B81084	mismatch repair pr
283	5	33.3	512	2	H84320	phycoene dehydroge	356	5	33.3	668	2	G87630	methylnalonyl-CoA
284	5	33.3	513	2	T38044	hypothetical prote	357	5	33.3	668	2	T13744	hypothetical prote
285	5	33.3	515	2	S67290	probable membrane	358	5	33.3	668	2	JC2363	protein kinase (EC
286	5	33.3	515	2	T43152	hypothetical prote	359	5	33.3	669	2	F84377	mismatch repair pr
287	5	33.3	516	2	S28060	serum response fac	360	5	33.3	671	2	D86479	annexin VI [valida
288	5	33.3	517	2	B87644	4-coumarate-CoA li	361	5	33.3	673	1	AQH068	annexin VI - rat
289	5	33.3	521	2	T06606	hypothetical prote	362	5	33.3	673	1	S01786	annexin VI - mouse
290	5	33.3	530	2	A84922	hypothetical prote	363	5	33.3	673	1	S52844	annexin VI - rat
291	5	33.3	539	2	T30327	hsdm protein - Kie	364	5	33.3	673	2	F87636	TPR domain protein
292	5	33.3	543	2	B34612	zinc finger protei	365	5	33.3	680	2	A43800	nuclear autoantige
293	5	33.3	544	2	Aei563	pyruvate dehydroge	366	5	33.3	681	2	JX0338	radphillin-3A - mou
294	5	33.3	546	2	AP1206	pyruvate dehydroge	367	5	33.3	684	2	I58166	radphillin-3A - rat
295	5	33.3	546	2	T24679	hypothetical prote	368	5	33.3	685	2	S46365	nuclear protein NO
296	5	33.3	547	2	T36550	hypothetical prote	369	5	33.3	694	2	C72761	hypothetical prote
297	5	33.3	548	1	S70146	mercury(II) reduct	370	5	33.3	696	2	T46394	hypothetical prote
298	5	33.3	549	2	D95979	probable amino aci	371	5	33.3	700	2	S57415	Hsp83 protein - Le
299	5	33.3	550	2	T19257	hypothetical prote	372	5	33.3	701	2	F84912	hypothetical prote
300	5	33.3	552	2	S50313	iron transport pro	373	5	33.3	704	2	T24517	hypothetical prote
301	5	33.3	559	2	F86479	hypothetical prote	374	5	33.3	706	2	S57374	probable DNA helic
302	5	33.3	560	2	JC2494	nuclear receptor R	375	5	33.3	721	2	T45495	probable beta-gala
303	5	33.3	560	2	C71155	hypothetical prote	376	5	33.3	722	2	T02421	gene CARSR12 prote
304	5	33.3	562	1	HMIW2	hemagglutinin prec	377	5	33.3	722	2	S27043	probable beta-gala
305	5	33.3	562	2	S38149	SIS2 protein - yea	378	5	33.3	727	2	I56506	hypothetical prote
306	5	33.3	563	2	T02720	beta-D-glucosidase	379	5	33.3	727	2	T47541	hypothetical prote
307	5	33.3	566	2	T45626	hypothetical prote	380	5	33.3	727	2	T25362	probable ABC trans
308	5	33.3	567	2	C84425	similar to axl 1 p	381	5	33.3	729	2	T04269	probable beta-gala
309	5	33.3	567	2	T15574	hypothetical prote	382	5	33.3	731	2	S16595	gene CARSR12 prote
310	5	33.3	568	2	C72129	probable outer mem	383	5	33.3	731	2	T17002	probable beta-gala
311	5	33.3	568	2	G86493	probable leader pe	384	5	33.3	732	2	T25937	hypothetical prote
312	5	33.3	569	2	T17779	hypothetical prote	385	5	33.3	736	2	A99279	hypothetical prote
313	5	33.3	570	2	T27407	hypothetical prote	386	5	33.3	736	2	T40080	probable ABC trans
314	5	33.3	570	2	H97244	membrane associate	387	5	33.3	736	2	T40510	beta transducin -
315	5	33.3	579	2	F72252	aspartate-tRNA lig	388	5	33.3	741	2	A41288	vascular cell adhe
316	5	33.3	579	2	T34331	zinc finger protei	389	5	33.3	741	2	B54908	phospholipase A2 c
317	5	33.3	586	1	S47452	probable serine/th	390	5	33.3	741	2	A26572	bsg25D protein A2 c
318	5	33.3	589	1	S42047	aspartate-tRNA lig	391	5	33.3	751	2	S38101	hypothetical prote
319	5	33.3	593	1	T37295	GTP-binding protei	392	5	33.3	753	2	C97510	hypothetical prote
320	5	33.3	595	2	AE2110	aspartate-tRNA lig	393	5	33.3	753	2	AB2729	succinylglycan bios
321	5	33.3	596	2	C70724	aspartate-tRNA lig	394	5	33.3	754	2	AH3004	vgrc protein [limpo

395	5	33.3	755	2	T48553	468	5	33.3	1061	2	D69799	cytochrome P450 /
396	5	33.3	756	2	G84866	469	5	33.3	1067	2	AC1439	B. subtilis yueB p
397	5	33.3	758	2	F75590	470	5	33.3	1071	2	D86279	hypothetical prote
398	5	33.3	760	2	T01383	471	5	33.3	1075	2	T07448	probable DNA-direc
399	5	33.3	765	2	AD0778	472	5	33.3	1088	1	PFRUGA	platelet-derived g
400	5	33.3	765	2	C64981	473	5	33.3	1089	1	PFRUGA	platelet-derived g
401	5	33.3	765	2	C91006	474	5	33.3	1089	1	S33727	platelet-derived g
402	5	33.3	765	2	D85850	475	5	33.3	1101	2	T33153	hypothetical prote
403	5	33.3	765	2	T35719	476	5	33.3	1104	2	S59310	probable membrane
404	5	33.3	784	2	T26585	477	5	33.3	1112	2	S46313	phytochrome E - Ar
405	5	33.3	786	2	T39585	478	5	33.3	1114	2	T14351	serine/threonine-s
406	5	33.3	787	1	JDVLM2	479	5	33.3	1121	2	I38127	phosphoprotein pho
407	5	33.3	788	1	JDVLM2	480	5	33.3	1121	2	T02764	myosin-I binding p
408	5	33.3	790	2	G02678	481	5	33.3	1127	2	T25804	hypothetical prote
409	5	33.3	792	2	G86564	482	5	33.3	1134	1	JN0711	protein-tyrosine k
410	5	33.3	792	2	D81608	483	5	33.3	1135	2	J02163	hypothetical 126.5
411	5	33.3	792	2	H72058	484	5	33.3	1138	1	S24066	protein-tyrosine k
412	5	33.3	799	2	T02456	485	5	33.3	1139	1	H64089	DNA-directed DNA p
413	5	33.3	808	2	S73947	486	5	33.3	1160	1	DJEC3A	DNA-directed DNA p
414	5	33.3	810	2	T33323	487	5	33.3	1160	1	A45915	DNA-directed DNA p
415	5	33.3	813	2	T02672	488	5	33.3	1160	2	B90652	DNA polymerase III
416	5	33.3	814	1	T39627	489	5	33.3	1160	2	B85503	DNA polymerase III
417	5	33.3	815	2	T57487	490	5	33.3	1160	2	A10530	DNA polymerase III
418	5	33.3	816	2	B96196	491	5	33.3	1164	2	G82100	DNA polymerase III
419	5	33.3	816	2	S16328	492	5	33.3	1171	2	AB0130	DNA-directed DNA p
420	5	33.3	816	2	AH3090	493	5	33.3	1173	2	I50620	nuclear envelope p
421	5	33.3	817	2	T25758	494	5	33.3	1199	2	A40670	prockr2 - chicken
422	5	33.3	824	2	T20477	495	5	33.3	1226	2	S15053	3c3.20c protein -
423	5	33.3	831	2	T05771	496	5	33.3	1321	2	T10929	dextranase - Strept
424	5	33.3	832	2	E84543	497	5	33.3	1337	2	T30291	LamDR1 protein - L
425	5	33.3	832	2	S41889	498	5	33.3	1341	2	JG0166	hypothetical prote
426	5	33.3	833	2	T24682	499	5	33.3	1341	2	T17285	hypothetical prote
427	5	33.3	835	2	T06590	500	5	33.3	1345	2	T00964	protein-tyrosine k
428	5	33.3	838	2	T40203	501	5	33.3	1404	1	A48196	hypothetical prote
429	5	33.3	839	2	C84685	502	5	33.3	1411	2	T18417	DNA polymerase III
430	5	33.3	842	2	H86220	503	5	33.3	1415	2	S52267	hypothetical prote
431	5	33.3	845	2	I48176	504	5	33.3	1417	2	T18418	DNA polymerase III
432	5	33.3	858	2	A46613	505	5	33.3	1438	2	C89900	DNA polymerase III
433	5	33.3	864	2	H85335	506	5	33.3	1474	2	B85188	retrotransposon II
434	5	33.3	864	2	T04518	507	5	33.3	1493	2	A38218	GAP-associated pro
435	5	33.3	875	2	AE1270	508	5	33.3	1499	2	B59431	Rho GTPase activat
436	5	33.3	875	2	AC1632	509	5	33.3	1501	2	T42274	p190-B protein - m
437	5	33.3	877	2	S49783	510	5	33.3	1535	2	T43902	hypothetical prote
438	5	33.3	880	2	S60137	511	5	33.3	1685	2	T43217	RNA polymerase (EC
439	5	33.3	886	2	C87031	512	5	33.3	1729	2	A49282	fusion protein Ia/
440	5	33.3	888	2	A55318	513	5	33.3	1751	2	G71518	hypothetical prote
441	5	33.3	888	2	JC5399	514	5	33.3	1771	2	S76851	hypothetical prote
442	5	33.3	913	2	T15278	515	5	33.3	1795	2	F97713	190K antigen precu
443	5	33.3	922	2	AC1827	516	5	33.3	1926	2	S01169	beta-glycosidase c
444	5	33.3	924	2	T09220	517	5	33.3	1994	2	D86452	protein F6N18.13 l
445	5	33.3	928	2	T10164	518	5	33.3	2088	2	E71436	hypothetical prote
446	5	33.3	931	2	D86222	519	5	33.3	2240	2	T37057	probable multi-dom
447	5	33.3	938	2	H83050	520	5	33.3	2288	2	T30568	acetyl-CoA carboxy
448	5	33.3	940	1	BVECUA	521	5	33.3	2332	1	GNNYF	genome polypotein
449	5	33.3	940	2	H91258	522	5	33.3	2332	1	GNNY4F	genome polypotein
450	5	33.3	940	2	D86099	523	5	33.3	2333	1	GNNY2F	genome polypotein
451	5	33.3	955	2	A47334	524	5	33.3	2336	2	S37077	genome polypotein
452	5	33.3	956	2	H81654	525	5	33.3	2342	2	T13412	hypothetical prote
453	5	33.3	957	2	T10633	526	5	33.3	2499	1	A30788	mannose 6-phosphat
454	5	33.3	965	2	S62935	527	5	33.3	2554	1	TVFF7L	kinase-related pro
455	5	33.3	968	2	T00353	528	5	33.3	2783	2	T34416	hypothetical prote
456	5	33.3	980	2	E72035	529	5	33.3	2793	2	B90784	hypothetical prote
457	5	33.3	980	2	E86589	530	5	33.3	2806	2	D85644	hypothetical prote
458	5	33.3	1003	2	T26746	531	5	33.3	3450	2	T26963	hypothetical prote
459	5	33.3	1008	2	T12532	532	5	33.3	3461	2	T26964	lysosomal traffick
460	5	33.3	1008	2	AE2304	533	5	33.3	3796	2	T18514	hypothetical prote
461	5	33.3	1021	2	A86421	534	5	33.3	3890	2	C89921	hypothetical prote
462	5	33.3	1021	2	T10748	535	5	33.3	4307	2	T20721	BIR repeat contain
463	5	33.3	1026	2	C71490	536	5	33.3	4845	10	T31067	Ig heavy chain CRD
464	5	33.3	1036	2	S55984	537	4	26.7	13	2	PT0309	T-cell antigen rec
465	5	33.3	1038	2	S06046	538	4	26.7	13	2	S47388	histone H2B - mous
466	5	33.3	1045	2	F90365	539	4	26.7	18	2	B27504	6-phosphofructo-2-
467	5	33.3	1054	2	D96519	540	4	26.7	20	2	I46940	

541	4	26.7	20	2	T44453	614	4	26.7	69	2	D70734	hypothetical prote
542	4	26.7	20	2	S78759	615	4	26.7	69	2	S41000	hypothetical prote
543	4	26.7	23	4	H0515	616	4	26.7	70	2	S42895	env polyprotein -
544	4	26.7	26	4	I59183	617	4	26.7	70	2	JU0103	hypothetical 8.5K
545	4	26.7	27	2	A49236	618	4	26.7	70	2	B46522	T-cell receptor et
546	4	26.7	27	2	I50161	619	4	26.7	70	2	C46522	T cell receptor et
547	4	26.7	29	2	S17147	620	4	26.7	71	1	H70587	probable mbh prot
548	4	26.7	29	2	S77569	621	4	26.7	71	2	S42909	envelope glycoprot
549	4	26.7	33	2	A60601	622	4	26.7	71	2	S42906	env polyprotein -
550	4	26.7	35	2	PC3291	623	4	26.7	71	2	S42908	env polyprotein -
551	4	26.7	37	2	G49050	624	4	26.7	71	2	S42910	env polyprotein -
552	4	26.7	38	2	E82424	625	4	26.7	71	2	S42911	env polyprotein -
553	4	26.7	38	2	B31194	626	4	26.7	71	2	S42912	env polyprotein -
554	4	26.7	39	2	B36207	627	4	26.7	71	2	S42916	env polyprotein -
555	4	26.7	39	2	S09645	628	4	26.7	71	2	S42917	env polyprotein -
556	4	26.7	41	2	G86110	629	4	26.7	71	2	S42918	env polyprotein -
557	4	26.7	42	2	T01609	630	4	26.7	71	2	S42897	env polyprotein -
558	4	26.7	44	2	S29785	631	4	26.7	71	2	S42901	env polyprotein -
559	4	26.7	44	2	AB1046	632	4	26.7	71	2	S42903	env polyprotein -
560	4	26.7	45	2	T37124	633	4	26.7	71	2	S42904	env polyprotein -
561	4	26.7	48	2	S62189	634	4	26.7	71	2	S42905	env polyprotein -
562	4	26.7	49	2	B56448	635	4	26.7	71	2	T38721	env polyprotein -
563	4	26.7	51	2	T08488	636	4	26.7	71	2	E82610	env polyprotein -
564	4	26.7	51	2	T29481	637	4	26.7	72	2	P70166	HLA-DRB sigma anti
565	4	26.7	53	2	H82784	638	4	26.7	72	2	T30373	hypothetical prote
566	4	26.7	54	2	I46202	639	4	26.7	72	2	G33172	C-ORF-B protein -
567	4	26.7	54	2	T35239	640	4	26.7	72	2	A42856	EPF autoantibody-r
568	4	26.7	56	2	A82565	641	4	26.7	72	2	B64299	probable archaeal
569	4	26.7	57	2	D49056	642	4	26.7	72	2	I79659	DRB1 transplanta
570	4	26.7	57	2	B95384	643	4	26.7	73	2	D90864	phage shock protei
571	4	26.7	58	2	A56448	644	4	26.7	73	2	E85754	phage shock protei
572	4	26.7	58	2	T08023	645	4	26.7	73	2	S17124	phage shock protei
573	4	26.7	58	2	AC1517	646	4	26.7	73	2	T05930	probable ribosomal
574	4	26.7	58	2	AP1158	647	4	26.7	74	2	T17549	hypothetical prote
575	4	26.7	59	2	T03588	648	4	26.7	74	2	H86993	hypothetical prote
576	4	26.7	59	2	S21332	649	4	26.7	75	2	AD3131	hypothetical prote
577	4	26.7	59	2	T37115	650	4	26.7	75	2	C33532	hypothetical prote
578	4	26.7	60	2	I55550	651	4	26.7	76	2	S35840	mucin SMUC-42 - hu
579	4	26.7	60	2	C71245	652	4	26.7	77	2	S35806	envelope protein -
580	4	26.7	60	2	E82516	653	4	26.7	77	2	S35841	envelope protein -
581	4	26.7	60	2	AC2981	654	4	26.7	77	2	S35804	envelope protein -
582	4	26.7	60	2	AE2514	655	4	26.7	77	2	S48322	SNP2 protein - yea
583	4	26.7	61	2	A36916	656	4	26.7	77	2	T29087	hypothetical prote
584	4	26.7	61	2	S18336	657	4	26.7	78	2	T30471	hypothetical prote
585	4	26.7	63	2	F82806	658	4	26.7	78	2	T17891	hypothetical prote
586	4	26.7	63	2	H82788	659	4	26.7	78	2	A56194	chromoxane A-2 re
587	4	26.7	63	2	AG3289	660	4	26.7	79	2	B87276	conserved hypotet
588	4	26.7	64	2	JX0060	661	4	26.7	79	2	G83089	hypothetical prote
589	4	26.7	64	2	S11950	662	4	26.7	79	2	T24150	hypothetical prote
590	4	26.7	64	2	T42161	663	4	26.7	80	2	T29855	hypothetical prote
591	4	26.7	64	2	PN0648	664	4	26.7	80	2	F82602	conserved hypotet
592	4	26.7	65	2	C87262	665	4	26.7	80	2	D43670	hypothetical prote
593	4	26.7	65	2	T17896	666	4	26.7	81	2	AD1825	hypothetical prote
594	4	26.7	65	2	S75236	667	4	26.7	81	2	AD2080	hypothetical prote
595	4	26.7	65	2	JN0802	668	4	26.7	82	2	S37112	class II histocomp
596	4	26.7	65	2	AD3359	669	4	26.7	82	2	T34039	hypothetical prote
597	4	26.7	66	2	T36517	670	4	26.7	82	2	E71321	hypothetical prote
598	4	26.7	66	2	D72580	671	4	26.7	83	2	H86911	hypothetical prote
599	4	26.7	66	2	AE1385	672	4	26.7	83	2	S15142	hypothetical prote
600	4	26.7	66	2	AG1760	673	4	26.7	83	2	B83556	hypothetical prote
601	4	26.7	67	2	T10832	674	4	26.7	83	2	AI0032	probable type III
602	4	26.7	67	2	T16372	675	4	26.7	83	2	AC3940	hypothetical prote
603	4	26.7	67	2	E96004	676	4	26.7	84	1	WMBPMB	gene P protein - p
604	4	26.7	67	2	H95418	677	4	26.7	84	2	B95079	hypothetical prote
605	4	26.7	67	2	A64321	678	4	26.7	84	2	F81128	probable lipoprote
606	4	26.7	67	2	D64416	679	4	26.7	84	2	G97946	hypothetical prote
607	4	26.7	67	2	D64513	680	4	26.7	85	2	E64855	ycfr protein precu
608	4	26.7	68	2	JH0100	681	4	26.7	85	2	F85674	hypothetical prote
609	4	26.7	68	2	B96942	682	4	26.7	85	2	B90815	hypothetical prote
610	4	26.7	68	2	AI1316	683	4	26.7	85	2	A69985	hypothetical prote
611	4	26.7	69	2	H83236	684	4	26.7	85	2	G86484	10.0K hypothetical
612	4	26.7	69	2	F83588	685	4	26.7	86	2	T42180	hypothetical prote
613	4	26.7	69	2	JQ1703	686	4	26.7	86	2		

687	4	26.7	86	2	A57292	signal recognition
688	4	26.7	86	2	A34731	signal recognition
689	4	26.7	86	2	S57500	signal recognition
690	4	26.7	87	2	E82736	conserved hypotet
691	4	26.7	87	2	H84234	hypothetical prote
692	4	26.7	87	2	T30424	hypothetical prote
693	4	26.7	87	2	B97749	hypothetical prote
694	4	26.7	88	2	C84912	hypothetical prote
695	4	26.7	88	2	A84342	hypothetical prote
696	4	26.7	88	2	E97543	hypothetical prote
697	4	26.7	88	2	AE7262	conserved hypotet
698	4	26.7	88	1	C36869	probable export pr
699	4	26.7	89	2	S35277	probable export pr
700	4	26.7	89	2	S78699	probable export pr
701	4	26.7	89	2	AE0753	flagellar biosynth
702	4	26.7	89	2	A10221	flagellar biosynth
703	4	26.7	89	2	H09064	probable export pr
704	4	26.7	89	2	D87338	hypothetical prote
705	4	26.7	89	2	H85812	flagellar biosynth
706	4	26.7	89	2	F97821	hypothetical prote
707	4	26.7	89	2	H86418	hypothetical prote
708	4	26.7	90	2	H82611	DNA-binding protei
709	4	26.7	91	2	J00903	bombayin B-1 homol
710	4	26.7	91	2	J00905	bombayin B-2 homol
711	4	26.7	91	2	I54248	apolipoprotein A-I
712	4	26.7	91	2	S02769	gag 75K protein pr
713	4	26.7	92	2	F83439	hypothetical prote
714	4	26.7	92	2	G69383	hypothetical prote
715	4	26.7	93	2	D48059	oncoprotein ZN-MYC
716	4	26.7	93	2	A13390	acyl carrier prote
717	4	26.7	94	2	S13265	heme oxygenase (de
718	4	26.7	94	2	C95249	PTS system, IIB co
719	4	26.7	94	2	F84497	En/Spm-like transp
720	4	26.7	94	2	T49851	hypothetical prote
721	4	26.7	94	2	H98113	hypothetical prote
722	4	26.7	94	2	AD2773	acgl carrier prote
723	4	26.7	95	2	A46422	calcium channel al
724	4	26.7	95	2	A70618	hypothetical prote
725	4	26.7	95	2	F84046	hypothetical prote
726	4	26.7	95	2	A97468	hypothetical prote
727	4	26.7	95	2	AD2686	hypothetical prote
728	4	26.7	96	2	T13540	hypothetical prote
729	4	26.7	97	2	AE2005	30S ribosomal prot
730	4	26.7	97	2	H84901	hypothetical prote
731	4	26.7	97	2	S43678	csamM protein - Chl
732	4	26.7	97	2	T28909	hypothetical prote
733	4	26.7	97	2	D64850	transcription fact
734	4	26.7	98	1	FERMX	ferredoxin [4Fe-4S
735	4	26.7	98	1	JC1001	ferredoxin [4Fe-4S
736	4	26.7	98	2	D95317	Flxx ferredoxin-11
737	4	26.7	98	2	I49562	alpha-1 type IIT c
738	4	26.7	98	2	E64763	probable alpha hel
739	4	26.7	98	2	D90680	hypothetical prote
740	4	26.7	98	2	E84589	hypothetical prote
741	4	26.7	98	2	A81902	hypothetical prote
742	4	26.7	98	2	B81120	hypothetical prote
743	4	26.7	98	2	S78727	protein YUL018c-a
744	4	26.7	98	2	H85530	probable alpha hel
745	4	26.7	99	1	WPBP2	repressor protein
746	4	26.7	99	2	S34301	galatinin - mouse
747	4	26.7	99	2	C83116	50S ribosomal prot
748	4	26.7	99	2	S22957	hypothetical prote
749	4	26.7	99	2	B82720	hypothetical prote
750	4	26.7	100	2	A82333	primosomal replica
751	4	26.7	100	2	H70586	hypothetical prote
752	4	26.7	100	2	E36905	ribosomal protein
753	4	26.7	100	2	B72664	hypothetical prote
754	4	26.7	100	2	AF2335	hypothetical prote
755	4	26.7	101	2	A43262	hypothetical prote
756	4	26.7	101	2	S11936	saif protein - Stre
757	4	26.7	101	2	C90564	lipoprotein [impor
758	4	26.7	101	2	A72742	hypothetical prote
759	4	26.7	102	2	S15454	cytochrome c - Eug
760	4	26.7	102	2	C81682	conserved hypotet
761	4	26.7	102	2	C96034	conserved hypotet
762	4	26.7	102	2	A87422	hypothetical prote
763	4	26.7	102	2	B87669	hypothetical prote
764	4	26.7	102	2	G97493	hypothetical prote
765	4	26.7	102	2	A12711	hypothetical prote
766	4	26.7	103	2	A41403	hypothetical prote
767	4	26.7	103	2	S04101	aldosterone secret
768	4	26.7	103	2	T08501	hemolysin A - prot
769	4	26.7	103	2	D49852	trbd protein - Ent
770	4	26.7	103	2	F70976	hypothetical prote
771	4	26.7	103	2	F72630	hypothetical prote
772	4	26.7	103	2	A97484	hypothetical prote
773	4	26.7	103	2	A12701	hypothetical prote
774	4	26.7	103	2	S70182	hypothetical prote
775	4	26.7	103	2	S72973	hypothetical prote
776	4	26.7	104	1	JC4694	proteic killer act
777	4	26.7	104	2	S32368	NNO-12.3 protein -
778	4	26.7	104	2	E95299	hypothetical prote
779	4	26.7	104	2	C98209	hypothetical prote
780	4	26.7	104	2	AE3077	conserved hypotet
781	4	26.7	104	2	H91204	hypothetical prote
782	4	26.7	104	2	T09471	hypothetical prote
783	4	26.7	105	2	S46311	ferredoxin -nitrile
784	4	26.7	105	2	AE0581	conserved hypotet
785	4	26.7	105	2	B75392	hypothetical prote
786	4	26.7	105	2	C87324	hypothetical prote
787	4	26.7	105	2	S77115	hypothetical prote
788	4	26.7	105	2	AC0430	primosomal replica
789	4	26.7	106	2	A85078	probable DNA-direc
790	4	26.7	106	2	C86142	hypothetical prote
791	4	26.7	106	2	E75371	hypothetical prote
792	4	26.7	106	2	E70897	hypothetical prote
793	4	26.7	106	2	G84541	hypothetical prote
794	4	26.7	106	2	B64350	hypothetical prote
795	4	26.7	107	2	AH2877	hypothetical prote
796	4	26.7	107	2	D70626	hypothetical prote
797	4	26.7	107	2	A72701	hypothetical prote
798	4	26.7	108	2	C83205	conserved hypotet
799	4	26.7	108	2	C72587	hypothetical prote
800	4	26.7	108	2	C83528	hypothetical prote
801	4	26.7	108	2	T27503	hypothetical prote
802	4	26.7	109	1	CABO	hypothetical prote
803	4	26.7	109	2	JC2440	biphenyl dioxygena
804	4	26.7	109	2	T32588	cytochrome-c oxida
805	4	26.7	109	2	F72743	probable Arpase in
806	4	26.7	109	2	T13121	hypothetical prote
807	4	26.7	109	2	E70956	protein gp35 - pha
808	4	26.7	109	2	D75538	hypothetical prote
809	4	26.7	109	2	F72684	conserved hypotet
810	4	26.7	109	2	D72604	hypothetical prote
811	4	26.7	109	2	A87425	hypothetical prote
812	4	26.7	110	2	S60591	tg light chain var
813	4	26.7	110	2	S55879	ribosomal protein
814	4	26.7	110	2	S55877	ribosomal protein
815	4	26.7	110	2	JN0329	ethidium efflux pr
816	4	26.7	110	2	F90830	integral membrane
817	4	26.7	110	2	C85688	hypothetical prote
818	4	26.7	110	2	C71134	hypothetical prote
819	4	26.7	110	2	T47180	hypothetical prote
820	4	26.7	111	2	JC1110	ferredoxin [2Fe-2S
821	4	26.7	111	2	AC0352	adrenodoxin family
822	4	26.7	111	2	A10823	ferredoxin [import
823	4	26.7	111	2	C85897	[2FE-2S] ferredoxi
824	4	26.7	111	2	G91052	[2FE-2S] ferredoxi
825	4	26.7	111	2	G72745	hypothetical prote
826	4	26.7	112	2	S34818	nifW protein - Rho
827	4	26.7	112	2	A84369	hypothetical prote
828	4	26.7	112	2	C98126	conserved hypotet
829	4	26.7	113	2	T44286	ferredoxin [2Fe-2S
830	4	26.7	113	2	P00275	polyprotein - hepa
831	4	26.7	113	2	P00276	polyprotein - hepa
832	4	26.7	113	2	F97624	csaa protein [limpo

833	4	26.7	113	2	AG2847	secretion chaperon
834	4	26.7	113	2	S66709	probable membrane
835	4	26.7	113	2	AG0396	hypothetical prote
836	4	26.7	113	2	H72528	hypothetical prote
837	4	26.7	113	2	T15547	hypothetical prote
838	4	26.7	113	2	A10723	conserved hypotet
839	4	26.7	113	2	I40399	flagellar protein
840	4	26.7	113	2	S23653	sensorin A - Calif
841	4	26.7	113	2	T12933	hypothetical prote
842	4	26.7	113	2	H71182	hypothetical prote
843	4	26.7	114	1	R1D1S1	somatostatin-14 pr
844	4	26.7	114	1	GM6ECP	cholecystokinin pr
845	4	26.7	114	1	R5HS2H	ribosomal protein
846	4	26.7	114	2	I50798	preprosomatostatin
847	4	26.7	114	2	F84266	50S ribosomal prot
848	4	26.7	114	2	A55010	neutrophil-activat
849	4	26.7	114	2	S09220	capsid protein - d
850	4	26.7	114	2	B75117	hypothetical prote
851	4	26.7	114	2	T17929	hypothetical prote
852	4	26.7	114	2	C75555	hypothetical prote
853	4	26.7	114	2	B98062	hypothetical prote
854	4	26.7	114	2	T50948	hypothetical prote
855	4	26.7	115	1	GMH0CP	cholecystokinin pr
856	4	26.7	115	2	I51064	somatostatin II pr
857	4	26.7	115	2	A48318	cholecystokinin pr
858	4	26.7	115	2	B75567	hypothetical prote
859	4	26.7	115	2	E90443	hypothetical prote
860	4	26.7	115	2	T14461	non intermediate f
861	4	26.7	115	2	T50477	hypothetical prote
862	4	26.7	115	2	T33703	hypothetical prote
863	4	26.7	115	2	G72493	hypothetical prote
864	4	26.7	116	2	S78094	endocuticular prot
865	4	26.7	116	2	PC4092	alanine carrier pr
866	4	26.7	116	2	F81796	hypothetical inner
867	4	26.7	116	2	D95280	hypothetical prote
868	4	26.7	116	2	D95385	protein [imported
869	4	26.7	116	2	D72560	hypothetical prote
870	4	26.7	117	1	ERAD01	early E3 13K glyco
871	4	26.7	117	2	E83526	probable arsenate
872	4	26.7	117	2	C81247	arsenate reductase
873	4	26.7	117	2	S73025	hypothetical prote
874	4	26.7	117	2	C59092	hypothetical prote
875	4	26.7	117	2	F72536	hypothetical prote
876	4	26.7	117	2	T49497	hypothetical prote
877	4	26.7	117	2	B83187	hypothetical prote
878	4	26.7	117	2	B86862	hypothetical prote
879	4	26.7	117	2	C72582	hypothetical prote
880	4	26.7	118	1	PSSMK3	phospholipase A2 (
881	4	26.7	118	2	H34860	C-type natriuretic
882	4	26.7	118	2	A75108	hypothetical prote
883	4	26.7	118	2	A75108	hypothetical prote
884	4	26.7	118	2	C84859	hypothetical prote
885	4	26.7	118	2	B86593	hypothetical prote
886	4	26.7	118	2	G95856	hypothetical prote
887	4	26.7	118	2	D72609	hypothetical prote
888	4	26.7	118	2	H72644	probable arabinoga
889	4	26.7	119	2	AH1817	single-stranded DN
890	4	26.7	119	2	T35859	hypothetical prote
891	4	26.7	119	2	S74932	hypothetical prote
892	4	26.7	119	2	F49804	hypothetical prote
893	4	26.7	119	2	A72651	hypothetical prote
894	4	26.7	119	2	J01327	anther-specific pr
895	4	26.7	119	2	E64940	hypothetical prote
896	4	26.7	119	2	B90942	hypothetical prote
897	4	26.7	119	2	F85790	hypothetical prote
898	4	26.7	119	2	S14292	transcription acti
899	4	26.7	120	2	AC0714	conserved hypotet
900	4	26.7	120	2	T02586	hypothetical prote
901	4	26.7	120	2	F81882	hypothetical prote
902	4	26.7	120	2	G86402	hypothetical prote
903	4	26.7	121	1	C69190	conserved hypotet
904	4	26.7	121	2	AB2314	ferredoxin-thiore
905	4	26.7	121	2	JC1138	xylokinase (EC 2
906	4	26.7	121	2	G71566	probable l19 ribos
907	4	26.7	121	2	G72768	hypothetical prote
908	4	26.7	121	2	B70767	hypothetical prote
909	4	26.7	121	2	S58088	sex-determining pr
910	4	26.7	121	2	S43481	matutase homolog -
911	4	26.7	121	2	G83684	hypothetical prote
912	4	26.7	122	1	SXAD9T	hexon-associated p
913	4	26.7	122	2	T14821	aldehyde dehydrog
914	4	26.7	122	2	B72637	hypothetical prote
915	4	26.7	122	2	H72279	conserved hypotet
916	4	26.7	123	1	RHHUN	galanin precursor
917	4	26.7	123	1	RHHOG	galanin precursor
918	4	26.7	123	1	RHPGN	galanin precursor
919	4	26.7	123	2	C61545	plasmin (EC 3.4.21
920	4	26.7	123	2	T43824	hypothetical prote
921	4	26.7	123	2	D84322	hypothetical prote
922	4	26.7	123	2	T20354	hypothetical prote
923	4	26.7	123	2	G75336	hypothetical prote
924	4	26.7	123	2	C71423	hypothetical prote
925	4	26.7	123	2	B87355	hypothetical prote
926	4	26.7	123	2	AH2525	hypothetical prote
927	4	26.7	123	2	C90432	conserved hypotet
928	4	26.7	123	2	D87238	hypothetical prote
929	4	26.7	123	2	G84592	hypothetical prote
930	4	26.7	123	2	G70969	hypothetical prote
931	4	26.7	123	2	C69282	conserved hypotet
932	4	26.7	123	2	T20279	hypothetical prote
933	4	26.7	124	1	RHRN	galanin precursor
934	4	26.7	124	2	JC5480	galanin precursor
935	4	26.7	124	2	A60218	galanin precursor
936	4	26.7	124	2	B83335	14k brain-specific
937	4	26.7	124	2	A70861	conserved hypotet
938	4	26.7	124	2	A72629	hypothetical prote
939	4	26.7	125	2	G47021	hypothetical prote
940	4	26.7	125	2	C32880	peptic enzyme secr
941	4	26.7	125	2	T36939	puls protein precu
942	4	26.7	125	2	T16848	hypothetical prote
943	4	26.7	125	2	F82974	hypothetical prote
944	4	26.7	125	2	B86051	hypothetical prote
945	4	26.7	125	2	C87560	hypothetical prote
946	4	26.7	125	2	E90350	hypothetical prote
947	4	26.7	125	2	E97414	hypothetical prote
948	4	26.7	125	2	G83555	hypothetical prote
949	4	26.7	126	1	AWHUC	natriuretic peptid
950	4	26.7	126	1	A36155	natriuretic peptid
951	4	26.7	126	1	H69178	conserved hypotet
952	4	26.7	126	2	S12988	brain natriuretic
953	4	26.7	126	2	A55688	natriuretic peptid
954	4	26.7	126	2	S29303	hypothetical prote
955	4	26.7	126	2	AF0356	holo-[acyl]-carrier
956	4	26.7	126	2	S65805	transcription acti
957	4	26.7	126	2	T03813	hypothetical prote
958	4	26.7	126	2	S64131	hypothetical prote
959	4	26.7	126	2	H72486	hypothetical prote
960	4	26.7	126	2	S74990	hypothetical prote
961	4	26.7	126	2	F89124	protein K07C11.10
962	4	26.7	126	2	AG2412	hypothetical prote
963	4	26.7	127	2	A70200	hypothetical prote
964	4	26.7	127	2	D54759	terminal oxidase (
965	4	26.7	127	2	T11004	MGCL36.12 protein
966	4	26.7	127	2	D75595	hypothetical prote
967	4	26.7	127	2	F69070	conserved hypotet
968	4	26.7	127	2	S53573	conserved hypotet
969	4	26.7	127	2	G82084	probable membrane
970	4	26.7	128	2	A33083	hypothetical prote
971	4	26.7	128	2	S33632	pancreatic ribonuc
972	4	26.7	128	2	B75531	l1r1 protein - ric
973	4	26.7	128	2	S53584	hypothetical prote
974	4	26.7	128	2	AE2364	probable membrane
975	4	26.7	128	2	F81310	hypothetical prote
976	4	26.7	129	2	F61187	alpha-7A integrin
977	4	26.7	129	2	S69862	hypothetical prote
978	4	26.7	129	2	T36732	hypothetical prote

979 4 26.7 129 2 T36916 hypothetical prote
980 4 26.7 129 2 T32313 hypothetical prote
981 4 26.7 129 2 H86673 single-strand bind
982 4 26.7 129 2 A72806 probable DNA prima
983 4 26.7 129 2 A72606 hypothetical prote
984 4 26.7 129 2 A97553 specialized acyl c
985 4 26.7 130 2 S30534 ig heavy chain V r
986 4 26.7 130 2 S31003 gene 58 protein -
987 4 26.7 130 2 H83150 hypothetical prote
988 4 26.7 130 2 T22920 hypothetical prote
989 4 26.7 130 2 T51879 hypothetical prote
990 4 26.7 130 2 E72697 hypothetical prote
991 4 26.7 130 2 A97549 hypothetical prote
992 4 26.7 130 2 AG2768 conserved hypotet
993 4 26.7 131 2 E25733 T-cell receptor al
994 4 26.7 131 2 B72557 probable ribosomal
995 4 26.7 131 2 T11557 tat protein - siml
996 4 26.7 131 2 S45059 AC1 protein (clone
997 4 26.7 131 2 AC0747 conserved hypotet
998 4 26.7 131 2 A69424 hypothetical prote
999 4 26.7 131 2 E70920 probable moab prot
1000 4 26.7 131 2 B75277 hypothetical prote

ALIGNMENTS

RESULT 1

S63683

C:Species: Homo sapiens (man)

C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999

C:Accession: S63683

R:Sahara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, T.; M

FEBS Lett. 381, 7-11, 1996

A>Title: Identification and characterization of presenilin 1-467, I-463 and I-374.

A:Reference number: S63683; MUID:96193901; PMID:8641442

A:Accession: S63683

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-463 <SAB>

A:Cross-references: EMBL:U40379; NID:q1244637; PIDN:AAB05894.1; PID:q1244638

C:Superfamily: Presenilin

Query Match

Best Local Similarity 100.0%; Score 15; DB 2; Length 467;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLGPRTSPESRAA 15

DB 342 SHLGPRTSPESRAA 356

RESULT 2

S58396

C:Species: Homo sapiens (man)

C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999

R:Sherrington, R.; Rogeev, E.I.; Liang, Y.; Rogeeva, E.A.; Levesque, G.; Ikeda, M.; Chl

E.; Romanus, J.M.; St George-Hyslop, P.H.

Nature 375, 754-760, 1995

A>Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer

A:Reference number: 158095; MUID:95319502; PMID:7596406

A:Accession: S58396

A:Molecule type: mRNA

A:Residues: 1-467 <SHE>

A:Cross-references: EMBL:L42110; NID:g904118; PIDN:AAB64416.1; PID:g904119

R:Vidal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.

FEBS Lett. 393, 19-23, 1996

A>Title: Alzheimer's presenilin 1 gene expression in platelets and megakaryocytes. Ident

A:Reference number: S71401; MUID:96397521; PMID:8804415
A:Accession: S71401
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 24-32;254-256,290-292;316-317,376-379 <VM>
A:Experimental source: Dam megakaryotic cell line (ATCC CRL-9792) and platelets
C:Genetics:
A:Gene: GDB:PSEN1; AD3; FAD; S182; PS1
A:Cross-references: GDB:135682; OMIM:104311
A:Map position: 14q24.3-14q24.3
C:Superfamily: Presenilin
C:Keywords: alternative splicing; Alzheimer's disease; glycoprotein; transmembrane pr
F:92-100/Domain: transmembrane #status predicted <TM1>
F:133-154/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:195-213/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:244-264/Domain: transmembrane #status predicted <TM6>
F:281-301/Domain: transmembrane #status predicted <TM7>
F:408-428/Domain: transmembrane #status predicted <TM8>
F:433-453/Domain: transmembrane #status predicted <TM9>
F:279,405/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 15; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLGPRTSPESRAA 15
DB 346 SHLGPRTSPESRAA 360

RESULT 3

I78388

C:Species: Mus musculus (house mouse)

C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999

C:Accession: I78388

R:Sherrington, R.; Rogeev, E.I.; Liang, Y.; Rogeeva, E.A.; Levesque, G.; Ikeda, M.; C

E.; Romanus, J.M.; St George-Hyslop, P.H.

Nature 375, 754-760, 1995

A>Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheim

A:Reference number: 158095; MUID:95319502; PMID:7596406

A:Accession: I78388

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <RES>

A:Cross-references: GB:L42177; NID:g904129; PIDN:AAC42094.1; PID:g904130

C:Superfamily: Presenilin

Query Match

Best Local Similarity 100.0%; Score 15; DB 2; Length 467;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLGPRTSPESRAA 15
DB 346 SHLGPRTSPESRAA 360

RESULT 4

H75253

C:Species: Deinococcus radiodurans (strain R1)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: H75253

R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J

S.; Shen, M.; Vamathevan, J.T.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.

Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: H75253

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <MWI>
 A:Cross-references: GB:AE002089; GB:AE000513; NID:g6460427; PIDN:AAF12144.1; PID:g646043
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2600
 A:Map position: 1

Query Match 53.3%; Score 8; DB 2; Length 347;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RSPESRA 14
 |||||
 DB 274 RSPESRA 281

RESULT 5
 F87541
 hypothetical protein CC2359 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
 C:Accession: F87541
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete genome sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: F87541
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-327 <STO>
 A:Cross-references: GB:AE005673; NID:g1342388; PIDN:AAK24330.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2359
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase

Query Match 46.7%; Score 7; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 15
 |||||
 DB 139 TPESRA 145

RESULT 6
 E95911
 probable transcription regulator, LacI family protein [imported] - Sinorhizobium meliloti

C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: E95911
 R:Finan, T.M.; Weidner, S.; Wong, J.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: E95911
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-343 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC4957.1; PID:g15140442; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welis, D.H.; Wong, K.; Yen, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation

C:Genetics:
 A:Gene: SMB20817
 A:Genome: plasmid

Query Match 46.7%; Score 7; DB 2; Length 343;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 15
 |||||
 DB 285 TPESRA 291

RESULT 7

JC5081
 presentin 1 protein isoform 463 - lesser mouse lemur

C:Species: Microcebus murinus (lesser mouse lemur)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
 C:Accession: JC5081
 R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Pelter, A.; Bons, N.; Bell
 Biochem. Biophys. Res. Commun. 228, 430-439, 1996
 A:Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene
 A:Reference number: JC5080; MUID:97079199; PMID:8920931
 A:Contents: brain
 A:Accession: JC5081
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-463 <CAL>
 A:Cross-references: EMBL:271333
 C:Comment: This protein is an intermembrane protein with seven transmembrane domains.
 C:Genetics:
 A:Gene: psi

A:Map position: 14
 C:Superfamily: presentin
 C:Keywords: transmembrane protein
 F:78-96/Domain: transmembrane #status predicted <TM1>
 F:129-150/Domain: transmembrane #status predicted <TM2>
 F:160-181/Domain: transmembrane #status predicted <TM3>
 F:191-209/Domain: transmembrane #status predicted <TM4>
 F:217-234/Domain: transmembrane #status predicted <TM5>
 F:240-257/Domain: transmembrane #status predicted <TM6>
 F:404-424/Domain: transmembrane #status predicted <TM7>

Query Match 46.7%; Score 7; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LGPHRST 9
 |||||
 DB 344 LGPHRST 350

RESULT 8

JC5080
 presentin 1 protein isoform 467 - lesser mouse lemur

C:Species: Microcebus murinus (lesser mouse lemur)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
 C:Accession: JC5080
 R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Pelter, A.; Bons, N.; Bell
 Biochem. Biophys. Res. Commun. 228, 430-439, 1996
 A:Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene
 A:Reference number: JC5080; MUID:97079199; PMID:8920931
 A:Accession: JC5080

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-467 <CAL>
 A:Cross-references: EMBL:271333; NID:g1707591; PIDN:CAA5930.1; PID:g1707592
 A:Experimental source: brain
 C:Comment: This protein is an intergal membrane protein with seven transmembrane dom

C:Genetics:
 A:Gene: psi
 A:Map position: 14
 C:Superfamily: presentin

C:Keywords: transmembrane protein
F:92-100/Domain: transmembrane #status predicted <TM1>
F:133-154/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:195-213/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:244-261/Domain: transmembrane #status predicted <TM6>
F:408-428/Domain: transmembrane #status predicted <TM7>

Query Match 46.7%; Score 7; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGPHRST 9
Db 348 LGPHRST 354

RESULT 9

S73457
methionine-tRNA ligase (EC 6.1.1.10) mets - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: hypothetical protein B01_orf512; methionyl-tRNA synthetase mets
C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342
C:Date: 26-Feb-1997 #sequence-revision 25-Apr-1997 #text-change 03-Jun-2002
C:Accession: S73457
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Plöckl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73457
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-512 <HIM>
A:Molecule type: DNA
A:Cross-references: EMBL:AE000015; GB:U00089; NID:g1673779; PIDN:AA95779.1; PID:g1673779
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Gene: mets
A:Genetic code: SGC3
C:Superfamily: methionine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 46.7%; Score 7; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TPESRAA 15
Db 180 TPESRAA 186

RESULT 10

FA5714
probable regulatory protein p13 II, alternative splice form - human T-cell lymphotropic
C:Species: human T-cell lymphotropic virus type 1, HTLV-1
C:Date: 22-Sep-1993 #sequence-revision 25-Apr-1997 #text-change 23-May-1997
C:Accession: FA5714
R:Gessain, A.; Boeri, E.; Yanagihara, R.; Gallo, R.C.; Franchini, G.
J. Virol. 67, 1015-1023, 1993

A:Title: Complete nucleotide sequence of a highly divergent human T-cell leukemia (lymph) from other geographical regions.
A:Reference number: A45714; MUID:93124536; PMID:8419636
A:Contents: HTLV-IMEL5
A:Accession: FA5714
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-87 <GES>
A:Note: sequence extracted from NCBI backbone (NCBIP:122473)

Query Match 40.0%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HLGPHR 7
Db 58 HLGPHR 63

RESULT 11

D61547
hypothetical protein II (px region) - human T-cell lymphotropic virus type 1 (isolate
C:Species: human T-cell lymphotropic virus type 1, HTLV-1
C:Date: 28-Oct-1994 #sequence-revision 28-Oct-1994 #text-change 08-Oct-1999
C:Accession: D61547

R:Tsutsui, A.; Teruuchi, T.; Imamura, J.; Shimotohno, K.; Miyoshi, I.; Miwa, M.
Mol. Biol. Med. 5, 29-42, 1988
A:Title: Nucleotide sequence analysis of a provirus derived from HTLV-1-associated my
A:Reference number: A61547; MUID:88232270; PMID:2897612
A:Accession: D61547

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <TSU>
A:Cross-references: GB:M37301; NID:g541634; PIDN:AAA5391.1; PID:g541638

Query Match 40.0%; Score 6; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HLGPHR 7
Db 58 HLGPHR 63

RESULT 12

D95289
hypothetical protein Sma0412 [imported] - Sinorhizobium meliloti (strain 1021) magap1
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence-revision 24-Aug-2001 #text-change 30-Sep-2001
C:Accession: D95289

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: D95289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <KUB>

A:Cross-references: GB:AE006469; PIDN:AAK64878.1; PID:g14523295; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, A.P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Kong, K.; Yeh,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:

A:Gene: Sma0412
A:Genome: plasmid

Query Match 40.0%; Score 6; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGPHRS 8
Db 109 LGPHRS 114

RESULT 13

T26722
hypothetical protein Y39A1A.18 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T26722
 R:Wall, M.
 submitted to the EMBL Data Library, September 1998
 A/Reference number: Z20257
 A/Accession: T26722
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-139 <Wt>
 A/Cross-references: EMBL:AL031633; PTDN:CAA21011.1; GSPDB:GN00021; CESP:Y39A1A.18
 A/Experimental source: clone Y39A1A
 C/Genetics:
 A:Gene: CESP:Y39A1A.18
 A:Map position: 3
 A/Introns: 37/3; 79/3

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 139;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 14
 |||||
 DB 19 TPESRA 24

RESULT 14
 E75257
 molybdenum cofactor biosynthesis protein C - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C/Accession: E75257
 R:White, O.; Eisen, J.A.; Weidberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: E75257
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-168 <Wt>
 A/Cross-references: GB:AE002086; GB:AE00513; NID:g6460395; PIDN:AAF12111.1; PID:g646039
 A/Experimental source: strain R1
 C/Genetics:
 A:Gene: DR2571
 A/Map position: 1
 C/Superfamily: molybdenum cofactor biosynthesis protein C

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 168;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PESRAA 15
 |||||
 DB 44 PESRAA 49

RESULT 15
 E45714
 probable regulatory function protein p30 II, alternative splice form - human T-cell lymph
 C/Species: human T-cell lymphotropic virus type 1, HTLV-1
 C/Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
 C/Accession: E45714
 R:Gessain, A.; Boert, E.; Yanagihara, R.; Gallo, R.C.; Franchini, G.
 J. Virol. 67, 1015-1023, 1993
 A/Title: Complete nucleotide sequence of a highly divergent human T-cell leukemia (lymph
 from other geographical regions.
 A/Reference number: A45714; MUID:93124536; PMID:8419636
 A/Contents: HTLV-IMEL5
 A/Accession: E45714
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-240 <GES>

A/Note: sequence extracted from NCBI backbone (NCBIP:122472)

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 240;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HLGPHR 7
 |||||
 DB 211 HLGPHR 216

RESULT 16
 C46181
 px-tax-orf II (alternatively spliced) - human T-cell lymphotropic virus type 1
 C/Species: human T-cell lymphotropic virus type 1, HTLV-1
 C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C/Accession: C46181; D46181
 R:Koralnik, I.J.; Gessain, A.; Klotman, M.E.; Lo Monaco, A.; Berneman, Z.N.; Franchin
 Proc. Natl. Acad. Sci. U.S.A. 89, 8813-8817, 1992
 A/Title: Protein isoforms encoded by the px region of human T-cell leukemia/lymphoc
 A/Reference number: A46181; MUID:92409607; PMID:1328697
 A/Accession: C46181
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-241 <KOR>
 A/Note: sequence extracted from NCBI backbone (NCBIP:114307)
 A/Accession: D46181
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 155-241 <KO2>
 A/Note: sequence extracted from NCBI backbone (NCBIP:114308)

Query Match
 Best Local Similarity 40.0%; Score 6; DB 2; Length 241;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HLGPHR 7
 |||||
 DB 212 HLGPHR 217

RESULT 17
 D96016
 probable exodeoxyribonuclease III (EC 3.1.11.2) [imported] - Sinorhizobium meliloti
 C/Species: Sinorhizobium meliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
 C/Accession: D96016
 R:Finan, T.M.; Weidner, S.; Wong, K.; Bhramare, J.; Chain, P.; Vorholter, F.J.; Hei
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing e
 A/Reference number: A95842; MUID:21396508; PMID:11481431
 A/Accession: D96016
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-257 <KUR>
 A/Cross-references: GB:AL591985; PIDN:CAC49796.1; PID:g15141283; GSPDB:GN00167
 A/Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub
 Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A:Gene: xtnA4; SMD20689
 A/Accession: SMD20689
 C/Superfamily: exodeoxyribonuclease III
 C/Keywords: hydrolase

Query Match
 40.0%; Score 6; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
Db 171 PESRAA 176

RESULT 18
F87498
exodeoxyribonuclease III [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: F87498
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Lau, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete genome sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:1259647
A:Accession: F87498
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-262 <SNQ>
A:Cross-references: GB:AE005673; NID:q13423482; PIDN:AAK23986.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2011
C:Superfamily: exodeoxyribonuclease III

Query Match 40.0%; Score 6; DB 2; Length 262;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
Db 176 PESRAA 181

RESULT 19
T37031
hypothetical protein SCJ12.12c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37031
R:Murphy, L.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21619
A:Accession: T37031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-301 <MUR>
A:Cross-references: EMBL:AL109989; PIDN:CAB53424.1; GSPDB:GN00070; SCQEDB:SCJ12.12c
C:Genetics:
A:Gene: SCQEDB:SCJ12.12c

Query Match 40.0%; Score 6; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
Db 13 PESRAA 18

RESULT 20
A82860
DNA replication and repair RecF protein XF0003 [imported] - Xylella fastidiosa (strain 9
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C:Accession: A82860
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: A82860
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <SIM>
A:Cross-references: GB:AE003855; GB:AE003849; NID:g9104760; PIDN:AAE82816.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0003
C:Superfamily: recF protein

Query Match 40.0%; Score 6; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LGPHRS 8
|||||
Db 254 LGPHRS 259

RESULT 21
S40693
opsin rh3 - fruit fly (*Drosophila pseudoobscura*)
C:Species: *Drosophila pseudoobscura*
C:Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C:Accession: S40693; S65548; S24607
R:Carulli, J.P.; Hartl, D.L.
Genetics 132, 193-204, 1992
A:Title: Variable rates of evolution among *Drosophila* opsin genes.
A:Reference number: S40691; MUID:93012921; PMID:1398053
A:Accession: S40693
A:Molecule type: DNA
A:Residues: 1-382 <CAR>
A:Cross-references: EMBL:X65879
A>Note: the authors translated the codon GCA for residue 25 as Gly
R:Carulli, J.P.
submitted to the EMBL Data Library, November 1992
A:Reference number: S65546
A:Accession: S65548
A:Molecule type: DNA
A:Residues: 1-123, 'L', 125-241, 'Q', 243-254, 'R', 256-382 <CAW>
A:Cross-references: EMBL:X65879; NID:g9081; PIDN:CAA46710.1; PID:g9082
C:Genetics:
A:Gene: FlyBase:Dpse/Rh3
A:Cross-references: FlyBase:FBgn0012709
C:Superfamily: vertebrate rhodopsin

Query Match 40.0%; Score 6; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
Db 362 PESRAA 367

RESULT 22

F69834
multidrug-efflux transporter homolog yhjO - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: F69834
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Bujalier, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabelt, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsveld, G.; Krogh, S.; Kumano, M.; Kurita, A.; Ladinolis,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauvel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Yamashita, A.; Tanaka, T.; Terpiltra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A9580; MUID:98044033; PMID:9384377
A:Accession: F69834
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-401 <KUN>
A:Molecule type: DNA
A:Cross-references: GB:299109; GB:AL009126; NID:g2633260; PIDN:CAB12898.1; PID:g2633394
C:Experimental source: strain 168
C:Genetics:
A:Gene: yhjO
C:Superfamily: tetracycline resistance protein

Query Match 40.0%; Score 6; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 STPESR 13
|||||
Db 131 STPESR 136

RESULT 23
T34535
hypothetical protein DKFZp434H0717.1 - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34535
R:Bioecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999
A:Reference number: 221539
A:Accession: T34535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <BLO>
A:Cross-references: EMBL:AL122102
A:Experimental source: adult testis; clone DKFZp434H0717
C:Genetics:
A:Note: DKFZp434H0717.1

Query Match 40.0%; Score 6; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RSTPES 12
|||||
Db 23 RSTPES 28

RESULT 24
D87297
conserved hypothetical protein CC0389 [Imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87297

R:Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87297
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <STO>
A:Cross-references: GB:AE005673; NID:913421548; PIDN:AAK22376.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0389

Query Match 40.0%; Score 6; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PESRAA 15
|||||
Db 117 PESRAA 122

RESULT 25
C95248
histidyl-tRNA synthetase [Imported] - *Streptococcus pneumoniae* (strain TIGR4)
C:Species: *Streptococcus pneumoniae*
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: C95248
R:Rettlein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
son, T.; Hickay, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-429 <KUN>
A:Cross-references: GB:AE005672; PIDN:AAK76180.1; PID:914973634; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2121
C:Superfamily: histidyl-tRNA ligase; histidyl-tRNA ligase homology

Query Match 40.0%; Score 6; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PESRAA 15
|||||
Db 171 PESRAA 176

RESULT 26
H98112
histidine-tRNA ligase (EC 6.1.1.21) [Imported] - *Streptococcus pneumoniae* (strain R6)
C:Species: *Streptococcus pneumoniae*
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
C:Accession: H98112
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAlhena, S.
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balitz, R.H.; Jaskunas, S.
A:Title: Genome of the Bacterium *Streptococcus pneumoniae* Strain R6.
A:Reference number: A87872; MUID:21429245; PMID:11544234
A:Accession: H98112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-429 <KUN>
A:Cross-references: GB:AE007317; PIDN:AAU00733.1; PID:915459628; GSPDB:GN00174

C:Genetics:
A:Gene: hist
C:Superfamily: histidine-trna ligase; histidine-trna ligase homology
C:Keywords: ligase

Query Match 40.0%; Score 6; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
DB 171 PESRAA 176

RESULT 27

JC5390
Presentin-alpha - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C:Accession: JC5390
R:Tsujiyama, A.; Yasojima, K.; Hashimoto-Gotoh, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997.
A:Title: Cloning of Xenopus presentin-alpha and -beta cDNAs and their differential exp
A:Reference number: JC5390; MUID:97223465; PMID:9070286
A:Accession: JC5390
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-433 <TSU>
A:Cross-references: DDBJ:DB4427; NID:g1944353; PIDN:BA19570.1; PID:g1944354
A:Experimental source: brain
C:Comment: This protein plays a role in negative regulation of apoptotic cascades during
C:Superfamily: presentin
F:48-66/Domain: transmembrane #status predicted <TM1>
F:99-119/Domain: transmembrane #status predicted <TM2>
F:130-149/Domain: transmembrane #status predicted <TM3>
F:161-178/Domain: transmembrane #status predicted <TM4>
F:187-203/Domain: transmembrane #status predicted <TM5>
F:210-227/Domain: transmembrane #status predicted <TM6>
F:314-394/Domain: transmembrane #status predicted <TM7>

Query Match 40.0%; Score 6; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 STPESR 13
|||||
DB 319 STPESR 324

RESULT 28

S31927
drop9 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
C:Accession: S31927
R:Kirsch, K.
submitted to the EMBL Data Library, February 1993
A:Reference number: S31927
A:Accession: S31927
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-475 <KIR>
A:Cross-references: EMBL:X70991; NID:g38459; PID:g38460

Query Match 40.0%; Score 6; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RSTPES 12
|||||
DB 139 RSTPES 144

RESULT 29

T03510
hypothetical protein - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C:Accession: T03510
R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus S81
A:Reference number: Z14955; MUID:97404404; PMID:9256491
A:Accession: T03510
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-617 <VLC>
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AC16163.1; PID:g3128311
C:Genetics:
A:Map position: 1

Query Match 40.0%; Score 6; DB 2; Length 617;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
DB 470 PESRAA 475

RESULT 30

AE1895
hypothetical protein all0711 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AE1895
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kultz, T.; Sasamoto, S.; Watanabe, A.; Itigun
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1895; MUID:21595285; PMID:11759840
A:Accession: AE1895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-640 <RUR>
A:Cross-references: GB:BA000019; PIDN:BA072668.1; PID:g17130056; GSPDB:GNO0179
C:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0711

Query Match 40.0%; Score 6; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PESRAA 15
|||||
DB 142 PESRAA 147

RESULT 31

I64207
preprotein translocase secA - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 17-Nov-2000
C:Accession: I64207
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.
M.; Fuhmann, J.; Nguyen, D.; Uitterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick,
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: I64207
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-806 <TIGR>

date?

A:Cross-references: GB:039687; GB:L43967; NID:g3844663; PIDN:AAC71290.1; PID:g1045748; I
A:Experimental source: strain G-37
C:Comment: The "nucleotide-binding motif B" and "DEAD motif" features as annotated are c
is adjacent to the identified motif and a third conserved motif is approximately 120-140
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: preprotein translocase secA
C:Keywords: ATP; membrane-associated complex; P-loop; protein transport
F:102-109/Region: nucleotide-binding motif A (P-loop) #status atypical
F:205-210/Region: nucleotide-binding motif B
F:209-212/Region: DEAD motif

Query Match 40.0%; Score 6; DB 2; Length 806;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PESRA 15
|||||
Db 255 PESRA 260

RESULT 32

RRVGT
RNA-directed RNA polymerase (EC 2.7.7.48) - tomato bushy stunt virus (strain cherry)
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: 33k protein
C:Species: tomato bushy stunt virus, TBSV
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 25-Oct-1996
R:Accession: A5315
R:Heuristics: P.O.; Knorr, D.A.; Hillman, B.I.; Morris, T.J.
Virology 177, 141-151, 1990
A:Title: The complete genome structure and synthesis of infectious RNA from clones of to
A:Reference number: A5315; MUID:90281577; PMID:2353450
A:Accession: A5315
A:Molecule type: genomic RNA
A:Residues: 1-817 <HEA>
A:Cross-references: EMBL:M31019
A:Note: readthrough of the terminator UAG occurs between codons AAA for 296-Lys and GGA
C:Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwarf v
C:Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication
F:1-296/Product: 33k protein #status predicted <P33>
F:527-694/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BYD>

Query Match 40.0%; Score 6; DB 1; Length 817;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 14
|||||
Db 766 TPESRA 771

RESULT 33

RRVGT
RNA-directed RNA polymerase (EC 2.7.7.48) - Cymbidium ringspot virus
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: 33k protein
C:Species: Cymbidium ringspot virus
C:Date: 31-Mar-1990 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
R:Accession: S05456; J50268
R:Giaco, F.; Burgan, J.; Russo, M.
Nucleic Acids Res. 17, 6383, 1989
A:Title: The nucleotide sequence of Cymbidium ringspot virus RNA.
A:Reference number: J50268; MUID:8936663; PMID:2771646
A:Accession: S05456
A:Status: preliminary; translation not shown
A:Molecule type: genomic RNA
A:Residues: 1-818 <GRI>
A:Cross-references: EMBL:X15511; NID:g59020; PIDN:CAB38439.1; PID:g4469160
A:Accession: J50268
A:Molecule type: genomic RNA
A:Residues: 1-296, 298-483, 1, 485-818 <GR2>
A:Cross-references: GB:X15511

A:Note: readthrough of the terminator TAG occurs between codons AAA for 296-Lys and G
C:Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwar
C:Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication
F:1-296/Product: 33k protein #status predicted <P33>
F:528-695/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BYD

Query Match 40.0%; Score 6; DB 1; Length 818;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 14
|||||
Db 767 TPESRA 772

RESULT 34

S52717
RNA-directed RNA polymerase (EC 2.7.7.48) - carnation Italian ringspot virus
N:Alternate names: RNA replicase
C:Species: carnation Italian ringspot virus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Jun-1999
R:Accession: S52717
R:Rubino, L.; Burgan, J.; Russo, M.
submitted to the EMBL Data Library, March 1995
A:Description: Molecular cloning and complete nucleotide sequence of carnation Italia
A:Reference number: S52717
A:Accession: S52717
A:Molecule type: genomic RNA
A:Residues: 1-851 <RUB>
A:Cross-references: EMBL:X85215; NID:g755716; PIDN:CA59478.1; PID:g755718
C:Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwar
C:Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication
F:561-728/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BYD

Query Match 40.0%; Score 6; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 14
|||||
Db 800 TPESRA 805

RESULT 35

VGBRB
glycoprotein B precursor - Marek's disease virus (strain RB1B)
C:Species: Marek's disease virus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000
R:Accession: A32402; B32402
R:Ross, L.J.N.; Sanderson, M.; Scott, S.D.; Blms, M.M.; Del, T.; Milne, B.
J. Gen. Virol. 70, 1789-1804, 1989
A:Title: Nucleotide sequence and characterization of the Marek's disease virus homolo
A:Reference number: A32402; MUID:89293086; PMID:2544666
A:Accession: A32402
A:Molecule type: DNA
A:Residues: 1-865 <ROS>
A:Cross-references: GB:D13713; EMBL:D00506; NID:g221836; PIDN:BA02866.1; PID:g221837
A:Accession: B32402
A:Molecule type: protein
A:Residues: 250-271;304-330 <ROS2>
C:Superfamily: herpesvirus glycoprotein B
C:Keywords: glycoprotein; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-865/Product: glycoprotein B #status predicted <GPB>
F:709-728/Domain: transmembrane #status predicted <TM1>
F:732-752/Domain: transmembrane #status predicted <TM2>
F:27,184,332,364,406,425,631/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 40.0%; Score 6; DB 1; Length 865;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 14

Db 174 TPESRA 179

RESULT 36

probable major core protein 113L - Molluscum contagiosum virus 1

N:Alternate names: MC113L

C:Species: Molluscum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000

C:Accession: T30715

R:Senkevitch, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Dairi, G.; Moss, B.

Science 273, 813-816, 1996

A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re

A:Reference number: Z20876; MUID:96325459; PMID:8670425

A:Accession: T30715

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-889 <SEN>

A:Cross-references: EMBL:U60315; NID:q1491943; PIDN:AC55241.1; PID:q1492056

C:Genetics:

A:Note: MC113L

C:Superfamily: vaccinia virus major core protein p4a

Query Match 40.0%; Score 6; DB 2; Length 889;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESRA 14

Db 211 TPESRA 216

RESULT 37

protein K07F5.12a [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: B88794

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: B88794

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-981 <STO>

A:Cross-references: GB:chr_IV; PIDN:CAA94287.1; PID:g44008375; GSPDB:GN00022; CESP:K07F5.

C:Genetics:

A:Gene: K07F5.12a

A:Map position: 4

Query Match 40.0%; Score 6; DB 2; Length 981;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PHRSTP 10

Db 533 PHRSTP 538

RESULT 38

platelet-derived growth factor receptor beta - Japanese pufferfish

C:Species: Fugu rubripes (Japanese pufferfish)

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000

C:Accession: T30815

R:How, G.F.; Venkatesh, B.; Brenner, S.

Genome Res. 6, 1185-1191, 1996

A:Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for pla

A:Reference number: Z20882; MUID:97129405; PMID:8973913

A:Accession: T30815

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1048 <HOW>

A:Cross-references: EMBL:U63926; NID:q1752706; PID:q1752707; PIDN:AC60062.1

C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo

Query Match 40.0%; Score 6; DB 2; Length 1048;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SHLGP 6

Db 652 SHLGP 657

RESULT 39

platelet-derived growth factor receptor beta precursor - mouse

N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 10-Sep-1999

C:Accession: A25742

R:Yarden, Y.; Escobedo, J.A.; Kuang, W.J.; Yang-Feng, T.L.; Daniel, T.O.; Tremble, P.

Nature 323, 226-232, 1986

A:Title: Structure of the receptor for platelet-derived growth factor helps define a

A:Reference number: A25742; MUID:87014762; PMID:3020426

A:Accession: A25742

A:Molecule type: mRNA

A:Residues: 1-1098 <YAR>

A:Cross-references: EMBL:X04367; NID:953618; PIDN:CA27882.1; PID:953619

A:Note: part of this sequence, including the amino end of the mature protein, was con

C:Comment: The extracellular domain is predicted to include five immunoglobulin-like

C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo

C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodim

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-1098/Product: platelet-derived growth factor receptor beta #status predicted <MA

F:32-530/Domain: extracellular #status predicted <EXT>

F:46-101/Domain: immunoglobulin homology <IMM1>

F:141-191/Domain: immunoglobulin homology <IMM2>

F:227-282/Domain: immunoglobulin homology <IMM3>

F:428-509/Domain: immunoglobulin homology <IMM4>

F:531-554/Domain: transmembrane #status predicted <TMN>

F:555-1098/Domain: intracellular #status predicted <INT>

F:557-964/Domain: protein kinase homology <KIN>

F:605-613/Region: protein kinase ATP-binding motif

F:44,88,102,214,291,306,353,370,444,467,478/Binding site: carbohydrate (Asn) (covalen

F:53-99,148-189,234-290,435-507/Disulfide bonds: #status predicted

F:633/Active site: Lys #status predicted

F:856/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 40.0%; Score 6; DB 1; Length 1098;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SHLGP 6

Db 655 SHLGP 660

RESULT 40

PFHUGB

platelet-derived growth factor receptor beta precursor - human

N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (hmn)

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999

C:Accession: A28206; A31195; A38268; A31925; B31925

R:Gronwald, R.G.K.; Grant, F.J.; Haldean, B.A.; Hart, C.E.; O'Hara, P.J.; Hegen, F.S

A:Title: Cloning and expression of a cDNA coding for the human platelet-derived growt

A:Reference number: A28206; MUID:88217915; PMID:2835772

A:Accession: A28206

A:Molecule type: mRNA
 A:Residues: 1-1106 <GR0>
 A:Cross-references: GB:J03278; NID:9189731; PIDN:AA60049.1; PID:9189732
 R:Classon-Welsh, L.; Eriksson, A.; Møren, A.; Severinsson, L.; Ek, B.; Oestman, A.; Bet
 Mol. Cell. Biol. 8, 3476-3486, 1988
 A:Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) r
 A:Reference number: A31195; MUID:89096941; PMID:2850496
 A:Accession: A31195
 A:Molecule type: mRNA
 A:Residues: 1-240, 'D', 242-1106 <CLA>
 A:Cross-references: GB:M21616; NID:9189729; PIDN:AA36427.1; PID:9189730
 R:Partanen, J.; Mäkelä, T.P.; Allitalo, R.; Lehteslahti, H.; Allitalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
 A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
 A:Reference number: A38268; MUID:91062389; PMID:2247464
 A:Accession: A38268
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 828-884 <PAR>
 R:Roberts, W.M.; Look, A.T.; Rousset, M.F.; Sherr, C.J.
 Cell 55, 655-661, 1988
 A:Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.
 A:Reference number: A90908; MUID:89028677; PMID:2846185
 A:Accession: A31925
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 676-727 <ROB>
 A:Accession: B31925
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 901-932 <RO2>
 A:Accession: C31925
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1047-1106 <RO3>
 C:Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
 C:Genetics:
 A:Gene: GDB:PDGFRB
 A:Cross-references: GDB:120710; OMIM:173410
 A:Map position: 5q31-q32
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
 C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:33-1106/Product: platelet-derived growth factor receptor beta #status predicted <MAT>
 F:33-531/Domain: extracellular #status predicted <EXT>
 F:47-102/Domain: immunoglobulin homology <IM1>
 F:142-192/Domain: immunoglobulin homology <IM2>
 F:228-293/Domain: immunoglobulin homology <IM3>
 F:429-510/Domain: immunoglobulin homology <IM4>
 F:532-555/Domain: transmembrane #status predicted <TM>
 F:556-1106/Domain: intracellular #status predicted <INT>
 F:598-965/Domain: protein kinase homology <KIN>
 F:606-614/Region: protein kinase ATP-binding motif
 F:45-89,103,215,230,292,307,354,371,468,479/Binding site: carbohydrate (Asn) (covalent)
 F:54-100,149-190,235-291,436-508/Disulfide bonds: #status predicted
 F:634/Active site: Lys #status predicted
 F:857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
 Query Match 40.0%; Score 6; DB 1; Length 1106;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SHLGH 6
 Db 656 SHLGH 661
 RESULT 41
 T01367
 hypothetical protein At2g34680 (imported) - Arabidopsis thaliana
 N:Alternate names: hypothetical protein T29F13.11
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001

C:Accession: T01367; F84759
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
 Submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
 A:Reference number: Z14179
 A:Accession: T01367
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1680 <ROU>
 A:Cross-references: EMBL:AC003096; NID:93132469; PID:93132477
 A:Experimental source: Cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
 M.; Ko, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umeyama, L.; Tallon,
 euss, D.; Niernmen, W.T.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-766, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: F84759
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1680 <STO>
 A:Cross-references: GB:AE002093; NID:93132477; PIDN:AA016266.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: T29F13.11; At2g34680
 A:Map position: 2
 A:Introns: 271/3; 295/3; 317/3; 341/3; 363/3; 384/3; 406/3; 440/1; 474/1; 551/3; 600/
 ; 1372/2; 1433/1; 1485/1; 1529/1; 1548/3; 1578/3; 1622/3
 Query Match 40.0%; Score 6; DB 2; Length 1680;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 STPESR 13
 Db 248 STPESR 253
 RESULT 42
 A47392
 Chromodomain-helicase-DNA-binding protein, CHD-1 - mouse
 N:Alternate names: KYP protein
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A47392; S21568
 R:Delmas, V.; Stokes, D.G.; Perry, R.P.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2414-2418, 1993
 A:Title: A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWI
 A:Reference number: A47392; MUID:93211972; PMID:8460153
 A:Accession: A47392
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1711
 A:Experimental source: S194 plasmacytoma cells
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:128272, NCBI:128273)
 R:Delmas, V.; Perry, R.P.
 submitted to the EMBL Data Library, May 1992
 A:Description: KYP, a mammalian protein that contains the SNF2/SWI2 helicase domain
 A:Reference number: S21568
 A:Accession: S21568
 A:Molecule type: mRNA
 A:Residues: 772-1711 <DE2>
 A:Cross-references: EMBL:X66028
 C:Superfamily: CHD-1 protein; chromobox homology
 C:Keywords: DNA binding
 F:293-336/Domain: chromobox homology <CB1>
 F:387-427/Domain: chromobox homology <CB2>
 Query Match 40.0%; Score 6; DB 1; Length 1711;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 HRSTPE 11

|||||
Db 1698 HRSTPE 1703

RESULT 43

variant-specific surface protein 2 - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T28626
R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herfeltdt, J.A.; Peterson, D.S.
Cell 82, 89-100, 1995
A:Title: The large diverse gene family var encodes proteins involved in cytoadherence an
A:Reference number: 220487; MUID:95330813; PMID:7606788
A:Accession: T28626
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2664 <SUX>
A:Cross-references: EMBL:L40609; NID:9886376; PID:9886378; PIDN:AAAT5398.1
C:Genetics:
A:introns: 2197/3
A>Note: var-2

Query Match 40.0%; Score 6; DB 2; Length 2664;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RSTPES 12
|||||
Db 1335 RSTPES 1340

RESULT 44

Insulin-like growth factor receptor type II - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C:Accession: S58277
R:Smrzka, O.W.; Stoger, R.; Kurzbauer, R.; Fae, I.; Fischer, G.F.; Barlow, D.P.
submitted to the EMBL Data Library, January 1995
A:Description: Conservation of a methylation imprint and a putative imprinting box at th
A:Reference number: S58277
A:Accession: S58277
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18 <SMR>
A:Cross-references: EMBL:X83702; NID:9929644; PIDN:CAAS8675.1; PID:9929645
C:Keywords: growth factor receptor

Query Match 33.3%; Score 5; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ESRAA 15
|||||
Db 6 ESRAA 10

RESULT 45

T04371
thaumatin-like protein - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04371
R:Skadsen, R.W.; Herbst, J.M.
submitted to the EMBL Data Library, July 1997
A:Reference number: Z15316
A:Accession: T04371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-26 <SKA>
A:Cross-references: EMBL:AF016328; NID:92454603; PIDN:AAAT1681.1; PID:92454604
A:Experimental source: cv. Morex

C:Genetics:
A:Gene: perm2

Query Match 33.3%; Score 5; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LGPHR 7
|||||
Db 19 LGPHR 23

RESULT 46

homeobox - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 15-Oct-1999
C:Accession: I37554
R:Moretti, P.; Simmons, P.; Thomas, P.; Haylock, D.; Rathjen, P.; Vadas, M.; D'Andrea
Gene 144, 213-219, 1994
A:Title: Identification of homeobox genes expressed in human haemopoietic progenitor
A:Reference number: I37554; MUID:94314219; PMID:7518789
A:Accession: I37554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-39 <RES>
A:Cross-references: EMBL:X74861; NID:9510992; PIDN:CAAS2854.1; PID:9510993
C:Genetics:
A:Gene: HPX-2
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 33.3%; Score 5; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESR 13
|||||
Db 32 TPESR 36

RESULT 47

F86491
hypothetical protein CPJ0006 [imported] - Chlamydomonas pneumoniae (strain J138)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: F86491
R:Shirai, M.; Hiraoka, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: F86491
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-51 <STO>
A:Cross-references: GB:BA000008; NID:98978379; PIDN:BAAG8216.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0006

Query Match 33.3%; Score 5; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RSTPE 11
|||||
Db 29 RSTPE 33

RESULT 48

C72131
hypothetical protein - Chlamydomonas pneumoniae (strain CWL029)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 C:Accession: C72131
 R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: C72131
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-51 <ARN>
 A:Cross-References: GB:AE001585; GB:AE001363; NID:g4376255; PIDN:AAD18164.1; PID:g437626
 A:Experimental source: strain CWL029
 C:Genetics:
 A:Gene: Cpn0006

Query Match 33.3%; Score 5; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RSPPE 11
 Db 29 RSPPE 33

RESULT 49

G72355

hypothetical protein - *Thermotoga maritima* (strain MSB8)C:Species: *Thermotoga maritima*

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: G72355

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: G72355

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-56 <ARN>

A:Cross-References: GB:AE001735; GB:AE000512; NID:g4981122; PIDN:AAD35696.1; PID:g498113

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0611

Query Match

33.3%; Score 5; DB 2; Length 56;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TPESR 13
 Db 22 TPESR 26

RESULT 50

QOECF7

ybeB protein - *Escherichia coli* (strain K-12)C:Species: *Escherichia coli*

C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 01-Mar-2002

C:Accession: A24995; C64798

R:Asob, S.; Matsuzawa, H.; Ishino, F.; Strominger, J.L.; Matsubashi, M.; Ohta, T.

Eur. J. Biochem. 160, 231-238, 1986

A:Title: Nucleotide sequence of the ybeB gene and characteristics of the deduced amino a

A:Reference number: A91176; MUID:87030266; PMID:3533535

A:Accession: A24995

A:Molecule type: DNA

A:Residues: 1-69 <ASO>

A:Cross-References: GB:X04516; GB:DD0001; GB:N00001; NID:g42313; PIDN:CAA28199.1; PID:g4

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64798

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-69 <BIAT>

A:Cross-References: GB:U00096; NID:g1786849; PIDN:AC73738.1; PID:g17868

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ybeB

A:Map position: 15 min

C:Superfamily: *Escherichia coli* ybeB protein

Query Match 33.3%; Score 5; DB 1; Length 69;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ESRRA 15
 Db 22 ESRRA 26

Search completed: February 6, 2003, 14:21:28
 Job time : 19.9025 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:17:41 : Search time 26.1598 Seconds
(Without alignments)
525.254 Million cell updates/sec

Title: US-09-689-159A-2

Perfect score: 467

Sequence: 1 MTELPAPLSTYFQNAQMSDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Issued_patents_AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	467	2	US-08-967-101-2
2	467	100.0	467	2	US-08-592-541-2
3	467	100.0	467	2	US-09-124-698-2
4	467	100.0	467	4	US-09-127-480-2
5	467	100.0	467	4	US-08-496-841C-2
6	467	100.0	467	4	US-09-124-523-2
7	438	93.8	463	3	US-08-888-077A-4
8	366	78.4	467	2	US-08-967-101-134
9	366	78.4	467	2	US-08-592-541-134
10	366	78.4	467	3	US-08-923-454A-10
11	366	78.4	467	3	US-08-670-964-2
12	366	78.4	467	3	US-08-888-077A-2
13	366	78.4	467	3	US-09-124-698-134
14	366	78.4	467	4	US-09-127-480-134
15	366	78.4	467	4	US-08-496-841C-134
16	366	78.4	467	4	US-08-832-867-3
17	366	78.4	467	4	US-09-227-725A-1
18	366	78.4	467	4	US-09-124-523-134
19	366	78.4	467	4	US-09-375-318-3
20	337	72.2	463	3	US-08-670-964-4
21	306	65.5	407	2	US-08-875-972-4
22	265	56.7	467	4	US-08-706-344C-2
23	204	43.7	467	4	US-08-706-344C-4
24	204	43.7	467	4	US-08-706-344C-28
25	204	43.7	467	4	US-08-706-344C-30
26	204	43.7	467	4	US-08-706-344C-32
27	189	40.5	462	3	US-08-788-231A-15

28	188	40.3	463	2	US-08-670-479-18	Sequence 18, Appl
29	97	20.8	467	2	US-08-967-101-4	Sequence 4, Appl
30	97	20.8	467	2	US-08-592-541-4	Sequence 17, Appl
31	97	20.8	467	3	US-08-888-077A-17	Sequence 4, Appl
32	97	20.8	467	3	US-09-124-698-4	Sequence 4, Appl
33	97	20.8	467	4	US-09-127-480-4	Sequence 4, Appl
34	97	20.8	467	4	US-08-496-841C-4	Sequence 136, App
35	97	20.8	467	4	US-08-496-841C-136	Sequence 4, Appl
36	97	20.8	467	4	US-09-124-523-4	Sequence 17, Appl
37	84	18.0	465	3	US-08-788-231A-17	Sequence 138, App
38	28	6.0	372	2	US-08-967-101-138	Sequence 138, App
39	28	6.0	372	2	US-08-592-541-138	Sequence 138, App
40	28	6.0	372	3	US-09-124-698-138	Sequence 138, App
41	28	6.0	372	4	US-09-127-480-138	Sequence 138, App
42	28	6.0	372	4	US-08-496-841C-138	Sequence 137, App
43	28	6.0	372	4	US-09-124-523-138	Sequence 137, App
44	28	6.0	447	2	US-08-875-972-29	Sequence 29, Appl
45	28	6.0	448	2	US-08-967-101-137	Sequence 137, App
46	28	6.0	448	2	US-08-592-541-137	Sequence 137, App
47	28	6.0	448	3	US-08-888-077A-19	Sequence 137, App
48	28	6.0	448	3	US-09-124-698-137	Sequence 137, App
49	28	6.0	448	4	US-09-127-480-137	Sequence 137, App
50	28	6.0	448	4	US-09-227-725A-2	Sequence 2, Appl
51	28	6.0	448	4	US-09-124-523-137	Sequence 137, App
52	28	6.0	448	4	US-09-375-318-2	Sequence 2, Appl
53	24	5.1	48	2	US-08-896-176-1	Sequence 1, Appl
54	23	4.7	29	2	US-08-896-176-4	Sequence 1, Appl
55	22	4.7	541	2	US-08-967-101-166	Sequence 166, App
56	22	4.7	541	2	US-08-592-541-166	Sequence 166, App
57	22	4.7	541	3	US-08-888-077A-21	Sequence 21, Appl
58	22	4.7	541	3	US-09-124-698-166	Sequence 166, App
59	22	4.7	541	4	US-09-127-480-166	Sequence 166, App
60	22	4.7	541	4	US-09-124-523-166	Sequence 166, App
61	20	4.3	376	2	US-08-896-176-2	Sequence 2, Appl
62	15	3.2	15	2	US-08-967-101-167	Sequence 167, App
63	15	3.2	15	2	US-08-592-541-167	Sequence 167, App
64	15	3.2	15	2	US-08-967-101-168	Sequence 168, App
65	15	3.2	15	2	US-08-967-101-169	Sequence 169, App
66	15	3.2	15	2	US-08-967-101-170	Sequence 170, App
67	15	3.2	15	2	US-08-592-541-167	Sequence 167, App
68	15	3.2	15	2	US-08-592-541-168	Sequence 168, App
69	15	3.2	15	2	US-08-592-541-169	Sequence 169, App
70	15	3.2	15	2	US-08-592-541-170	Sequence 170, App
71	15	3.2	15	3	US-09-124-698-167	Sequence 167, App
72	15	3.2	15	3	US-09-124-698-168	Sequence 168, App
73	15	3.2	15	3	US-09-124-698-169	Sequence 169, App
74	15	3.2	15	3	US-09-124-698-170	Sequence 170, App
75	15	3.2	15	4	US-08-496-841C-165	Sequence 165, App
76	15	3.2	15	4	US-08-496-841C-166	Sequence 166, App
77	15	3.2	15	4	US-08-496-841C-167	Sequence 167, App
78	15	3.2	15	4	US-09-124-523-167	Sequence 167, App
79	15	3.2	15	4	US-09-124-523-168	Sequence 168, App
80	15	3.2	15	4	US-09-124-523-169	Sequence 169, App
81	15	3.2	15	4	US-09-124-523-170	Sequence 170, App
82	15	3.2	15	4	US-08-896-176-3	Sequence 3, Appl
83	15	3.2	15	4	US-09-375-318-41	Sequence 41, Appl
84	15	3.2	15	4	US-08-896-176-9	Sequence 9, Appl
85	15	3.2	15	4	US-08-788-649A-2	Sequence 2, Appl
86	15	3.2	15	4	US-08-583-276-19	Sequence 19, Appl
87	15	3.2	15	4	US-08-752-447-2	Sequence 2, Appl
88	15	3.2	15	4	US-09-316-167-2	Sequence 2, Appl
89	11	2.4	20	4	US-08-896-176-1	Sequence 1, Appl
90	9	1.9	9	2	US-08-896-176-4	Sequence 4, Appl
91	8	1.7	1279	2	US-08-788-649A-2	Sequence 2, Appl
92	8	1.7	1280	2	US-08-583-276-19	Sequence 19, Appl
93	8	1.7	1280	2	US-08-752-447-2	Sequence 2, Appl
94	8	1.7	1280	4	US-09-316-167-2	Sequence 2, Appl
95	8	1.7	1280	6	US-08-896-176-1	Sequence 1, Appl
96	7	1.5	31	1	US-08-090-036-1	Sequence 1, Appl
97	7	1.5	38	4	US-09-319-730-17	Sequence 17, Appl
98	7	1.5	61	4	US-09-319-730-15	Sequence 15, Appl
99	7	1.5	61	4	US-09-319-730-19	Sequence 19, Appl
100	7	1.5	74	4	US-09-177-249-56	Sequence 56, Appl

101	7	1.5	118	2	US-08-767-026-4	Sequence 4, Appli	174	6	1.3	12	5	PCT-US95-02044-22	Sequence 22, Appl
102	7	1.5	118	2	US-08-846-021A-2	Sequence 2, Appli	175	6	1.3	14	1	US-08-199-776-18	Sequence 18, Appl
103	7	1.5	118	2	US-08-846-021A-7	Sequence 7, Appli	176	6	1.3	14	3	US-08-663-731-18	Sequence 18, Appl
104	7	1.5	154	1	US-08-366-783-5	Sequence 5, Appli	177	6	1.3	14	3	US-08-879-338-18	Sequence 18, Appl
105	7	1.5	173	1	US-08-366-783-2	Sequence 2, Appli	178	6	1.3	14	3	US-09-293-238B-18	Sequence 18, Appl
106	7	1.5	173	1	US-08-313-098A-2	Sequence 2, Appli	179	6	1.3	14	5	PCT-US95-02044-18	Sequence 18, Appl
107	7	1.5	173	2	US-08-767-026-2	Sequence 2, Appli	180	6	1.3	15	1	US-08-199-776-20	Sequence 20, Appl
108	7	1.5	173	2	US-08-831-575-6	Sequence 6, Appli	181	6	1.3	15	3	US-08-663-731-20	Sequence 20, Appl
109	7	1.5	187	2	US-08-846-021A-5	Sequence 5, Appli	182	6	1.3	15	3	US-08-879-338-20	Sequence 20, Appl
110	7	1.5	202	4	US-09-615-192A-386	Sequence 386, App	183	6	1.3	15	4	US-09-009-953-234	Sequence 234, App
111	7	1.5	213	4	US-09-134-001C-3556	Sequence 3556, Ap	184	6	1.3	15	4	US-09-009-953-252	Sequence 252, App
112	7	1.5	231	2	US-08-808-550-33	Sequence 33, Appli	185	6	1.3	15	4	PCT-US95-02044-20	Sequence 20, Appl
113	7	1.5	234	1	US-08-366-783-4	Sequence 4, Appli	186	6	1.3	15	5	PCT-US95-02044-20	Sequence 20, Appl
114	7	1.5	254	2	US-08-767-026-7	Sequence 7, Appli	187	6	1.3	16	4	US-08-602-999A-220	Sequence 220, App
115	7	1.5	323	4	US-09-293-858B-22	Sequence 22, Appli	188	6	1.3	16	4	US-09-500-124-220	Sequence 220, App
116	7	1.5	366	4	US-09-210-843-2	Sequence 2, Appli	189	6	1.3	19	4	US-09-177-249-232	Sequence 232, App
117	7	1.5	392	4	US-09-026-408-2	Sequence 2, Appli	190	6	1.3	20	1	US-08-199-776-21	Sequence 21, Appl
118	7	1.5	405	4	US-09-026-408-13	Sequence 13, Appli	191	6	1.3	20	3	US-08-663-731-21	Sequence 21, Appl
119	7	1.5	434	2	US-08-989-925-1	Sequence 1, Appli	192	6	1.3	20	3	US-08-879-338-21	Sequence 21, Appl
120	7	1.5	482	3	US-09-135-639-2	Sequence 2, Appli	193	6	1.3	20	4	US-09-293-238B-21	Sequence 21, Appl
121	7	1.5	527	4	US-09-370-838-216	Sequence 216, App	194	6	1.3	20	5	PCT-US95-02044-21	Sequence 21, Appl
122	7	1.5	564	4	US-09-134-001C-5139	Sequence 5139, Ap	195	6	1.3	21	1	US-08-199-776-5	Sequence 5, Appli
123	7	1.5	571	4	US-09-134-001C-3865	Sequence 3865, Ap	196	6	1.3	21	3	US-08-663-731-5	Sequence 5, Appli
124	7	1.5	689	4	US-09-177-249-2	Sequence 2, Appli	197	6	1.3	21	3	US-08-879-338-5	Sequence 5, Appli
125	7	1.5	689	4	US-09-061-769A-2	Sequence 2, Appli	198	6	1.3	21	3	US-08-879-338-26	Sequence 26, Appli
126	7	1.5	714	2	US-08-990-114-3	Sequence 3, Appli	199	6	1.3	21	4	US-09-336-536-25	Sequence 25, Appli
127	7	1.5	714	2	US-09-241-333-3	Sequence 3, Appli	200	6	1.3	21	4	US-09-293-238B-5	Sequence 5, Appli
128	7	1.5	740	4	US-09-022-983-5	Sequence 5, Appli	201	6	1.3	21	4	US-09-293-238B-26	Sequence 26, Appli
129	7	1.5	830	4	US-09-562-737-31	Sequence 31, Appli	202	6	1.3	21	5	PCT-US95-02044-5	Sequence 5, Appli
130	7	1.5	830	4	US-09-562-737-33	Sequence 33, Appli	203	6	1.3	25	4	US-09-149-876-431	Sequence 431, App
131	7	1.5	830	4	US-09-562-737-34	Sequence 34, Appli	204	6	1.3	25	4	US-09-911-927-35	Sequence 35, Appli
132	7	1.5	830	4	US-09-562-737-35	Sequence 35, Appli	205	6	1.3	25	4	US-09-911-882-35	Sequence 35, Appli
133	7	1.5	830	4	US-09-562-737-36	Sequence 36, Appli	206	6	1.3	26	4	US-08-965-762-35	Sequence 35, Appli
134	7	1.5	979	4	US-08-878-474-5	Sequence 5, Appli	207	6	1.3	27	4	US-09-227-357-642	Sequence 642, App
135	7	1.5	1023	2	US-08-475-891A-2	Sequence 2, Appli	208	6	1.3	29	4	US-09-143-124-24	Sequence 24, Appli
136	7	1.5	1023	2	US-08-567-375-2	Sequence 2, Appli	209	6	1.3	32	1	US-08-190-802A-119	Sequence 119, App
137	7	1.5	1023	2	US-08-587-600A-2	Sequence 2, Appli	210	6	1.3	32	4	US-08-477-946-119	Sequence 119, App
138	7	1.5	1162	2	US-08-728-333A-2	Sequence 2, Appli	211	6	1.3	32	4	US-08-473-089-119	Sequence 119, App
139	7	1.5	1162	2	US-09-298-568-2	Sequence 2, Appli	212	6	1.3	32	4	US-08-487-072A-119	Sequence 119, App
140	7	1.5	2647	2	US-08-583-562B-8	Sequence 8, Appli	213	6	1.3	37	4	US-09-149-476-694	Sequence 694, App
141	7	1.5	2647	2	US-08-779-113-8	Sequence 8, Appli	214	6	1.3	39	5	PCT-US92-07813-9	Sequence 9, Appli
142	7	1.5	2987	2	US-08-970-269A-29	Sequence 29, Appli	215	6	1.3	41	2	US-08-366-800-3	Sequence 3, Appli
143	7	1.5	2987	2	US-09-407-562-29	Sequence 29, Appli	216	6	1.3	43	2	US-08-499-676A-29	Sequence 29, Appli
144	7	1.5	3959	2	US-08-970-269A-30	Sequence 30, Appli	217	6	1.3	43	2	US-08-499-676A-30	Sequence 30, Appli
145	7	1.5	3959	2	US-09-407-562-30	Sequence 30, Appli	218	6	1.3	43	2	US-08-499-676A-31	Sequence 31, Appli
146	6	1.3	6	3	US-08-738-381-49	Sequence 49, Appli	219	6	1.3	44	4	US-09-314-268-157	Sequence 157, App
147	6	1.3	6	3	US-08-738-381-50	Sequence 50, Appli	220	6	1.3	44	4	US-08-905-223-345	Sequence 345, App
148	6	1.3	6	3	US-08-738-381-52	Sequence 52, Appli	221	6	1.3	45	1	US-08-062-472B-24	Sequence 24, Appli
149	6	1.3	6	1	US-08-199-776-13	Sequence 13, Appli	222	6	1.3	46	4	US-09-227-357-278	Sequence 278, App
150	6	1.3	10	1	US-08-199-776-14	Sequence 14, Appli	223	6	1.3	50	1	US-09-314-268-160	Sequence 160, App
151	6	1.3	10	1	US-08-199-776-15	Sequence 15, Appli	224	6	1.3	55	4	US-08-199-776-4	Sequence 4, Appli
152	6	1.3	10	1	US-08-199-776-16	Sequence 16, Appli	225	6	1.3	55	3	US-08-663-731-4	Sequence 4, Appli
153	6	1.3	10	3	US-08-663-731-13	Sequence 13, Appli	226	6	1.3	55	3	US-08-879-338-4	Sequence 4, Appli
154	6	1.3	10	3	US-08-663-731-14	Sequence 14, Appli	227	6	1.3	55	4	US-09-293-238B-4	Sequence 4, Appli
155	6	1.3	10	3	US-08-663-731-15	Sequence 15, Appli	228	6	1.3	55	5	PCT-US95-02044-4	Sequence 4, Appli
156	6	1.3	10	3	US-08-663-731-16	Sequence 16, Appli	229	6	1.3	60	3	US-08-955-337A-6	Sequence 6, Appli
157	6	1.3	10	3	US-08-879-338-13	Sequence 13, Appli	230	6	1.3	62	4	US-09-300-985-6	Sequence 6, Appli
158	6	1.3	10	3	US-08-879-338-14	Sequence 14, Appli	231	6	1.3	62	1	US-08-083-947-4	Sequence 4, Appli
159	6	1.3	10	3	US-08-879-338-15	Sequence 15, Appli	232	6	1.3	62	1	US-08-083-947-9	Sequence 9, Appli
160	6	1.3	10	3	US-08-879-338-16	Sequence 16, Appli	233	6	1.3	62	1	US-08-083-947-13	Sequence 13, Appli
161	6	1.3	10	4	US-09-293-238B-13	Sequence 13, Appli	234	6	1.3	62	5	PCT-US94-07088-4	Sequence 4, Appli
162	6	1.3	10	4	US-09-293-238B-14	Sequence 14, Appli	235	6	1.3	62	5	PCT-US94-07088-5	Sequence 5, Appli
163	6	1.3	10	4	US-09-293-238B-15	Sequence 15, Appli	236	6	1.3	62	5	PCT-US94-07088-13	Sequence 13, Appli
164	6	1.3	10	4	US-09-293-238B-16	Sequence 16, Appli	237	6	1.3	71	1	US-08-083-947-2	Sequence 2, Appli
165	6	1.3	10	5	PCT-US95-02044-13	Sequence 13, Appli	238	6	1.3	71	1	US-08-083-947-5	Sequence 5, Appli
166	6	1.3	10	5	PCT-US95-02044-14	Sequence 14, Appli	239	6	1.3	71	1	US-08-083-947-10	Sequence 10, Appli
167	6	1.3	10	5	PCT-US95-02044-15	Sequence 15, Appli	240	6	1.3	71	1	US-08-083-947-14	Sequence 14, Appli
168	6	1.3	10	5	PCT-US95-02044-16	Sequence 16, Appli	241	6	1.3	71	5	PCT-US94-07088-2	Sequence 2, Appli
169	6	1.3	12	3	US-08-199-776-22	Sequence 22, Appli	242	6	1.3	71	5	PCT-US94-07088-5	Sequence 5, Appli
170	6	1.3	12	3	US-08-663-731-22	Sequence 22, Appli	243	6	1.3	71	5	PCT-US94-07088-10	Sequence 10, Appli
171	6	1.3	12	3	US-08-879-338-22	Sequence 22, Appli	244	6	1.3	71	5	PCT-US94-07088-14	Sequence 14, Appli
172	6	1.3	12	4	US-09-752-165-53	Sequence 53, Appli	245	6	1.3	77	5	US-08-530-550-6	Sequence 6, Appli
173	6	1.3	12	4	US-09-293-238B-22	Sequence 22, Appli	246	6	1.3	77	5	PCT-US95-13660-6	Sequence 6, Appli

247	6	1.3	77	6	5175095-5	Patent No. 5175095	320	6	1.3	137	4	US-09-325-932A-170	Sequence 170, App
248	6	1.3	80	4	US-09-145-828A-3	Sequence 3, Appl1	321	6	1.3	140	2	US-08-483-636-4	Sequence 4, Appl1
249	6	1.3	81	1	US-08-083-947-1	Sequence 1, Appl1	322	6	1.3	140	2	US-08-483-637-4	Sequence 4, Appl1
250	6	1.3	81	1	US-08-083-947-6	Sequence 6, Appl1	323	6	1.3	142	4	US-09-134-001C-4136	Sequence 4136, Ap
251	6	1.3	81	1	US-08-083-947-11	Sequence 11, Appl1	324	6	1.3	144	2	US-08-186-895-10	Sequence 10, Appl
252	6	1.3	81	1	US-08-083-947-15	Sequence 15, Appl1	325	6	1.3	144	2	US-08-888-497-37	Sequence 37, Appl
253	6	1.3	81	1	US-08-530-550-4	Sequence 4, Appl1	326	6	1.3	144	2	US-09-362-230-37	Sequence 37, Appl
254	6	1.3	81	1	US-08-530-550-7	Sequence 7, Appl1	327	6	1.3	144	5	PCT-US94-07926-37	Sequence 37, Appl
255	6	1.3	81	1	US-08-530-550-8	Sequence 8, Appl1	328	6	1.3	144	6	5187153-18	Patent No. 5187153
256	6	1.3	81	1	US-08-530-550-9	Sequence 9, Appl1	329	6	1.3	145	2	US-08-832-535-11	Sequence 11, Appl
257	6	1.3	81	1	US-08-530-550-10	Sequence 10, Appl1	330	6	1.3	146	2	US-08-791-522-3	Sequence 3, Appl1
258	6	1.3	81	1	US-08-530-550-11	Sequence 11, Appl1	331	6	1.3	146	3	US-08-744-138-3	Sequence 4, Appl1
259	6	1.3	81	1	US-08-530-550-12	Sequence 12, Appl1	332	6	1.3	146	3	US-09-019-485-4	Sequence 3, Appl1
260	6	1.3	81	1	US-08-530-550-13	Sequence 13, Appl1	333	6	1.3	146	3	US-09-314-777-3	Sequence 3, Appl1
261	6	1.3	81	1	US-08-530-550-14	Sequence 14, Appl1	334	6	1.3	146	4	US-09-431-480-6	Sequence 6, Appl1
262	6	1.3	81	1	US-08-530-550-15	Sequence 15, Appl1	335	6	1.3	146	4	US-09-617-302-6	Sequence 6, Appl1
263	6	1.3	81	5	PCT-US94-07088-1	Sequence 1, Appl1	336	6	1.3	146	4	US-09-241-376-3	Sequence 3, Appl1
264	6	1.3	81	5	PCT-US94-07088-6	Sequence 11, Appl1	337	6	1.3	146	5	PCT-US95-07135-9	Sequence 9, Appl1
265	6	1.3	81	5	PCT-US94-07088-11	Sequence 15, Appl1	338	6	1.3	146	6	5432264-6	Patent No. 5432264
266	6	1.3	81	5	PCT-US95-13660-4	Sequence 4, Appl1	339	6	1.3	151	2	US-08-637-759B-349	Sequence 349, App
267	6	1.3	81	5	PCT-US95-13660-7	Sequence 7, Appl1	340	6	1.3	151	3	US-08-871-355A-349	Sequence 349, App
268	6	1.3	81	5	PCT-US95-13660-8	Sequence 8, Appl1	341	6	1.3	151	4	US-09-201-942-349	Sequence 349, App
269	6	1.3	81	5	PCT-US95-13660-9	Sequence 9, Appl1	342	6	1.3	153	3	US-08-943-173-1	Sequence 1, Appl1
270	6	1.3	81	5	PCT-US95-13660-10	Sequence 10, Appl1	343	6	1.3	155	1	US-08-530-010-13	Sequence 13, Appl1
271	6	1.3	81	5	PCT-US95-13660-11	Sequence 11, Appl1	344	6	1.3	155	2	US-08-484-101B-13	Sequence 13, Appl1
272	6	1.3	81	5	PCT-US95-13660-12	Sequence 12, Appl1	345	6	1.3	155	4	US-08-714-524D-13	Sequence 13, Appl1
273	6	1.3	81	5	PCT-US95-13660-13	Sequence 13, Appl1	346	6	1.3	157	2	US-08-883-070-3	Sequence 3, Appl1
274	6	1.3	81	5	PCT-US95-13660-14	Sequence 14, Appl1	347	6	1.3	159	1	US-07-853-985A-8	Sequence 8, Appl1
275	6	1.3	81	5	PCT-US95-13660-15	Sequence 15, Appl1	348	6	1.3	159	1	US-07-681-703B-8	Sequence 8, Appl1
276	6	1.3	81	5	PCT-US95-13660-16	Sequence 16, Appl1	349	6	1.3	159	1	US-08-184-236-8	Sequence 8, Appl1
277	6	1.3	83	2	US-08-499-676A-10	Sequence 10, Appl1	350	6	1.3	159	2	US-08-407-410B-8	Sequence 8, Appl1
278	6	1.3	83	2	US-08-499-676A-11	Sequence 11, Appl1	351	6	1.3	159	2	US-08-485-500-8	Sequence 8, Appl1
279	6	1.3	83	2	US-08-499-676A-12	Sequence 12, Appl1	352	6	1.3	159	5	PCT-US91-02370-8	Sequence 8, Appl1
280	6	1.3	84	1	US-08-083-947-8	Sequence 8, Appl1	353	6	1.3	159	5	PCT-US94-04174-8	Sequence 8, Appl1
281	6	1.3	84	1	US-08-530-550-21	Sequence 21, Appl1	354	6	1.3	160	4	US-09-247-155-156	Sequence 156, App
282	6	1.3	84	5	PCT-US94-07088-8	Sequence 21, Appl1	355	6	1.3	162	1	US-07-879-685B-4	Sequence 4, Appl1
283	6	1.3	84	5	PCT-US95-13660-21	Sequence 21, Appl1	356	6	1.3	170	2	US-08-820-170A-22	Sequence 22, Appl1
284	6	1.3	89	4	US-08-444-818-22	Sequence 408, App	357	6	1.3	170	2	US-08-918-723-1	Sequence 1, Appl1
285	6	1.3	92	4	US-08-905-223-408	Sequence 2, Appl1	358	6	1.3	170	2	US-09-237-507-1	Sequence 2, Appl1
286	6	1.3	93	1	US-08-083-947-7	Sequence 7, Appl1	359	6	1.3	170	3	US-09-055-699-22	Sequence 22, Appl1
287	6	1.3	93	1	US-08-083-947-12	Sequence 12, Appl1	360	6	1.3	170	3	US-09-069-896-1	Sequence 1, Appl1
288	6	1.3	93	5	PCT-US94-07088-7	Sequence 7, Appl1	361	6	1.3	170	4	US-09-273-565-22	Sequence 22, Appl1
289	6	1.3	93	5	PCT-US94-07088-12	Sequence 12, Appl1	362	6	1.3	170	4	US-09-565-538-22	Sequence 22, Appl1
290	6	1.3	93	5	PCT-US94-07088-12	Sequence 12, Appl1	363	6	1.3	170	4	US-09-661-468-22	Sequence 22, Appl1
291	6	1.3	98	4	US-09-020-846-40	Sequence 40, Appl1	364	6	1.3	170	4	US-09-661-468-1	Sequence 1, Appl1
292	6	1.3	102	1	US-08-350-884-80	Sequence 80, Appl1	365	6	1.3	173	2	US-08-537-811-43	Sequence 43, Appl1
293	6	1.3	102	1	US-08-709-173-80	Sequence 80, Appl1	366	6	1.3	178	2	US-08-487-031-23	Sequence 23, Appl1
294	6	1.3	102	2	US-08-411-913-9	Sequence 9, Appl1	367	6	1.3	178	3	US-08-473-034-23	Sequence 23, Appl1
295	6	1.3	102	2	US-08-709-177-80	Sequence 80, Appl1	368	6	1.3	178	4	US-08-259-451-15	Sequence 15, Appl1
296	6	1.3	102	2	US-08-444-818-144	Sequence 144, App	369	6	1.3	180	1	US-08-062-472B-7	Sequence 7, Appl1
297	6	1.3	105	2	US-08-487-031-20	Sequence 20, Appl1	370	6	1.3	182	1	US-08-466-603-5	Sequence 5, Appl1
298	6	1.3	105	3	US-08-473-034-20	Sequence 20, Appl1	371	6	1.3	182	1	US-08-314-503A-5	Sequence 5, Appl1
299	6	1.3	105	4	US-09-149-476-479	Sequence 479, App	372	6	1.3	182	1	US-08-468-066-5	Sequence 5, Appl1
300	6	1.3	106	1	US-08-290-919-11	Sequence 11, Appl1	373	6	1.3	182	2	US-08-466-717-5	Sequence 5, Appl1
301	6	1.3	107	2	US-08-647-144-6	Sequence 6, Appl1	374	6	1.3	182	3	US-08-466-741-5	Sequence 5, Appl1
302	6	1.3	115	4	US-09-145-828A-15	Sequence 15, Appl1	375	6	1.3	182	5	PCT-US95-12414-5	Sequence 5, Appl1
303	6	1.3	116	3	US-08-621-018B-4	Sequence 4, Appl1	376	6	1.3	186	1	US-07-853-985A-10	Sequence 10, Appl1
304	6	1.3	120	4	US-08-751-359-25	Sequence 25, Appl1	377	6	1.3	186	1	US-07-681-703B-10	Sequence 10, Appl1
305	6	1.3	120	4	US-08-907-146-25	Sequence 25, Appl1	378	6	1.3	186	1	US-08-184-236-10	Sequence 10, Appl1
306	6	1.3	123	1	US-08-398-613A-20	Sequence 20, Appl1	379	6	1.3	186	2	US-08-407-410B-10	Sequence 10, Appl1
307	6	1.3	123	1	US-08-398-612A-20	Sequence 20, Appl1	380	6	1.3	186	2	US-08-485-500-10	Sequence 10, Appl1
308	6	1.3	123	1	US-08-398-611A-20	Sequence 20, Appl1	381	6	1.3	186	5	PCT-US91-02370-10	Sequence 10, Appl1
309	6	1.3	123	2	US-08-491-334A-20	Sequence 20, Appl1	382	6	1.3	186	5	PCT-US94-04174-10	Sequence 10, Appl1
310	6	1.3	123	2	US-08-822-573-2	Sequence 2, Appl1	383	6	1.3	190	4	US-08-918-428D-3	Sequence 3, Appl1
311	6	1.3	123	3	US-09-027-449-17	Sequence 17, Appl1	384	6	1.3	194	4	US-08-959-004-9	Sequence 9, Appl1
312	6	1.3	123	3	US-08-804-444A-17	Sequence 17, Appl1	385	6	1.3	196	3	US-09-122-443-4	Sequence 4, Appl1
313	6	1.3	123	4	US-09-026-985-17	Sequence 17, Appl1	386	6	1.3	199	4	US-09-134-001C-4391	Sequence 4391, Ap
314	6	1.3	123	4	US-09-121-952A-17	Sequence 17, Appl1	387	6	1.3	200	4	US-08-469-260A-395	Sequence 395, App
315	6	1.3	123	4	US-09-234-340A-17	Sequence 17, Appl1	388	6	1.3	201	2	US-08-716-317-1	Sequence 13, Appl1
316	6	1.3	123	6	5466783-22	Patent No. 5466783	389	6	1.3	207	3	US-08-559-397A-13	Sequence 13, Appl1
317	6	1.3	124	4	US-08-307-499-2	Sequence 2, Appl1	390	6	1.3	209	3	US-08-559-397A-11	Sequence 11, Appl1
318	6	1.3	124	4	US-09-299-268-2	Sequence 2, Appl1	391	6	1.3	212	4	US-08-937-067-4	Sequence 4, Appl1
319	6	1.3	125	4	US-08-905-223-320	Sequence 320, App	392	6	1.3	219	1	US-08-441-629-13	Sequence 13, Appl1

393	6	1.3	219	3	US-08-776-207-13	Sequence 13, Appl
394	6	1.3	219	4	US-09-507-773-13	Sequence 13, Appl
395	6	1.3	219	5	PCT-US95-09172-13	Sequence 13, Appl
396	6	1.3	222	1	US-07-688-352C-46	Sequence 46, Appl
397	6	1.3	222	4	US-09-134-001C-4748	Sequence 4748, Ap
398	6	1.3	222	5	PCT-US91-02274-43	Sequence 43, Appl
399	6	1.3	222	5	PCT-US91-02274-54	Sequence 54, Appl
400	6	1.3	228	1	US-08-278-091-10	Sequence 10, Appl
401	6	1.3	228	1	US-08-483-859-10	Sequence 10, Appl
402	6	1.3	228	1	US-08-472-173-10	Sequence 10, Appl
403	6	1.3	228	2	US-08-487-167-10	Sequence 10, Appl
404	6	1.3	228	2	US-08-482-816-10	Sequence 10, Appl
405	6	1.3	228	2	US-08-296-149-10	Sequence 10, Appl
406	6	1.3	228	2	US-08-801-499-10	Sequence 10, Appl
407	6	1.3	228	2	US-08-615-271-10	Sequence 10, Appl
408	6	1.3	228	3	US-09-074-660-10	Sequence 10, Appl
409	6	1.3	228	3	US-09-074-659-10	Sequence 10, Appl
410	6	1.3	228	3	US-09-106-468-10	Sequence 10, Appl
411	6	1.3	228	4	US-09-106-468A-10	Sequence 10, Appl
412	6	1.3	228	4	US-09-106-467-10	Sequence 10, Appl
413	6	1.3	231	1	US-08-220-379B-7	Sequence 7, Appl
414	6	1.3	231	1	US-08-243-545-2	Sequence 2, Appl
415	6	1.3	231	2	US-08-993-962-2	Sequence 2, Appl
416	6	1.3	231	4	US-09-160-841-2	Sequence 2, Appl
417	6	1.3	231	5	PCT-US94-05365-2	Sequence 2, Appl
418	6	1.3	231	5	PCT-US95-03866-6	Sequence 6, Appl
419	6	1.3	233	1	US-08-032-848C-12	Sequence 12, Appl
420	6	1.3	235	3	US-08-836-236-6	Sequence 6, Appl
421	6	1.3	236	1	US-08-118-270-74	Sequence 74, Appl
422	6	1.3	236	5	PCT-US93-08528-74	Sequence 74, Appl
423	6	1.3	237	1	US-08-398-612A-28	Sequence 28, Appl
424	6	1.3	237	1	US-08-398-611A-28	Sequence 28, Appl
425	6	1.3	237	2	US-08-491-334A-28	Sequence 28, Appl
426	6	1.3	237	3	US-09-027-449-25	Sequence 25, Appl
427	6	1.3	237	3	US-08-804-444A-25	Sequence 25, Appl
428	6	1.3	237	4	US-09-026-985-25	Sequence 25, Appl
429	6	1.3	237	4	US-09-121-952A-25	Sequence 25, Appl
430	6	1.3	237	4	US-09-234-340A-25	Sequence 25, Appl
431	6	1.3	238	1	US-08-398-613A-28	Sequence 28, Appl
432	6	1.3	238	4	US-09-111-470-8	Sequence 8, Appl
433	6	1.3	240	1	US-08-278-091-11	Sequence 11, Appl
434	6	1.3	240	1	US-08-483-859-11	Sequence 11, Appl
435	6	1.3	240	1	US-08-472-173-11	Sequence 11, Appl
436	6	1.3	240	2	US-08-114-555A-6	Sequence 6, Appl
437	6	1.3	240	2	US-08-114-555A-8	Sequence 8, Appl
438	6	1.3	240	2	US-08-487-167-11	Sequence 11, Appl
439	6	1.3	240	2	US-08-482-816-11	Sequence 11, Appl
440	6	1.3	240	2	US-08-296-149-11	Sequence 11, Appl
441	6	1.3	240	2	US-08-801-499-11	Sequence 11, Appl
442	6	1.3	240	2	US-08-760-745-3	Sequence 3, Appl
443	6	1.3	240	2	US-08-615-271-11	Sequence 11, Appl
444	6	1.3	240	3	US-09-074-660-11	Sequence 11, Appl
445	6	1.3	240	3	US-09-074-659-11	Sequence 11, Appl
446	6	1.3	240	3	US-08-559-397A-12	Sequence 12, Appl
447	6	1.3	240	3	US-08-559-397A-14	Sequence 14, Appl
448	6	1.3	240	3	US-09-106-468-11	Sequence 11, Appl
449	6	1.3	240	4	US-09-106-466A-11	Sequence 11, Appl
450	6	1.3	240	4	US-09-106-467-11	Sequence 11, Appl
451	6	1.3	246	4	US-08-634-475-3	Sequence 3, Appl
452	6	1.3	246	4	US-09-709-791-3	Sequence 3, Appl
453	6	1.3	249	1	US-08-466-603-2	Sequence 2, Appl
454	6	1.3	249	1	US-08-314-503A-2	Sequence 2, Appl
455	6	1.3	249	1	US-08-468-066-2	Sequence 2, Appl
456	6	1.3	249	2	US-08-466-717-2	Sequence 2, Appl
457	6	1.3	249	2	US-08-766-738-4	Sequence 4, Appl
458	6	1.3	249	2	US-09-154-802-1	Sequence 1, Appl
459	6	1.3	249	3	US-09-373-029-1	Sequence 1, Appl
460	6	1.3	249	3	US-08-466-743-2	Sequence 2, Appl
461	6	1.3	249	4	US-09-262-610-4	Sequence 4, Appl
462	6	1.3	249	5	PCT-US95-12414-2	Sequence 2, Appl
463	6	1.3	251	4	US-08-766-738-3	Sequence 3, Appl
464	6	1.3	251	4	US-09-262-610-3	Sequence 3, Appl
465	6	1.3	253	2	US-08-474-379C-46	Sequence 46, Appl
466	6	1.3	253	3	US-09-146-249A-46	Sequence 46, Appl
467	6	1.3	253	3	US-08-206-188B-46	Sequence 46, Appl
468	6	1.3	254	4	US-09-134-001C-4582	Sequence 4582, Ap
469	6	1.3	256	4	US-09-325-932A-57	Sequence 57, Appl
470	6	1.3	260	4	US-09-216-295-23	Sequence 23, Appl
471	6	1.3	263	4	US-09-216-295-24	Sequence 24, Appl
472	6	1.3	266	4	US-08-444-818-32	Sequence 32, Appl
473	6	1.3	266	4	US-08-850-328-7	Sequence 7, Appl
474	6	1.3	266	4	US-09-417-721-9	Sequence 9, Appl
475	6	1.3	266	4	US-09-417-721-15	Sequence 15, Appl
476	6	1.3	266	6	5175383-5	Patent No. 5175383
477	6	1.3	267	1	US-08-462-159B-13	Sequence 13, Appl
478	6	1.3	267	3	US-09-103-079-13	Sequence 13, Appl
479	6	1.3	267	4	US-08-871-572B-7	Sequence 7, Appl
480	6	1.3	268	1	US-08-439-725A-12	Sequence 12, Appl
481	6	1.3	268	1	US-08-464-590A-17	Sequence 17, Appl
482	6	1.3	268	2	US-08-207-412B-12	Sequence 12, Appl
483	6	1.3	268	2	US-08-867-471-12	Sequence 12, Appl
484	6	1.3	268	2	US-08-438-439C-8	Sequence 8, Appl
485	6	1.3	268	2	US-08-951-822-33	Sequence 33, Appl
486	6	1.3	268	3	US-08-705-245-14	Sequence 14, Appl
487	6	1.3	268	3	US-08-718-904-14	Sequence 14, Appl
488	6	1.3	268	3	US-09-023-082A-15	Sequence 15, Appl
489	6	1.3	268	3	US-09-093-585-17	Sequence 17, Appl
490	6	1.3	268	4	US-09-240-952-2	Sequence 2, Appl
491	6	1.3	268	4	US-09-368-951-13	Sequence 13, Appl
492	6	1.3	269	2	US-08-438-439C-18	Sequence 18, Appl
493	6	1.3	270	2	US-07-857-224B-76	Sequence 76, Appl
494	6	1.3	270	4	US-09-399-913-59	Sequence 59, Appl
495	6	1.3	272	1	US-08-350-884-84	Sequence 84, Appl
496	6	1.3	272	1	US-08-709-173-84	Sequence 84, Appl
497	6	1.3	272	2	US-08-709-177-84	Sequence 84, Appl
498	6	1.3	280	4	US-09-720-817-1	Sequence 1, Appl
499	6	1.3	280	4	US-09-145-828A-21	Sequence 21, Appl
500	6	1.3	283	4	US-09-134-001C-5491	Sequence 5491, Ap
501	6	1.3	289	4	US-09-145-828A-17	Sequence 17, Appl
502	6	1.3	293	4	US-09-145-828A-12	Sequence 12, Appl
503	6	1.3	295	3	US-08-511-759B-2	Sequence 2, Appl
504	6	1.3	295	4	US-09-592-197-2	Sequence 2, Appl
505	6	1.3	295	4	US-08-892-704-2	Sequence 2, Appl
506	6	1.3	296	4	US-09-134-001C-4473	Sequence 4473, Ap
507	6	1.3	297	3	US-09-187-049-10	Sequence 10, Appl
508	6	1.3	297	4	US-09-134-001C-3397	Sequence 3397, Ap
509	6	1.3	298	1	US-08-393-985-10	Sequence 10, Appl
510	6	1.3	298	4	US-09-134-001C-3631	Sequence 3631, Ap
511	6	1.3	300	4	US-09-194-146-6	Sequence 6, Appl
512	6	1.3	302	3	US-08-511-759B-9	Sequence 9, Appl
513	6	1.3	302	4	US-09-592-197-9	Sequence 9, Appl
514	6	1.3	302	4	US-08-892-704-9	Sequence 9, Appl
515	6	1.3	313	3	US-08-926-842B-62	Sequence 62, Appl
516	6	1.3	315	4	US-09-720-817-3	Sequence 3, Appl
517	6	1.3	315	4	US-09-720-817-6	Sequence 6, Appl
518	6	1.3	317	4	US-09-145-828A-7	Sequence 7, Appl
519	6	1.3	318	4	US-08-878-474-3	Sequence 3, Appl
520	6	1.3	318	4	US-09-483-371-2	Sequence 2, Appl
521	6	1.3	318	4	US-09-145-828A-19	Sequence 19, Appl
522	6	1.3	319	4	US-09-008-697A-6	Sequence 6, Appl
523	6	1.3	320	1	US-08-365-103B-10	Sequence 10, Appl
524	6	1.3	320	4	US-09-134-001C-4133	Sequence 4133, Ap
525	6	1.3	321	1	US-08-365-103B-8	Sequence 8, Appl
526	6	1.3	324	4	US-09-134-001C-3365	Sequence 3365, Ap
527	6	1.3	327	4	US-09-134-001C-2889	Sequence 2889, Ap
528	6	1.3	332	4	US-09-134-001C-3199	Sequence 3199, Ap
529	6	1.3	333	1	US-08-148-215A-4	Sequence 4, Appl
530	6	1.3	333	3	US-08-988-876-6	Sequence 6, Appl
531	6	1.3	347	1	US-08-249-420-2	Sequence 2, Appl
532	6	1.3	347	2	US-08-737-663-2	Sequence 2, Appl
533	6	1.3	347	4	US-09-145-828A-16	Sequence 16, Appl
534	6	1.3	348	4	US-08-430-286A-11	Sequence 11, Appl
535	6	1.3	348	4	US-09-134-001C-4857	Sequence 4857, Ap
536	6	1.3	350	6	5352575-7	Patent No. 5352575
537	6	1.3	351	3	US-08-688-988-28	Sequence 28, Appl
538	6	1.3	353	4	US-09-134-001C-4252	Sequence 4252, Ap

539	6	1.3	354	3	US-08-688-988-29	Sequence 29, Appl	612	6	1.3	452	1	US-07-937-609-16	Sequence 16, Appl
540	6	1.3	359	3	US-08-688-988-32	Sequence 32, Appl	613	6	1.3	452	4	US-08-029-170-16	Sequence 16, Appl
541	6	1.3	359	3	US-09-082-089-3	Sequence 3, Appl	614	6	1.3	453	1	US-07-937-609-26	Sequence 26, Appl
542	6	1.3	363	3	US-09-082-089-5	Sequence 5, Appl	615	6	1.3	453	1	US-07-937-609-27	Sequence 27, Appl
543	6	1.3	366	1	US-08-700-359-22	Sequence 22, Appl	616	6	1.3	453	1	US-07-978-892A-5	Sequence 5, Appl
544	6	1.3	369	1	US-08-844-055-2	Sequence 2, Appl	617	6	1.3	453	1	US-08-570-157-4	Sequence 4, Appl
545	6	1.3	370	3	US-09-006-849-2	Sequence 2, Appl	618	6	1.3	453	4	US-08-029-170-26	Sequence 26, Appl
546	6	1.3	369	3	US-09-325-932A-169	Sequence 169, App	619	6	1.3	453	4	US-08-029-170-27	Sequence 27, Appl
547	6	1.3	372	3	US-09-082-089-2	Sequence 2, Appl	620	6	1.3	453	4	US-09-076-510-4	Sequence 4, Appl
548	6	1.3	386	4	US-09-293-322C-5	Sequence 5, Appl	621	6	1.3	457	4	US-08-821-818-1	Sequence 1, Appl
549	6	1.3	386	4	US-09-134-001C-3809	Sequence 3809, Ap	622	6	1.3	457	4	US-08-821-818-5	Sequence 5, Appl
550	6	1.3	390	3	US-08-689-421-21	Sequence 21, Appl	623	6	1.3	463	3	US-09-082-310-1	Sequence 1, Appl
551	6	1.3	390	3	US-08-650-766-7	Sequence 7, Appl	624	6	1.3	463	3	US-09-575-205-1	Sequence 1, Appl
552	6	1.3	390	3	US-08-922-635-6	Sequence 6, Appl	625	6	1.3	465	2	US-08-114-555A-2	Sequence 2, Appl
553	6	1.3	390	3	US-09-389-528-21	Sequence 21, Appl	626	6	1.3	465	2	US-08-833-678A-2	Sequence 2, Appl
554	6	1.3	390	4	US-09-181-827A-21	Sequence 21, Appl	627	6	1.3	465	3	US-08-553-397A-2	Sequence 2, Appl
555	6	1.3	391	4	US-09-134-001C-3442	Sequence 3442, Ap	628	6	1.3	465	4	US-08-529-169A-2	Sequence 2, Appl
556	6	1.3	392	4	US-09-378-088A-90	Sequence 90, Appl	629	6	1.3	470	2	US-08-466-906B-8	Sequence 8, Appl
557	6	1.3	393	1	US-07-629-1041-3	Sequence 3, Appl	630	6	1.3	470	2	US-09-201-746-8	Sequence 8, Appl
558	6	1.3	393	2	US-08-977-554-2	Sequence 2, Appl	631	6	1.3	475	2	US-08-861-464-14	Sequence 14, Appl
559	6	1.3	393	4	US-09-225-967-2	Sequence 2, Appl	632	6	1.3	475	2	US-08-396-001-14	Sequence 14, Appl
560	6	1.3	393	4	US-09-227-806-2	Sequence 2, Appl	633	6	1.3	475	2	US-09-323-433A-14	Sequence 14, Appl
561	6	1.3	397	4	US-09-459-113-2	Sequence 2, Appl	634	6	1.3	479	4	US-08-416-788-2	Sequence 2, Appl
562	6	1.3	398	2	US-08-288-663A-15	Sequence 15, Appl	635	6	1.3	481	1	US-08-286-856C-2	Sequence 2, Appl
563	6	1.3	400	1	US-07-989-991A-2	Sequence 2, Appl	636	6	1.3	481	1	US-08-477-831-2	Sequence 2, Appl
564	6	1.3	400	3	US-08-621-255-2	Sequence 2, Appl	637	6	1.3	486	3	US-08-904-452-2	Sequence 2, Appl
565	6	1.3	400	4	US-09-352-574-2	Sequence 2, Appl	638	6	1.3	486	4	US-08-295-451-13	Sequence 13, Appl
566	6	1.3	402	1	US-08-553-703A-1	Sequence 1, Appl	639	6	1.3	486	4	US-09-517-639-2	Sequence 2, Appl
567	6	1.3	402	1	US-08-553-703A-4	Sequence 4, Appl	640	6	1.3	493	2	US-09-031-392-10	Sequence 10, Appl
568	6	1.3	402	2	US-09-006-021-1	Sequence 1, Appl	641	6	1.3	493	4	US-09-299-549-10	Sequence 10, Appl
569	6	1.3	406	2	US-09-006-021-4	Sequence 4, Appl	642	6	1.3	493	4	US-09-610-417-10	Sequence 10, Appl
570	6	1.3	406	3	US-08-434-881-2	Sequence 2, Appl	643	6	1.3	494	4	US-09-134-001C-1176	Sequence 4176, Ap
571	6	1.3	406	3	US-08-977-771-2	Sequence 2, Appl	644	6	1.3	496	4	US-09-350-268-2	Sequence 2, Appl
572	6	1.3	406	4	US-09-361-773-2	Sequence 2, Appl	645	6	1.3	496	4	US-09-558-679-2	Sequence 2, Appl
573	6	1.3	406	4	US-09-336-536-23	Sequence 23, Appl	646	6	1.3	496	2	US-08-702-598-2	Sequence 2, Appl
574	6	1.3	410	6	5177197-1	Patent No. 5177197	647	6	1.3	498	4	US-09-134-607A-17	Sequence 17, Appl
575	6	1.3	414	1	US-07-667-276A-4	Sequence 11, Appl	648	6	1.3	498	4	US-09-134-607A-18	Sequence 18, Appl
576	6	1.3	415	4	US-08-795-430-11	Sequence 11, Appl	649	6	1.3	498	4	US-09-134-607A-19	Sequence 19, Appl
577	6	1.3	415	4	US-09-355-700-11	Sequence 11, Appl	650	6	1.3	500	1	US-07-755-573C-8	Sequence 8, Appl
578	6	1.3	415	4	US-08-601-132-41	Sequence 41, Appl	651	6	1.3	500	2	US-08-316-601-2	Sequence 2, Appl
579	6	1.3	418	1	US-07-816-283-10	Sequence 10, Appl	652	6	1.3	501	2	PCT-US95-13051-2	Sequence 40, Appl
580	6	1.3	418	1	US-08-417-103-3	Sequence 10, Appl	653	6	1.3	501	2	US-08-577-492A-10	Sequence 40, Appl
581	6	1.3	419	1	US-08-615-170-16	Sequence 16, Appl	654	6	1.3	501	2	US-08-408-095-31	Sequence 31, Appl
582	6	1.3	418	4	US-09-134-001C-3441	Sequence 3441, Ap	655	6	1.3	501	4	US-09-079-630-40	Sequence 40, Appl
583	6	1.3	421	3	US-09-002-567B-1	Sequence 1, Appl	656	6	1.3	505	1	US-09-041-075A-8	Sequence 8, Appl
584	6	1.3	421	3	US-09-002-567B-3	Sequence 3, Appl	657	6	1.3	506	1	US-08-286-856C-3	Sequence 3, Appl
585	6	1.3	421	4	US-09-020-846-68	Sequence 68, Appl	658	6	1.3	506	1	US-08-472-831-3	Sequence 3, Appl
586	6	1.3	421	4	US-09-571-347-1	Sequence 1, Appl	659	6	1.3	508	2	US-08-850-293-5	Sequence 5, Appl
587	6	1.3	421	4	US-09-571-347-3	Sequence 3, Appl	660	6	1.3	513	4	US-08-867-611-59	Sequence 59, Appl
588	6	1.3	424	4	US-09-134-001C-5009	Sequence 5009, Ap	661	6	1.3	517	3	US-08-688-421-33	Sequence 33, Appl
589	6	1.3	426	1	US-08-615-170-6	Sequence 6, Appl	662	6	1.3	517	4	US-09-388-528-33	Sequence 33, Appl
590	6	1.3	426	1	US-08-615-170-15	Sequence 15, Appl	663	6	1.3	517	4	US-09-181-827A-33	Sequence 33, Appl
591	6	1.3	428	1	US-07-816-283-12	Sequence 12, Appl	664	6	1.3	521	4	US-09-258-349-2	Sequence 2, Appl
592	6	1.3	429	1	US-08-906-744A-2	Sequence 2, Appl	665	6	1.3	532	1	US-08-333-152A-32	Sequence 32, Appl
593	6	1.3	431	1	US-09-093-134-2	Sequence 2, Appl	666	6	1.3	534	4	US-09-029-348-5	Sequence 5, Appl
594	6	1.3	431	1	US-08-190-802A-37	Sequence 37, Appl	667	6	1.3	535	4	US-09-029-348-1	Sequence 1, Appl
595	6	1.3	431	4	US-08-477-346-37	Sequence 37, Appl	668	6	1.3	537	4	US-09-029-348-4	Sequence 4, Appl
596	6	1.3	431	4	US-08-473-089-37	Sequence 37, Appl	669	6	1.3	538	4	US-09-647-390-16	Sequence 16, Appl
597	6	1.3	431	4	US-08-487-072A-37	Sequence 37, Appl	670	6	1.3	542	1	US-08-140-729A-5	Sequence 5, Appl
598	6	1.3	437	4	US-09-134-001C-4808	Sequence 4808, Ap	671	6	1.3	542	1	US-08-701-380-2	Sequence 2, Appl
599	6	1.3	437	2	US-08-577-492-38	Sequence 38, Appl	672	6	1.3	542	1	US-08-546-666-5	Sequence 5, Appl
600	6	1.3	438	4	US-09-079-630-38	Sequence 38, Appl	673	6	1.3	542	2	US-08-916-745-5	Sequence 5, Appl
601	6	1.3	438	4	US-09-339-838-5	Sequence 5, Appl	674	6	1.3	542	2	US-08-948-569A-2	Sequence 2, Appl
602	6	1.3	438	4	US-09-339-838-7	Sequence 7, Appl	675	6	1.3	542	2	US-08-663-808-4	Sequence 2, Appl
603	6	1.3	441	4	US-09-522-666-4	Sequence 4, Appl	676	6	1.3	542	2	US-09-042-929-5	Sequence 5, Appl
604	6	1.3	441	1	US-07-937-609-29	Sequence 29, Appl	677	6	1.3	542	2	US-08-546-661-5	Sequence 5, Appl
605	6	1.3	447	1	US-07-978-892A-6	Sequence 6, Appl	678	6	1.3	542	2	US-09-042-960-5	Sequence 5, Appl
606	6	1.3	447	1	US-08-029-170-29	Sequence 29, Appl	679	6	1.3	542	2	US-09-188-469-2	Sequence 2, Appl
607	6	1.3	448	1	US-08-570-157-3	Sequence 3, Appl	680	6	1.3	542	3	US-09-198-650-5	Sequence 5, Appl
608	6	1.3	448	1	US-09-076-510-3	Sequence 3, Appl	681	6	1.3	542	3	US-09-332-740-4	Sequence 4, Appl
609	6	1.3	451	4	US-08-570-157-2	Sequence 2, Appl	682	6	1.3	542	3	US-09-042-913-5	Sequence 5, Appl
610	6	1.3	451	4	US-09-076-510-2	Sequence 2, Appl	683	6	1.3	542	3	US-09-188-496-4	Sequence 4, Appl
611	6	1.3	451	4	US-09-184-964-3	Sequence 3, Appl	684	6	1.3	542	3	US-09-042-937-5	Sequence 5, Appl

685	6	1.3	542	3	US-09-032-365A-13	Sequence 13, Appl	758	6	1.3	609	4	US-09-315-850-40	Sequence 40, Appl
686	6	1.3	542	4	US-09-397-283A-2	Sequence 2, Appl	759	6	1.3	631	1	US-08-700-356-1	Sequence 1, Appl
687	6	1.3	542	4	US-09-368-282-4	Sequence 4, Appl	760	6	1.3	631	2	US-08-936-865-1	Sequence 1, Appl
688	6	1.3	542	4	US-09-566-708A-4	Sequence 4, Appl	761	6	1.3	631	2	US-08-833-678A-1	Sequence 1, Appl
689	6	1.3	542	4	US-09-042-709A-5	Sequence 5, Appl	762	6	1.3	631	2	US-09-128-314-2	Sequence 2, Appl
690	6	1.3	543	2	US-08-469-412A-7	Sequence 7, Appl	763	6	1.3	631	4	US-08-529-169A-1	Sequence 1, Appl
691	6	1.3	543	4	US-09-021-715-7	Sequence 7, Appl	764	6	1.3	632	4	US-09-198-723A-23	Sequence 23, Appl
692	6	1.3	543	4	US-09-042-709A-18	Sequence 18, Appl	765	6	1.3	646	4	US-09-198-723A-60	Sequence 60, Appl
693	6	1.3	544	2	US-08-935-760-2	Sequence 2, Appl	766	6	1.3	646	4	US-09-198-723A-60	Sequence 60, Appl
694	6	1.3	544	2	US-08-559-397A-19	Sequence 19, Appl	767	6	1.3	646	4	US-09-198-723A-63	Sequence 63, Appl
695	6	1.3	544	2	US-08-559-397A-29	Sequence 29, Appl	768	6	1.3	646	4	US-09-198-723A-66	Sequence 66, Appl
696	6	1.3	548	2	US-08-469-412A-2	Sequence 2, Appl	769	6	1.3	646	4	US-09-198-723A-66	Sequence 66, Appl
697	6	1.3	548	2	US-09-032-315-4	Sequence 4, Appl	770	6	1.3	651	3	US-08-650-766-6	Sequence 6, Appl
698	6	1.3	548	2	US-08-993-318A-4	Sequence 4, Appl	771	6	1.3	651	3	US-08-922-635-5	Sequence 5, Appl
699	6	1.3	548	4	US-09-399-886-4	Sequence 4, Appl	772	6	1.3	656	2	US-08-523-669A-6	Sequence 6, Appl
700	6	1.3	548	4	US-09-396-260-4	Sequence 4, Appl	773	6	1.3	656	4	US-08-487-072A-34	Sequence 34, Appl
701	6	1.3	548	4	US-09-021-715-2	Sequence 2, Appl	774	6	1.3	658	4	US-08-477-346-34	Sequence 34, Appl
702	6	1.3	549	4	US-09-576-281-4	Sequence 4, Appl	775	6	1.3	658	4	US-08-473-089-34	Sequence 34, Appl
703	6	1.3	549	4	US-08-828-199A-3	Sequence 3, Appl	776	6	1.3	658	4	US-08-473-089-34	Sequence 34, Appl
704	6	1.3	553	2	US-08-943-087-2	Sequence 2, Appl	777	6	1.3	658	4	US-08-473-089-34	Sequence 34, Appl
705	6	1.3	553	2	US-08-943-087-14	Sequence 14, Appl	778	6	1.3	658	4	US-08-473-089-34	Sequence 34, Appl
706	6	1.3	553	2	US-08-943-087-16	Sequence 16, Appl	779	6	1.3	658	4	US-08-487-072A-34	Sequence 34, Appl
707	6	1.3	553	2	US-08-943-087-18	Sequence 18, Appl	780	6	1.3	661	1	US-08-514-014-4	Sequence 4, Appl
708	6	1.3	553	2	US-08-943-087-20	Sequence 20, Appl	781	6	1.3	661	1	US-08-232-538-12	Sequence 12, Appl
709	6	1.3	553	2	US-08-943-087-22	Sequence 22, Appl	782	6	1.3	661	2	US-08-786-164-12	Sequence 12, Appl
710	6	1.3	553	2	US-08-943-087-24	Sequence 24, Appl	783	6	1.3	661	2	US-08-833-823-4	Sequence 4, Appl
711	6	1.3	553	2	US-08-943-087-26	Sequence 26, Appl	784	6	1.3	666	2	US-08-737-716-14	Sequence 14, Appl
712	6	1.3	553	2	US-08-943-087-28	Sequence 28, Appl	785	6	1.3	666	4	US-09-138-723A-11	Sequence 11, Appl
713	6	1.3	553	2	US-08-943-087-30	Sequence 30, Appl	786	6	1.3	666	4	US-09-138-723A-12	Sequence 12, Appl
714	6	1.3	553	2	US-08-943-087-32	Sequence 32, Appl	787	6	1.3	666	4	US-09-138-723A-13	Sequence 13, Appl
715	6	1.3	553	2	US-08-943-087-34	Sequence 34, Appl	788	6	1.3	666	4	US-09-138-723A-14	Sequence 14, Appl
716	6	1.3	553	2	US-08-943-087-36	Sequence 36, Appl	789	6	1.3	666	4	US-09-138-723A-15	Sequence 15, Appl
717	6	1.3	553	2	US-08-943-087-38	Sequence 38, Appl	790	6	1.3	666	4	US-09-138-723A-16	Sequence 16, Appl
718	6	1.3	553	2	US-08-943-087-40	Sequence 40, Appl	791	6	1.3	666	4	US-09-138-723A-17	Sequence 17, Appl
719	6	1.3	553	2	US-08-943-087-42	Sequence 42, Appl	792	6	1.3	666	4	US-09-138-723A-18	Sequence 18, Appl
720	6	1.3	553	2	US-08-943-087-44	Sequence 44, Appl	793	6	1.3	667	2	US-08-718-661-2	Sequence 2, Appl
721	6	1.3	553	2	US-08-943-087-46	Sequence 46, Appl	794	6	1.3	668	4	US-09-134-001C-4816	Sequence 4816, Ap
722	6	1.3	553	2	US-08-943-087-48	Sequence 48, Appl	795	6	1.3	670	2	US-08-366-547-2	Sequence 2, Appl
723	6	1.3	556	1	US-08-943-087-11	Sequence 11, Appl	796	6	1.3	672	4	US-09-138-723A-19	Sequence 19, Appl
724	6	1.3	566	2	US-07-930-548A-11	Sequence 11, Appl	797	6	1.3	672	4	US-09-138-723A-20	Sequence 20, Appl
725	6	1.3	571	1	US-07-955-905A-25	Sequence 25, Appl	798	6	1.3	674	3	US-08-893-852A-1	Sequence 1, Appl
726	6	1.3	573	4	US-09-042-709A-19	Sequence 19, Appl	799	6	1.3	675	1	US-08-439-818A-9	Sequence 9, Appl
727	6	1.3	574	1	US-08-140-729A-7	Sequence 7, Appl	800	6	1.3	675	2	US-08-751-965-9	Sequence 9, Appl
728	6	1.3	574	1	US-08-546-666-7	Sequence 7, Appl	801	6	1.3	675	2	US-08-728-926-9	Sequence 9, Appl
729	6	1.3	574	2	US-08-916-745-7	Sequence 7, Appl	802	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
730	6	1.3	574	2	US-08-948-569A-4	Sequence 4, Appl	803	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
731	6	1.3	574	2	US-08-663-808-6	Sequence 6, Appl	804	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
732	6	1.3	574	2	US-09-042-929-7	Sequence 7, Appl	805	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
733	6	1.3	574	2	US-08-546-661-7	Sequence 7, Appl	806	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
734	6	1.3	574	2	US-09-042-960-7	Sequence 7, Appl	807	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
735	6	1.3	574	2	US-08-906-713-2	Sequence 2, Appl	808	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
736	6	1.3	574	2	US-09-188-469-4	Sequence 4, Appl	809	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
737	6	1.3	574	2	US-09-198-650-7	Sequence 7, Appl	810	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
738	6	1.3	574	3	US-09-332-740-6	Sequence 6, Appl	811	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
739	6	1.3	574	3	US-09-042-913-7	Sequence 6, Appl	812	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
740	6	1.3	574	3	US-09-188-496-6	Sequence 6, Appl	813	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
741	6	1.3	574	3	US-09-042-937-7	Sequence 7, Appl	814	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
742	6	1.3	574	3	US-09-397-238A-4	Sequence 4, Appl	815	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
743	6	1.3	574	4	US-09-368-282-6	Sequence 6, Appl	816	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
744	6	1.3	574	4	US-09-566-708A-6	Sequence 6, Appl	817	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
745	6	1.3	574	4	US-09-042-709A-7	Sequence 7, Appl	818	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
746	6	1.3	574	4	US-09-134-001C-4730	Sequence 4730, Ap	819	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
747	6	1.3	574	4	US-08-850-328-3	Sequence 3, Appl	820	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
748	6	1.3	590	4	US-09-197-814-3	Sequence 3, Appl	821	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
749	6	1.3	604	4	US-09-134-001C-4425	Sequence 4425, Ap	822	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
750	6	1.3	605	4	US-09-577-492-32	Sequence 32, Appl	823	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
751	6	1.3	606	2	US-08-620-077B-3	Sequence 3, Appl	824	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
752	6	1.3	606	3	US-08-079-630-32	Sequence 32, Appl	825	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
753	6	1.3	608	4	US-09-095-385-4	Sequence 4, Appl	826	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
754	6	1.3	608	4	US-09-134-001C-4751	Sequence 4751, Ap	827	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
755	6	1.3	609	1	US-08-324-977-40	Sequence 40, Appl	828	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
756	6	1.3	609	1	US-08-384-616-40	Sequence 40, Appl	829	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl
757	6	1.3	609	2	US-08-904-686A-40	Sequence 40, Appl	830	6	1.3	675	2	US-08-808-599A-9	Sequence 9, Appl

831	6	1.3	763	1	US-08-155-331-13	Sequence 13, Appl	504	6	1.3	1106	1	US-08-477-329-2	Sequence 2, Appl
832	6	1.3	763	1	US-08-424-022-13	Sequence 13, Appl	505	6	1.3	1106	2	US-08-475-458-2	Sequence 2, Appl
833	6	1.3	763	2	US-08-424-022-13	Sequence 13, Appl	506	6	1.3	1106	2	US-08-475-458-2	Sequence 2, Appl
834	6	1.3	763	5	PCT-US93-11696-13	Sequence 13, Appl	507	6	1.3	1106	2	US-08-460-50-2	Sequence 2, Appl
835	6	1.3	780	1	US-08-232-538-14	Sequence 14, Appl	508	6	1.3	1106	3	US-08-980-400-2	Sequence 4, Appl
836	6	1.3	780	2	US-08-786-164-14	Sequence 14, Appl	509	6	1.3	1106	3	US-08-462-728-4	Sequence 4, Appl
837	6	1.3	781	4	US-08-867-611-4	Sequence 4, Appl	510	6	1.3	1106	4	US-09-583-459A-2	Sequence 2, Appl
838	6	1.3	781	4	US-09-766-387-2	Sequence 4, Appl	511	6	1.3	1106	4	US-09-583-459A-2	Sequence 2, Appl
839	6	1.3	781	4	US-09-766-387-4	Sequence 4, Appl	512	6	1.3	1106	4	US-09-583-459A-2	Sequence 2, Appl
840	6	1.3	781	5	PCT-US92-06865A-9	Sequence 9, Appl	513	6	1.3	1106	4	US-09-433-039-2	Sequence 2, Appl
841	6	1.3	784	4	US-09-740-235-1	Sequence 9, Appl	514	6	1.3	1106	4	US-08-461-917-4	Sequence 4, Appl
842	6	1.3	790	2	US-08-359-705B-9	Sequence 9, Appl	515	6	1.3	1106	5	PCT-US92-00730-2	Sequence 2, Appl
843	6	1.3	790	2	US-08-286-846A-9	Sequence 9, Appl	516	6	1.3	1106	5	PCT-US92-00862-2	Sequence 2, Appl
844	6	1.3	790	2	US-08-457-880A-9	Sequence 9, Appl	517	6	1.3	1135	2	US-08-574-959A-7	Sequence 7, Appl
845	6	1.3	790	3	US-08-444-622A-9	Sequence 9, Appl	518	6	1.3	1135	2	US-09-357-014-7	Sequence 7, Appl
846	6	1.3	790	3	US-08-942-562-9	Sequence 9, Appl	519	6	1.3	1145	4	US-09-470-443-2	Sequence 4, Appl
847	6	1.3	790	4	US-09-156-923-9	Sequence 9, Appl	520	6	1.3	1145	4	US-09-470-443-4	Sequence 4, Appl
848	6	1.3	829	4	US-08-444-818-69	Sequence 69, Appl	521	6	1.3	1178	1	US-08-199-776-2	Sequence 2, Appl
849	6	1.3	829	4	US-09-562-737-40	Sequence 40, Appl	522	6	1.3	1178	3	US-08-663-731-2	Sequence 2, Appl
850	6	1.3	830	4	US-09-562-737-32	Sequence 32, Appl	523	6	1.3	1178	3	US-08-879-338-2	Sequence 2, Appl
851	6	1.3	830	4	US-09-562-737-37	Sequence 37, Appl	524	6	1.3	1178	5	PCT-US95-02044-2	Sequence 2, Appl
852	6	1.3	830	4	US-09-562-737-39	Sequence 39, Appl	525	6	1.3	1179	4	US-09-293-228B-2	Sequence 2, Appl
853	6	1.3	841	1	US-08-350-884-86	Sequence 86, Appl	526	6	1.3	1194	4	US-08-538-526-1	Sequence 2, Appl
854	6	1.3	841	1	US-08-709-173-86	Sequence 86, Appl	527	6	1.3	1196	4	US-08-881-706-2	Sequence 2, Appl
855	6	1.3	841	2	US-08-709-177-86	Sequence 86, Appl	528	6	1.3	1229	3	US-09-310-293-2	Sequence 2, Appl
856	6	1.3	859	2	US-08-444-818-30	Sequence 30, Appl	529	6	1.3	1229	3	US-09-579-376-2	Sequence 2, Appl
857	6	1.3	865	1	US-07-803-633A-13	Sequence 13, Appl	530	6	1.3	1244	5	PCT-US93-10500-2	Sequence 2, Appl
858	6	1.3	866	4	US-09-556-877-189	Sequence 189, App	531	6	1.3	1248	4	US-08-882-046-6	Sequence 6, Appl
859	6	1.3	866	4	US-09-620-412C-189	Sequence 189, App	532	6	1.3	1257	4	US-09-220-641-3	Sequence 3, Appl
860	6	1.3	873	4	US-09-540-824-28	Sequence 28, Appl	533	6	1.3	1259	4	US-09-134-001C-3757	Sequence 3757, Ap
861	6	1.3	880	4	US-09-556-877-175	Sequence 175, App	534	6	1.3	1311	1	US-08-340-011-5	Sequence 5, Appl
862	6	1.3	880	4	US-09-620-412C-175	Sequence 175, App	535	6	1.3	1311	3	US-08-901-710-5	Sequence 5, Appl
863	6	1.3	905	1	US-08-072-574-2	Sequence 2, Appl	536	6	1.3	1332	2	US-08-921-244-2	Sequence 2, Appl
864	6	1.3	905	2	US-08-574-959A-9	Sequence 9, Appl	537	6	1.3	1332	4	US-09-286-831-2	Sequence 2, Appl
865	6	1.3	905	4	US-09-357-014-9	Sequence 9, Appl	538	6	1.3	1338	4	US-08-750-141A-3	Sequence 3, Appl
866	6	1.3	906	1	US-08-486-270-2	Sequence 2, Appl	539	6	1.3	1362	2	US-08-874-678-33	Sequence 33, Appl
867	6	1.3	906	3	US-08-367-264-2	Sequence 2, Appl	540	6	1.3	1362	3	US-08-643-839-33	Sequence 33, Appl
868	6	1.3	906	4	US-09-153-757-2	Sequence 2, Appl	541	6	1.3	1362	4	US-09-348-886-33	Sequence 33, Appl
869	6	1.3	907	3	US-08-783-774-2	Sequence 2, Appl	542	6	1.3	1366	4	US-08-965-825-19	Sequence 19, Appl
870	6	1.3	907	4	US-09-328-559A-1	Sequence 1, Appl	543	6	1.3	1366	4	US-09-500-811-19	Sequence 19, Appl
871	6	1.3	907	5	PCT-US95-04611A-19	Sequence 19, Appl	544	6	1.3	1366	6	US-09-570-678-19	Sequence 19, Appl
872	6	1.3	913	1	US-08-445-640-4	Sequence 4, Appl	545	6	1.3	1366	4	US-09-548-603-19	Sequence 19, Appl
873	6	1.3	913	3	US-08-170-558-4	Sequence 4, Appl	546	6	1.3	1366	4	US-09-585-887-10	Sequence 10, Appl
874	6	1.3	913	3	US-08-447-314-4	Sequence 4, Appl	547	6	1.3	1366	4	US-09-289-578-10	Sequence 10, Appl
875	6	1.3	913	3	US-08-445-461-4	Sequence 4, Appl	548	6	1.3	1394	6	5177197-30	Patent No. 5177197
876	6	1.3	914	1	US-08-484-105-2	Sequence 2, Appl	549	6	1.3	1420	2	US-08-540-804-14	Sequence 14, Appl
877	6	1.3	914	1	US-08-484-106-2	Sequence 2, Appl	550	6	1.3	1420	2	US-08-218-265-14	Sequence 14, Appl
878	6	1.3	918	2	US-08-843-530B-35	Sequence 35, Appl	551	6	1.3	1420	2	US-08-521-872-14	Sequence 14, Appl
879	6	1.3	919	1	US-08-336-343A-2	Sequence 2, Appl	552	6	1.3	1420	4	US-08-559-399-14	Sequence 14, Appl
880	6	1.3	967	1	US-08-188-281B-13	Sequence 13, Appl	553	6	1.3	1648	1	US-08-188-281B-12	Sequence 12, Appl
881	6	1.3	967	4	US-09-130-481-2	Sequence 2, Appl	554	6	1.3	1648	5	PCT-US94-07280-12	Sequence 12, Appl
882	6	1.3	967	5	PCT-US94-07280-13	Sequence 13, Appl	555	6	1.3	1648	5	PCT-US95-01087-12	Sequence 12, Appl
883	6	1.3	967	5	PCT-US95-01087-13	Sequence 13, Appl	556	6	1.3	1676	4	US-08-487-283A-2	Sequence 2, Appl
884	6	1.3	971	4	US-08-867-611-52	Sequence 52, Appl	557	6	1.3	1692	4	US-09-263-933-4	Sequence 4, Appl
885	6	1.3	973	3	US-08-904-452-4	Sequence 4, Appl	558	6	1.3	1692	4	US-09-263-933-11	Sequence 11, Appl
886	6	1.3	973	4	US-08-867-611-53	Sequence 53, Appl	559	6	1.3	1692	4	US-09-263-933-18	Sequence 18, Appl
887	6	1.3	973	4	US-09-517-639-4	Sequence 4, Appl	560	6	1.3	1719	2	US-08-455-568-4	Sequence 4, Appl
888	6	1.3	992	4	US-08-867-611-54	Sequence 54, Appl	561	6	1.3	1719	2	US-08-399-411-4	Sequence 4, Appl
889	6	1.3	1021	4	US-08-497-025-3	Sequence 3, Appl	562	6	1.3	1719	2	US-08-516-859A-4	Sequence 4, Appl
890	6	1.3	1021	1	US-07-910-760-12	Sequence 12, Appl	563	6	1.3	1719	4	US-09-586-472-4	Sequence 4, Appl
891	6	1.3	1021	1	US-08-440-519-12	Sequence 12, Appl	564	6	1.3	1719	4	US-09-528-706-4	Sequence 4, Appl
892	6	1.3	1021	4	US-08-440-549-12	Sequence 12, Appl	565	6	1.3	1732	2	US-08-477-451-14	Sequence 14, Appl
893	6	1.3	1036	2	US-08-720-484A-5	Sequence 5, Appl	566	6	1.3	1786	4	US-08-444-818-54	Sequence 54, Appl
894	6	1.3	1036	4	US-08-953-823A-5	Sequence 5, Appl	567	6	1.3	1872	4	US-08-188-582-14	Sequence 14, Appl
895	6	1.3	1036	4	US-09-398-239-5	Sequence 5, Appl	568	6	1.3	1872	4	US-08-646-715-14	Sequence 14, Appl
896	6	1.3	1044	2	US-08-777-405A-2	Sequence 2, Appl	569	6	1.3	1893	1	US-08-188-582-11	Sequence 11, Appl
897	6	1.3	1044	2	US-08-977-871A-2	Sequence 2, Appl	570	6	1.3	1893	1	US-08-646-715-11	Sequence 11, Appl
898	6	1.3	1044	2	US-09-225-951-2	Sequence 2, Appl	571	6	1.3	2004	1	US-08-375-709-15	Sequence 15, Appl
899	6	1.3	1049	3	US-08-772-270A-11	Sequence 11, Appl	572	6	1.3	2004	1	US-08-752-929-15	Sequence 15, Appl
900	6	1.3	1070	3	US-08-922-635-22	Sequence 22, Appl	573	6	1.3	2004	4	US-09-090-793-9	Sequence 9, Appl
901	6	1.3	1076	4	US-09-470-443-6	Sequence 6, Appl	574	6	1.3	2013	1	US-08-324-977-12	Sequence 12, Appl
902	6	1.3	1106	1	US-08-180-195-2	Sequence 2, Appl	575	6	1.3	2013	2	US-08-384-616-12	Sequence 12, Appl
903	6	1.3	1106	1	US-08-168-917-2	Sequence 2, Appl	576	6	1.3	2013	2	US-08-904-686A-12	Sequence 12, Appl

977 6 1.3 2013 4 US-09-315-850-12 Sequence 12, Appl
978 6 1.3 2201 4 US-08-952-981A-2 Sequence 2, Appl
979 6 1.3 2233 2 US-08-569-853-1 Sequence 1, Appl
980 6 1.3 2233 3 US-08-569-853-2 Sequence 2, Appl
981 6 1.3 2233 3 US-08-987-439-1 Sequence 1, Appl
982 6 1.3 2261 4 US-08-444-818-66 Sequence 66, Appl
983 6 1.3 2307 4 US-09-263-933-2 Sequence 2, Appl
984 6 1.3 2307 4 US-09-263-933-9 Sequence 9, Appl
985 6 1.3 2307 4 US-09-263-933-16 Sequence 16, Appl
986 6 1.3 2318 4 US-09-091-219-24 Sequence 24, Appl
987 6 1.3 2353 4 US-08-984-709A-50 Sequence 50, Appl
988 6 1.3 2436 4 US-08-444-818-75 Sequence 75, Appl
989 6 1.3 2476 2 US-08-324-977-32 Sequence 2, Appl
990 6 1.3 2620 2 US-08-384-616-32 Sequence 32, Appl
991 6 1.3 2620 2 US-08-904-686A-32 Sequence 32, Appl
992 6 1.3 2620 2 US-09-315-850-32 Sequence 32, Appl
993 6 1.3 2621 1 US-08-324-977-36 Sequence 36, Appl
994 6 1.3 2621 2 US-08-384-616-36 Sequence 36, Appl
995 6 1.3 2621 2 US-09-315-850-36 Sequence 36, Appl
996 6 1.3 2621 4 US-08-375-709-11 Sequence 11, Appl
997 6 1.3 2756 1 US-08-752-929-11 Sequence 11, Appl
998 6 1.3 2756 1 US-09-090-793-7 Sequence 7, Appl
1000 6 1.3 2756 4 US-09-090-793-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-08-967-101-2

Sequence 2, Application US/08967101

Patent No. 5840540

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/967,101

FILING DATE: 10-NOV-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/592,541

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-967-101-2

Query Match 100.0%; Score 467; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEELPAPISFCNNAQMSQDNHLSNTVRSQNDNRQENHSDRSLSGHPPELSNGRQNSR 60
1 MEELPAPISFCNNAQMSQDNHLSNTVRSQNDNRQENHSDRSLSGHPPELSNGRQNSR 60
Db 1 MEELPAPISFCNNAQMSQDNHLSNTVRSQNDNRQENHSDRSLSGHPPELSNGRQNSR 60
QY 61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPPE 120
61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPPE 120
Db 61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPPE 120
QY 121 DTEYQORALHSILNAAIMISYIVMTLLVLYRYRCYKVIHAWLIISLLFFFSFI 180
121 DTEYQORALHSILNAAIMISYIVMTLLVLYRYRCYKVIHAWLIISLLFFFSFI 180
Db 121 DTEYQORALHSILNAAIMISYIVMTLLVLYRYRCYKVIHAWLIISLLFFFSFI 180
QY 181 YLGEVFKYNNVAVDITVAALLIWNIGVGMISIHKGPLRQOATLIMISALMALVFITY 240
181 YLGEVFKYNNVAVDITVAALLIWNIGVGMISIHKGPLRQOATLIMISALMALVFITY 240
Db 181 YLGEVFKYNNVAVDITVAALLIWNIGVGMISIHKGPLRQOATLIMISALMALVFITY 240
QY 241 LPEWTAMTILAVISYDVAVLCPKGPLMLVETAQERNETLFPALITYSTPWMLVYMAE 300
241 LPEWTAMTILAVISYDVAVLCPKGPLMLVETAQERNETLFPALITYSTPWMLVYMAE 300
Db 241 LPEWTAMTILAVISYDVAVLCPKGPLMLVETAQERNETLFPALITYSTPWMLVYMAE 300
QY 301 GDPFAQRVRSKNSKYNAESTERESQDTVAENDGGFSEWEAQRDSHLGPRTSPESRAA 360
301 GDPFAQRVRSKNSKYNAESTERESQDTVAENDGGFSEWEAQRDSHLGPRTSPESRAA 360
Db 301 GDPFAQRVRSKNSKYNAESTERESQDTVAENDGGFSEWEAQRDSHLGPRTSPESRAA 360
QY 361 VOELSSSLIAGEDPERKVKLGDFITFYSVYVGAASATGADWNTTACVAILIGLCL 420
361 VOELSSSLIAGEDPERKVKLGDFITFYSVYVGAASATGADWNTTACVAILIGLCL 420
Db 361 VOELSSSLIAGEDPERKVKLGDFITFYSVYVGAASATGADWNTTACVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVFEATDYLVOFPMDLAFHOFYI 467
421 TLLLAIFKKALPALPISITFGVFEATDYLVOFPMDLAFHOFYI 467
Db 421 TLLLAIFKKALPALPISITFGVFEATDYLVOFPMDLAFHOFYI 467

RESULT 2

US-08-592-541-2

Sequence 2, Application US/08592541

Patent No. 5986054

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,541

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-541-2

Query Match 100.0%; Score 467; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNMQMSDNLSTNVRSONDRERQEHNDRLSGHPPLSNGRQNSR 60
DB 1 MTELPAPLSTYFQNMQMSDNLSTNVRSONDRERQEHNDRLSGHPPLSNGRQNSR 60
QY 61 QVDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATISVSFYTRKDGOLITPTPE 120
DB 61 QVDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATISVSFYTRKDGOLITPTPE 120
QY 121 DTEVGRALHSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFESFI 180
DB 121 DTEVGRALHSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFESFI 180
QY 181 YLGEVFTYNAVDYITVALLIMNLGVGMISIHKGPLRQOAVLIMISALMALVFTKY 240
DB 181 YLGEVFTYNAVDYITVALLIMNLGVGMISIHKGPLRQOAVLIMISALMALVFTKY 240
QY 241 LPEWTAMILAVISYDVAVLCPKGPLRMLVETAQERNETLFPALISSTWMLVNAE 300
DB 241 LPEWTAMILAVISYDVAVLCPKGPLRMLVETAQERNETLFPALISSTWMLVNAE 300
QY 301 GDEPQORVSKNSKYNAESTERESODTVAENDGGFSEWEAQRDRLGPHRSTPESRAA 360
DB 301 GDEPQORVSKNSKYNAESTERESODTVAENDGGFSEWEAQRDRLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLIATFKKALPALPISITFGLVFYFATDYLVOFMDQLAFHOFYI 467
DB 421 TLLLIATFKKALPALPISITFGLVFYFATDYLVOFMDQLAFHOFYI 467

RESULT 3
US-09-124-698-2
Sequence 2, Application US/09124698
GENERAL INFORMATION:
PATENT NO. 611978
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-698-2

Query Match 100.0%; Score 467; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNMQMSDNLSTNVRSONDRERQEHNDRLSGHPPLSNGRQNSR 60
DB 1 MTELPAPLSTYFQNMQMSDNLSTNVRSONDRERQEHNDRLSGHPPLSNGRQNSR 60
QY 61 QVDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATISVSFYTRKDGOLITPTPE 120
DB 61 QVDEDEDEDELTKYGAHVIMLFVPTLCMVVAVATISVSFYTRKDGOLITPTPE 120
QY 121 DTEVGRALHSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFESFI 180
DB 121 DTEVGRALHSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFESFI 180
QY 181 YLGEVFTYNAVDYITVALLIMNLGVGMISIHKGPLRQOAVLIMISALMALVFTKY 240
DB 181 YLGEVFTYNAVDYITVALLIMNLGVGMISIHKGPLRQOAVLIMISALMALVFTKY 240
QY 241 LPEWTAMILAVISYDVAVLCPKGPLRMLVETAQERNETLFPALISSTWMLVNAE 300
DB 241 LPEWTAMILAVISYDVAVLCPKGPLRMLVETAQERNETLFPALISSTWMLVNAE 300
QY 301 GDEPQORVSKNSKYNAESTERESODTVAENDGGFSEWEAQRDRLGPHRSTPESRAA 360
DB 301 GDEPQORVSKNSKYNAESTERESODTVAENDGGFSEWEAQRDRLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
QY 421 TLLLIATFKKALPALPISITFGLVFYFATDYLVOFMDQLAFHOFYI 467
DB 421 TLLLIATFKKALPALPISITFGLVFYFATDYLVOFMDQLAFHOFYI 467

RESULT 4
US-09-127-480-2
Sequence 2, Application US/09127480
PATENT NO. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-480-2

Query Match 100.0%; Score 467; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRROEHNDRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRROEHNDRSLGHPPLSNGRPOGNSR 60
QY 61 QVVEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSFYTRKDGQILYTPETE 120
DB 61 QVVEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSFYTRKDGQILYTPETE 120
QY 121 DTEVGGRAHLSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFFSFI 180
DB 121 DTEVGGRAHLSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFFSFI 180
QY 181 YLGEVFTYNAVVDYITVALLIMNLGVVGMISIMKGPRLQOAYLIMISALMALVFITY 240
DB 181 YLGEVFTYNAVVDYITVALLIMNLGVVGMISIMKGPRLQOAYLIMISALMALVFITY 240
QY 241 LPEWTAMLILAVISYVDLVAVLCRGPRLMLVETAQERNETLFPALITYSSTMVWLVNMAE 300
DB 241 LPEWTAMLILAVISYVDLVAVLCRGPRLMLVETAQERNETLFPALITYSSTMVWLVNMAE 300
QY 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEEMEAORDSHLGHRSIPESRAA 360
DB 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEEMEAORDSHLGHRSIPESRAA 360
QY 361 VOELSSSILAGEDEBERGVKLGIDFTFYSVLYGKASATASGDMNTTIACFVALILIGLCL 420
DB 361 VOELSSSILAGEDEBERGVKLGIDFTFYSVLYGKASATASGDMNTTIACFVALILIGLCL 420
QY 421 TLLILAIFFKALPALPISITFGVLFYATDYLVOPFMDQLAFHQFYI 467
DB 421 TLLILAIFFKALPALPISITFGVLFYATDYLVOPFMDQLAFHQFYI 467

RESULT 5
US-08-496-841C-2

Sequence 2, Application US/08496841C
Patent No. 6210919

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H

ROMMENS, JOHANNA M
FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-496-841C-2

Query Match 100.0%; Score 467; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRROEHNDRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRROEHNDRSLGHPPLSNGRPOGNSR 60
QY 61 QVVEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSFYTRKDGQILYTPETE 120
DB 61 QVVEDEDEDELTKYGAHVIMLFVPTLCMVVAVATIKSVSFYTRKDGQILYTPETE 120
QY 121 DTEVGGRAHLSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFFSFI 180
DB 121 DTEVGGRAHLSILNAIMISVIYVMTLLVLYKRCYKVIHAWLITSSLLFFFSFI 180
QY 181 YLGEVFTYNAVVDYITVALLIMNLGVVGMISIMKGPRLQOAYLIMISALMALVFITY 240
DB 181 YLGEVFTYNAVVDYITVALLIMNLGVVGMISIMKGPRLQOAYLIMISALMALVFITY 240
QY 241 LPEWTAMLILAVISYVDLVAVLCRGPRLMLVETAQERNETLFPALITYSSTMVWLVNMAE 300
DB 241 LPEWTAMLILAVISYVDLVAVLCRGPRLMLVETAQERNETLFPALITYSSTMVWLVNMAE 300
QY 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEEMEAORDSHLGHRSIPESRAA 360
DB 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEEMEAORDSHLGHRSIPESRAA 360
QY 361 VOELSSSILAGEDEBERGVKLGIDFTFYSVLYGKASATASGDMNTTIACFVALILIGLCL 420
DB 361 VOELSSSILAGEDEBERGVKLGIDFTFYSVLYGKASATASGDMNTTIACFVALILIGLCL 420
QY 421 TLLILAIFFKALPALPISITFGVLFYATDYLVOPFMDQLAFHQFYI 467
DB 421 TLLILAIFFKALPALPISITFGVLFYATDYLVOPFMDQLAFHQFYI 467

RESULT 6
US-09-124-523-2

Sequence 2, Application US/09124523
Patent No. 6395960

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-523-2

Query Match 100.0%; Score 467; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTELPAPLSYFQNAQMSQDNHLSNTVRSQNDNRQEHNDRLSLGHPPLSNGRPGNSR 60
DB 1 MTELPAPLSYFQNAQMSQDNHLSNTVRSQNDNRQEHNDRLSLGHPPLSNGRPGNSR 60
QY 61 QVVEDDEDEDELTKYGAHHVIMLFVPTLCMVVVVATIKSVFTTRDQGLITPPE 120
DB 61 QVVEDDEDEDELTKYGAHHVIMLFVPTLCMVVVVATIKSVFTTRDQGLITPPE 120
QY 121 DTEYGOALHSILNAAMISIVVMTLLVLYKRYCYVIAHMLIISLLFFFSFI 180
DB 121 DTEYGOALHSILNAAMISIVVMTLLVLYKRYCYVIAHMLIISLLFFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIMHKGPLRLOQAVLIMISALMAVFIKY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIMHKGPLRLOQAVLIMISALMAVFIKY 240
QY 241 LPEWTAAMLLAVISYDVAVLCPRKPLMLVETAOERNETLFPALITYSTWMLVMAE 300
DB 241 LPEWTAAMLLAVISYDVAVLCPRKPLMLVETAOERNETLFPALITYSTWMLVMAE 300
QY 301 GPEAORARYSKSKYNAESTERESODTVAENDDGFSEMEARORDSLGPHRSTPESRAA 360
DB 301 GPEAORARYSKSKYNAESTERESODTVAENDDGFSEMEARORDSLGPHRSTPESRAA 360
QY 361 VOELSSILAGDEPBERGVKLGDFIFYSVLGKASATASGDMNTTACFAAILGLCL 420
DB 361 VOELSSILAGDEPBERGVKLGDFIFYSVLGKASATASGDMNTTACFAAILGLCL 420
QY 421 TLLLLAIFKKAIPALPISITFGIVFATDYLQPPMDLAFHOFYI 467
DB 421 TLLLLAIFKKAIPALPISITFGIVFATDYLQPPMDLAFHOFYI 467

RESULT 7
US-08-888-077A-4
Sequence 4, Application US/08888077A
Patent No. 602013
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-077A-4
Query Match 93.8%; Score 438; DB 3; Length 463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 NNREROEHNDRLSLGHPPLSNGRPGNSRQVVEDDEDEDELTKYGAHHVIMLFV 89
DB 26 NNREROEHNDRLSLGHPPLSNGRPGNSRQVVEDDEDEDELTKYGAHHVIMLFV 85
QY 90 TLCMVVVVATIKSVFTTRDQGLITPPTEDTETVGOALHSILNAAMISIVVMTLL 149
DB 86 TLCMVVVVATIKSVFTTRDQGLITPPTEDTETVGOALHSILNAAMISIVVMTLL 145
QY 150 LVLYKRYCYVIAHMLIISLLFFFSFIYLGEVFKTYNVAVDYITVALLIMNLGV 209
DB 146 LVLYKRYCYVIAHMLIISLLFFFSFIYLGEVFKTYNVAVDYITVALLIMNLGV 205
QY 210 MTSIMHKGPLRLOQAVLIMISALMAVFIKYLPREWTAAMLLAVISYDVAVLCPR 269
DB 206 MTSIMHKGPLRLOQAVLIMISALMAVFIKYLPREWTAAMLLAVISYDVAVLCPR 265
QY 270 MLVETAOERNETLFPALITYSTWMLVMAEGDPEAORARYSKSKYNAESTERESODTVA 329
DB 266 MLVETAOERNETLFPALITYSTWMLVMAEGDPEAORARYSKSKYNAESTERESODTVA 325
QY 330 ENDDGFSSEMEARORDSLGPHRSTPESRAA VOELSSILAGDEPBERGVKLGDFIF 389
DB 326 ENDDGFSSEMEARORDSLGPHRSTPESRAA VOELSSILAGDEPBERGVKLGDFIF 385


```

QY 181 YLGEVFKTYNAVDYITVALLIWNLGVMGMSIMHKGPLRLOQAYLIMISALMALVFRTKY 240
D 181 YLGEVFKTYNAVDYITVALLIWNLGVMGMSIMHKGPLRLOQAYLIMISALMALVFRTKY 240
QY 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAQERNETLFPALIVSSTMVNLVNNAE 300
D 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAQERNETLFPALIVSSTMVNLVNNAE 300
QY 301 GDPAQRVRSKNSKYNNAESTERESODTYVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
D 301 GDPAQRVRSKNSKYNNAESTERESODTYVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFITFYSVLGKASATASGDMNTTACFVAILIGLCL 420
D 361 VOELSSSILAGEDPEERGVKLGDFITFYSVLGKASATASGDMNTTACFVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVLFYFATDYLVQPFMDQLAFHOFYI 467
D 421 TLLLLAIFKKALPALPISITFGVLFYFATDYLVQPFMDQLAFHOFYI 467

```

```

RESULT 10
US-08-923-454A-10
: Sequence 10, Application US/08923454A
: Patent No. 6004794
: GENERAL INFORMATION:
: APPLICANT: Creasy, Caretha
: APPLICANT: Liyi, George
: APPLICANT: Kairan, Eric
: APPLICANT: Clinkenbeard, Helen
: APPLICANT: Browne, Michael
: APPLICANT: Southan, Christopher
: TITLE OF INVENTION: HUMAN SERINE PROTEASE
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: IBM Compatible
: SOFTWARE: FASTED Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/923,454A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/025436
: FILING DATE: 06-SEPT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumeister, Kirk
: REGISTRATION NUMBER: 33,833
: REFERENCE/DOCKET NUMBER: P50547
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5096
: TELEFAX: 610-270-5090
: TELEX:
: INFORMATION FOR SRO ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:

```

US-08-923-454A-10

Query Match 78.4% Score 366: DB 3: Length 467:
 Best Local Similarity 99.8% Pred. No. 0:
 Matches 466: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

```

QY 1 MTELPAPLSTYQONOMSNDNLSTNVRSONDNREOEHNDRSRIGHPPLSNGRPOGNSR 60
D 1 MTELPAPLSTYQONOMSNDNLSTNVRSONDNREOEHNDRSRIGHPPLSNGRPOGNSR 60
QY 61 QVODEDEDEDELTKYGAHVIMLFVPTLCMVVAVTIKSVSEFYTRKQDLITYPTE 120
D 61 QVODEDEDEDELTKYGAHVIMLFVPTLCMVVAVTIKSVSEFYTRKQDLITYPTE 120
QY 121 DTEVGGRAALSLTAAIMISYIVYMTLLVLYKRYCYKIHAMLLISLLFFESFI 180
D 121 DTEVGGRAALSLTAAIMISYIVYMTLLVLYKRYCYKIHAMLLISLLFFESFI 180
QY 181 YLGEVFKTYNAVDYITVALLIWNLGVMGMSIMHKGPLRLOQAYLIMISALMALVFRTKY 240
D 181 YLGEVFKTYNAVDYITVALLIWNLGVMGMSIMHKGPLRLOQAYLIMISALMALVFRTKY 240
QY 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAQERNETLFPALIVSSTMVNLVNNAE 300
D 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAQERNETLFPALIVSSTMVNLVNNAE 300
QY 301 GDPAQRVRSKNSKYNNAESTERESODTYVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
D 301 GDPAQRVRSKNSKYNNAESTERESODTYVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFITFYSVLGKASATASGDMNTTACFVAILIGLCL 420
D 361 VOELSSSILAGEDPEERGVKLGDFITFYSVLGKASATASGDMNTTACFVAILIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVLFYFATDYLVQPFMDQLAFHOFYI 467
D 421 TLLLLAIFKKALPALPISITFGVLFYFATDYLVQPFMDQLAFHOFYI 467

```

```

RESULT 11
US-08-670-964-2
: Sequence 2, Application US/08670964
: Patent No. 6010874
: GENERAL INFORMATION:
: APPLICANT: Hardy, John A.
: TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road - UW2220; P.O. Box 15
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: IBM Compatible
: SOFTWARE: FASTED for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/670,964
: FILING DATE: 26-JUN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/001,142
: FILING DATE: 13-JUL-1995
: APPLICATION NUMBER: 60/001,501
: FILING DATE: 18-JUL-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Han, William T
: REGISTRATION NUMBER: 34,344
: REFERENCE/DOCKET NUMBER: P50358

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-670-964-2

Query Match

78.4%; Score 366; DB 3; Length 467;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MTELPAPLSTYFQNAQMSDNHLSNTVRSQNDNREROHNDNRSLGHPPLSNRPOGNSR 60
D 1 MTELPAPLSTYFQNAQMSDNHLSNTVRSQNDNREROHNDNRSLGHPPLSNRPOGNSR 60
QY 61 QVVEODEEDELTLTKYGAHVIMLEVPVTLCAVNVVATIKVSFTYRKDGQILYTPETE 120
D 61 QVVEODEEDELTLTKYGAHVIMLEVPVTLCAVNVVATIKVSFTYRKDGQILYTPETE 120
QY 121 DTEVGGRAHSLILNAIMISVIVMTLLVLYTKRCYVIAHMLIISLLFFESFI 180
D 121 DTEVGGRAHSLILNAIMISVIVMTLLVLYTKRCYVIAHMLIISLLFFESFI 180
QY 181 YLGEVFTYNAVDYITVALLINMGVGMISIMKGPLRQOAYLIMISALMALVFIKY 240
D 181 YLGEVFTYNAVDYITVALLINMGVGMISIMKGPLRQOAYLIMISALMALVFIKY 240
QY 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAOERNETLFPALYSTWLVNMAE 300
D 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAOERNETLFPALYSTWLVNMAE 300
QY 301 GDPAQRVSKNSKYNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHRSTPESRAA 360
D 301 GDPAQRVSKNSKYNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHRSTPESRAA 360
QY 361 VOELSSILAGEDPEERGVKLGDFIFYSVLGKASATASGDMNTTIACFVALILGLCL 420
D 361 VOELSSILAGEDPEERGVKLGDFIFYSVLGKASATASGDMNTTIACFVALILGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVFFATDYLVPFMDQLAFHQFYI 467
D 421 TLLLAIFKKALPALPISITFGVFFATDYLVPFMDQLAFHQFYI 467
```

RESULT 12

US-08-888-077A-2

Sequence 2, Application US/0888077A

Patent No. 6020143

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: LERNER, DAVID, LITTENBERG, KRONHOLZ & MENTLIK

STREET: 600 SOUTH AVENUE WEST

CITY: WESTFIELD

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,077A

FILING DATE: 03-JUL-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/892,541

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: PALISI, THOMAS M

REGISTRATION NUMBER: 36,629

REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 654-5000

TELEFAX: (908) 654-7866

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-888-077A-2

Query Match

78.4%; Score 366; DB 3; Length 467;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MTELPAPLSTYFQNAQMSDNHLSNTVRSQNDNREROHNDNRSLGHPPLSNRPOGNSR 60
D 1 MTELPAPLSTYFQNAQMSDNHLSNTVRSQNDNREROHNDNRSLGHPPLSNRPOGNSR 60
QY 61 QVVEODEEDELTLTKYGAHVIMLEVPVTLCAVNVVATIKVSFTYRKDGQILYTPETE 120
D 61 QVVEODEEDELTLTKYGAHVIMLEVPVTLCAVNVVATIKVSFTYRKDGQILYTPETE 120
QY 121 DTEVGGRAHSLILNAIMISVIVMTLLVLYTKRCYVIAHMLIISLLFFESFI 180
D 121 DTEVGGRAHSLILNAIMISVIVMTLLVLYTKRCYVIAHMLIISLLFFESFI 180
QY 181 YLGEVFTYNAVDYITVALLINMGVGMISIMKGPLRQOAYLIMISALMALVFIKY 240
D 181 YLGEVFTYNAVDYITVALLINMGVGMISIMKGPLRQOAYLIMISALMALVFIKY 240
QY 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAOERNETLFPALYSTWLVNMAE 300
D 241 LPEWTAMLLIAVISYVDLVAVLCPKGPLRMLVETAOERNETLFPALYSTWLVNMAE 300
QY 301 GDPAQRVSKNSKYNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHRSTPESRAA 360
D 301 GDPAQRVSKNSKYNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHRSTPESRAA 360
QY 361 VOELSSILAGEDPEERGVKLGDFIFYSVLGKASATASGDMNTTIACFVALILGLCL 420
D 361 VOELSSILAGEDPEERGVKLGDFIFYSVLGKASATASGDMNTTIACFVALILGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVFFATDYLVPFMDQLAFHQFYI 467
D 421 TLLLAIFKKALPALPISITFGVFFATDYLVPFMDQLAFHQFYI 467
```

RESULT 13

US-09-124-698-134

Sequence 134, Application US/09124698

Patent No. 6117978

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURNITZ & THIBEAULT

STREET: High Street tower - 125 High Street

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-698-134

Query Match 78.4%; Score 366; DB 3; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLNSGRPGNSR 60
DB 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLNSGRPGNSR 60
QY 61 OVEODEEDEDLTLKYGAKHVIMLFVPTLCWVVVATIKSVFTRKDGQLITPPT 120
DB 61 OVEODEEDEDLTLKYGAKHVIMLFVPTLCWVVVATIKSVFTRKDGQLITPPT 120
QY 121 DRETGQALHSLNAINMISVIVMTILLVLYKYRCYKVIHAWLISSLLFFFSFT 180
DB 121 DRETGQALHSLNAINMISVIVMTILLVLYKYRCYKVIHAWLISSLLFFFSFT 180
QY 181 YGGEVKTNNVADVITVALLIMNLCVGMISTHMGKPLRLQOAYLIMISALMALVFIRY 240
DB 181 YGGEVKTNNVADVITVALLIMNLCVGMISTHMGKPLRLQOAYLIMISALMALVFIRY 240
QY 241 LPEWTAMLAVISYDVAVLCPRKPLRLVETAOERNETLFPALISSTWMLVNM 300
DB 241 LPEWTAMLAVISYDVAVLCPRKPLRLVETAOERNETLFPALISSTWMLVNM 300
QY 301 GDEPAORRVSKSKYNAESTERESQDTVAENDGCFSEMEARDSHLGPHRSTPESRAA 360
DB 301 GDEPAORRVSKSKYNAESTERESQDTVAENDGCFSEMEARDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGDEPBERGVKLGIDPFIYSVLGKASATASGDMNTTICFAVAILGLCL 420
DB 361 VOELSSIIAGDEPBERGVKLGIDPFIYSVLGKASATASGDMNTTICFAVAILGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFVFATDYLVOPMDOLAFHOFT 467
DB 421 TLLLLAIFKKALPALPISITFGLVFVFATDYLVOPMDOLAFHOFT 467

RESULT 14
US-09-127-480-134
Sequence 134, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-480-134

Query Match 78.4%; Score 366; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLNSGRPGNSR 60
DB 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNREOHNDRLSLGHPPLNSGRPGNSR 60
QY 61 OVEODEEDEDLTLKYGAKHVIMLFVPTLCWVVVATIKSVFTRKDGQLITPPT 120
DB 61 OVEODEEDEDLTLKYGAKHVIMLFVPTLCWVVVATIKSVFTRKDGQLITPPT 120
QY 121 DRETGQALHSLNAINMISVIVMTILLVLYKYRCYKVIHAWLISSLLFFFSFT 180
DB 121 DRETGQALHSLNAINMISVIVMTILLVLYKYRCYKVIHAWLISSLLFFFSFT 180
QY 181 YGGEVKTNNVADVITVALLIMNLCVGMISTHMGKPLRLQOAYLIMISALMALVFIRY 240
DB 181 YGGEVKTNNVADVITVALLIMNLCVGMISTHMGKPLRLQOAYLIMISALMALVFIRY 240
QY 241 LPEWTAMLAVISYDVAVLCPRKPLRLVETAOERNETLFPALISSTWMLVNM 300
DB 241 LPEWTAMLAVISYDVAVLCPRKPLRLVETAOERNETLFPALISSTWMLVNM 300
QY 301 GDEPAORRVSKSKYNAESTERESQDTVAENDGCFSEMEARDSHLGPHRSTPESRAA 360
DB 301 GDEPAORRVSKSKYNAESTERESQDTVAENDGCFSEMEARDSHLGPHRSTPESRAA 360
QY 361 VOELSSIIAGDEPBERGVKLGIDPFIYSVLGKASATASGDMNTTICFAVAILGLCL 420
DB 361 VOELSSIIAGDEPBERGVKLGIDPFIYSVLGKASATASGDMNTTICFAVAILGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFVFATDYLVOPMDOLAFHOFT 467
DB 421 TLLLLAIFKKALPALPISITFGLVFVFATDYLVOPMDOLAFHOFT 467

RESULT 15

US-08-496-841C-134

; Sequence 134, Application US/08496841C
; Patent No. 6210919

; GENERAL INFORMATION:

; APPLICANT: ST. GEORGE-HYSLOP, PETER H

; ROMMENS, JOHANNA M

; FRASER, PAUL E

; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Darryl & Darby, PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/496,841C

; FILING DATE: 28-JUN-1995

; CLASSIFICATION: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul F. Fehner, Ph.D.

; REGISTRATION NUMBER: 35,135

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 527-7700

; TELEFAX: (212) 753-6237

; INFORMATION FOR SEQ ID NO: 134:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 467 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 134:

US-08-496-841C-134

Query Match 78.4%; Score 366; DB 4; Length 467;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRQGNR 60
  |||||||
DB 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRQGNR 60
QY 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120
  |||||||
DB 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120
QY 121 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
  |||||||
DB 121 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
QY 122 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
  |||||||
DB 122 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
QY 181 YLGEVFKTYNNAVDYITVALLIMNGVVGMI SIHKGPLRLQOAYLIMISALMALVFITY 240
  |||||||
DB 181 YLGEVFKTYNNAVDYITVALLIMNGVVGMI SIHKGPLRLQOAYLIMISALMALVFITY 240
QY 181 YLGEVFKTYNNAVDYITVALLIMNGVVGMI SIHKGPLRLQOAYLIMISALMALVFITY 240
  |||||||
DB 181 YLGEVFKTYNNAVDYITVALLIMNGVVGMI SIHKGPLRLQOAYLIMISALMALVFITY 240
QY 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
  |||||||
DB 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
QY 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
  |||||||
DB 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
QY 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
  |||||||
DB 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
QY 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
  |||||||
DB 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360

```

RESULT 16

US-08-832-867-3

; Sequence 3, Application US/08832867C

; Patent No. 6376239

; GENERAL INFORMATION:

; APPLICANT: BAUMEISTER, Ralf

; TITLE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF

; TITLE OF INVENTION: CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN

; TITLE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.

; FILE REFERENCE: 674503-2004

; CURRENT APPLICATION NUMBER: US/08/832,867C

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 3

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-08-832-867-3

Query Match 78.4%; Score 366; DB 4; Length 467;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRQGNR 60
  |||||||
DB 1 MTELPAPLSYFONAOQSEDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRQGNR 60
QY 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120
  |||||||
DB 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120
QY 121 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
  |||||||
DB 121 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
QY 121 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
  |||||||
DB 121 DTEYGORALHSILNAAIMISYIVMTLLVLYKYRCYKVIHAMLITSSLLFFESFI 180
QY 181 YLGEVFKTYNNAVDYITVALLIMNGVVGMI SIHKGPLRLQOAYLIMISALMALVFITY 240
  |||||||
DB 181 YLGEVFKTYNNAVDYITVALLIMNGVVGMI SIHKGPLRLQOAYLIMISALMALVFITY 240
QY 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
  |||||||
DB 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
QY 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
  |||||||
DB 241 LPEWTAMILLAVISYDLYAVLCPPKPLRLMVLVETAOERNETLFPALITSSIMVWLNNAE 300
QY 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
  |||||||
DB 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
QY 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
  |||||||
DB 301 GDPFAORRYSKSKYNASTERESODTVAENDGGFSEMEWQORDSHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPERGVKGLGDFITYSYLVGKASATASGDWMTTACVAILIGLCL 420
  |||||||
DB 361 VOELSSSILAGDEPERGVKGLGDFITYSYLVGKASATASGDWMTTACVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVOFPMQLAFHQFYI 467
  |||||||
DB 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVOFPMQLAFHQFYI 467

```

RESULT 17

US-09-227-725A-1

; Sequence 1, Application US/09227725A

; Patent No. 6383758

; GENERAL INFORMATION:

; APPLICANT: St. George-Hyslop, Peter H.

APPLICANT: Rommens, Johanna
APPLICANT: Fraser, Paul E.
TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
TITLE OF INVENTION: of use
FILE REFERENCE: 1034/1810-US1
CURRENT APPLICATION NUMBER: US/09/227,725A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 467
TYPE: PRT
ORGANISM: Homo Sapien
US-09-227-725A-1

Query Match 78.4%; Score 366; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAFLSYFONAKSEDNHLSNTVRSONDNREHNDRLSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAFLSYFONAKSEDNHLSNTVRSONDNREHNDRLSLGHPPLSNGRPOGNSR 60
QY 61 QVEQDEDEDELTLYGAKHVMLEFPVTLQVWVAVATIKSVFTRKDGOLITPPE 120
DB 61 QVEQDEDEDELTLYGAKHVMLEFPVTLQVWVAVATIKSVFTRKDGOLITPPE 120
QY 121 DRETVQGRALHSLNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
DB 121 DRETVQGRALHSLNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
QY 181 YLGEVETKYNVAVDYITVALLINNLGVGMISIMHKGPRLOQAYLIMISALMALVFIRY 240
DB 181 YLGEVETKYNVAVDYITVALLINNLGVGMISIMHKGPRLOQAYLIMISALMALVFIRY 240
QY 241 LPEWTAMLILAVISYVDLVAVLCPKGPLRMLVETAOERNETLPALISSTWMLVMAE 300
DB 241 LPEWTAMLILAVISYVDLVAVLCPKGPLRMLVETAOERNETLPALISSTWMLVMAE 300
QY 301 GDEPAQRVSKSKYNAESTERESODTVAENDGGSSEMEAOQSDSHLGHSTPESRAA 360
DB 301 GDEPAQRVSKSKYNAESTERESODTVAENDGGSSEMEAOQSDSHLGHSTPESRAA 360
QY 361 VOELSSILAGEDPEERGVKLGIDFTFYSVLGKASATASGDMNTTIACFVAIILGLCL 420
DB 361 VOELSSILAGEDPEERGVKLGIDFTFYSVLGKASATASGDMNTTIACFVAIILGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFATDYLQPFMDQLAFHOFTY 467
DB 421 TLLLLAIFKKALPALPISITFGLVFATDYLQPFMDQLAFHOFTY 467

RESULT 18
US-09-124-523-134
Sequence 134, Application US/09124523
Patent No. 6395960

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HUMMITS & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-523-134

Query Match 78.4%; Score 366; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAFLSYFONAKSEDNHLSNTVRSONDNREHNDRLSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAFLSYFONAKSEDNHLSNTVRSONDNREHNDRLSLGHPPLSNGRPOGNSR 60
QY 61 QVEQDEDEDELTLYGAKHVMLEFPVTLQVWVAVATIKSVFTRKDGOLITPPE 120
DB 61 QVEQDEDEDELTLYGAKHVMLEFPVTLQVWVAVATIKSVFTRKDGOLITPPE 120
QY 121 DRETVQGRALHSLNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
DB 121 DRETVQGRALHSLNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
QY 181 YLGEVETKYNVAVDYITVALLINNLGVGMISIMHKGPRLOQAYLIMISALMALVFIRY 240
DB 181 YLGEVETKYNVAVDYITVALLINNLGVGMISIMHKGPRLOQAYLIMISALMALVFIRY 240
QY 241 LPEWTAMLILAVISYVDLVAVLCPKGPLRMLVETAOERNETLPALISSTWMLVMAE 300
DB 241 LPEWTAMLILAVISYVDLVAVLCPKGPLRMLVETAOERNETLPALISSTWMLVMAE 300
QY 301 GDEPAQRVSKSKYNAESTERESODTVAENDGGSSEMEAOQSDSHLGHSTPESRAA 360
DB 301 GDEPAQRVSKSKYNAESTERESODTVAENDGGSSEMEAOQSDSHLGHSTPESRAA 360
QY 361 VOELSSILAGEDPEERGVKLGIDFTFYSVLGKASATASGDMNTTIACFVAIILGLCL 420
DB 361 VOELSSILAGEDPEERGVKLGIDFTFYSVLGKASATASGDMNTTIACFVAIILGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGLVFATDYLQPFMDQLAFHOFTY 467
DB 421 TLLLLAIFKKALPALPISITFGLVFATDYLQPFMDQLAFHOFTY 467

RESULT 19
US-09-375-318-3
Sequence 3, Application US/09375318
Patent No. 6468791

GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
Schellenberg, Gerard D.
Masco, Wilma

Levy-Lahad, Ephrat
Bird, Thomas D.
Galas, David J.
TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BEERY LLP
STREET: 701 Fifth Ave, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,318
FILING DATE: 16-Aug-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Verna, James M.
REGISTRATION NUMBER: 33,287
REFERENCE/DOCKET NUMBER: 920010.571C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-375-318-3
Query Match 78.4%; Score 366; DB 4; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSYFQNAQMSQEDNHLSTNTYRSQNDNREROEHRSLGHPLELSNGRPGNSR 60
DB 1 MTELPAPLSYFQNAQMSQEDNHLSTNTYRSQNDNREROEHRSLGHPLELSNGRPGNSR 60
QY 61 QVVEDEDEDELTLTKYGAHVIMLFVPTLCMVVVVATIKSVFTRKDGOLITPTPE 120
DB 61 QVVEDEDEDELTLTKYGAHVIMLFVPTLCMVVVVATIKSVFTRKDGOLITPTPE 120
QY 121 DFEYGOARLHSLNAAIMISIVYVMTLLVLYKYRCYKVIHAWLIISLLLEFESPI 180
DB 121 DFEYGOARLHSLNAAIMISIVYVMTLLVLYKYRCYKVIHAWLIISLLLEFESPI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVFIRY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVFIRY 240
QY 241 LPEWTAWLLAVISYVDLAVLCPEKGPLRLMVLTAOERNETLFPALIIYSTWMLVNAE 300
DB 241 LPEWTAWLLAVISYVDLAVLCPEKGPLRLMVLTAOERNETLFPALIIYSTWMLVNAE 300
QY 301 GDPPEORRRYSKSKYNAESTERESODTVAENDGGFSEWEAQRSDSHLGPSTESRA 360
DB 301 GDPPEORRRYSKSKYNAESTERESODTVAENDGGFSEWEAQRSDSHLGPSTESRA 360
QY 361 VOELSSSILAGDPBERGVKLGLGDFIFYSVLVKASATASGDWNTTIACFVAILIGLCL 420
DB 361 VOELSSSILAGDPBERGVKLGLGDFIFYSVLVKASATASGDWNTTIACFVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISTITGVLVYFATDYLVOPMDQLAFHOFYI 467
DB 421 TLLLAIFKKALPALPISTITGVLVYFATDYLVOPMDQLAFHOFYI 467
RESULT 20
US-08-670-964-4
Sequence 4, Application US/08670964

Patent No. 6010874
GENERAL INFORMATION:
APPLICANT: Hardy, John A.
TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
TITLE OF INVENTION: GENE AND GENE PRODUCTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road - UW2220; P.O. Box 15
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,964
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,142
FILING DATE: 3-JUL-1995
APPLICATION NUMBER: 60/001,501
FILING DATE: 18-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50358
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-964-4
Query Match 72.2%; Score 337; DB 3; Length 463;
Best Local Similarity 99.8%; Pred. No. 5.8e-313;
Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 30 NDNREORHNDRRSLGHPLELSNGRPGNSRQVYQDEDEDELTLKYGAHVIMLFV 89
DB 26 NDNREORHNDRRSLGHPLELSNGRPGNSRQVYQDEDEDELTLKYGAHVIMLFV 85
QY 90 TLCMVVVVATIKSVFTRKDGOLITPTPEDETFYGOARLHSLNAAIMISIVYVMTL 149
DB 86 TLCMVVVVATIKSVFTRKDGOLITPTPEDETFYGOARLHSLNAAIMISIVYVMTL 145
QY 150 LVVLYKYRCYKVIHAWLIISLLLEFESFYTLGVEFKTYNVAVDYITVALLIMNLGVG 209
DB 146 LVVLYKYRCYKVIHAWLIISLLLEFESFYTLGVEFKTYNVAVDYITVALLIMNLGVG 205
QY 210 MISHMKGPLRLQOAVLIMISALMALVFIRYKLPENTAWLLAVISYVDLAVLCPKGPLR 269
DB 206 MISHMKGPLRLQOAVLIMISALMALVFIRYKLPENTAWLLAVISYVDLAVLCPKGPLR 265
QY 270 MIVETAOERNETLFPALIIYSTWMLVNAEGDPEAQRYSKSKYNAESTERESODTVA 329
DB 266 MIVETAOERNETLFPALIIYSTWMLVNAEGDPEAQRYSKSKYNAESTERESODTVA 325
QY 330 ENDDGFESEWEAQRSDSHLGPSTESRAVVOELSSSILAGDPBERGVKLGLGDFIF 389
DB 326 ENDDGFESEWEAQRSDSHLGPSTESRAVVOELSSSILAGDPBERGVKLGLGDFIF 385
QY 390 SVLVKASATASGDWNTTIACFVAILIGLCLTLLLAIFKKALPALPISTITGVLVYFAT 449

|||||
Db 386 SYLVAKASATASGDMNTTACFAVAILIGLCTLLLAIFKKALPALPISITFGLVFEAT 445
Oy 450 DYLVOPMDQLAFHOFYI 467
|||||
Db 446 DILVOPMDQLAFHOFYI 463

RESULT 21
US-08-875-972-4

; Sequence 4, Application US/08875972
; Patent No. 5985564
; GENERAL INFORMATION:
; APPLICANT: Huntington Potter and Jinhue Li
; TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
; TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,972
; FILING DATE: 08-AUG-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,448
; FILING DATE: 16-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan Esq., Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-03PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 407 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-972-4

Query Match 65.5%; Score 306; DB 2; Length 407;

Best Local Similarity 99.8%; Pred. No. 1.8e-283;
Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 61 OVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSYTRDGLIYTPETE 120
|||||
Db 1 OVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSYTRDGLIYTPETE 60
121 DTEVGORALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
Oy 121 DTEVGORALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
|||||
Db 61 DTEVGORALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 120
Oy 161 YLGEVFKTYNAVVDYITVALLIWNLCVGMISIHMKGPLRLOQAVLIMISALMALVFIRY 240
Db 121 YLGEVFKTYNAVVDYITVALLIWNLCVGMISIHMKGPLRLOQAVLIMISALMALVFIRY 180
Oy 241 LPETVAMILAVISYVDLAVAVCPKGPLMLVETAOERRETLFPALISSTWVWLVNME 300
Db 181 LPETVAMILAVISYVDLAVAVCPKGPLMLVETAOERRETLFPALISSTWVWLVNME 240
Oy 301 GDEAQRVSKNSKYNAESTERESODTVAENDDGFSEEMEQRSHLGPHRSTPESRAA 360
|||||

Db 241 GDEAQRVSKNSKYNAESTERESODTVAENDDGFSEEMEQRSHLGPHRSTPESRAA 300
Oy 361 VOELSSSILAGDPERGVKLGIDGFIYSYVGRASATASGDMNTTACFAVAILIGLCL 420
Db 301 VOELSSSILAGDPERGVKLGIDGFIYSYVGRASATASGDMNTTACFAVAILIGLCL 360
Oy 421 TLLLAIFKKALPALPISITFGLVFATDYLVOPMDQLAFHOFYI 467
|||||
Db 361 TLLLAIFKKALPALPISITFGLVFATDYLVOPMDQLAFHOFYI 407

RESULT 22
US-08-706-344C-2

; Sequence 2, Application US/08706344C
; Patent No. 6248555
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; APPLICANT: WASCO, WILMA
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; TITLE OF INVENTION: Alzheimer's Disease
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (Epo)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,344C
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/003,054
; FILING DATE: 31-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0609.4180001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-706-344C-2

Query Match 56.7%; Score 265; DB 4; Length 467;

Best Local Similarity 99.6%; Pred. No. 2.5e-244;
Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MTELPAPLSYFQNAQSEDNHLSNTRVSONDREROEHNDRLSLGHPPLSGRPGQNSR 60
Db 1 MTELPAPLSYFQNAQSEDNHLSNTRVSONDREROEHNDRLSLGHPPLSGRPGQNSR 60
Oy 61 OVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSYTRDGLIYTPETE 120
Db 61 OVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVSYTRDGLIYTPETE 120
Oy 121 DTEVGORALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
Db 121 DTEVGORALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
Oy 181 YLGEVFKTYNAVVDYITVALLIWNLCVGMISIHMKGPLRLOQAVLIMISALMALVFIRY 240
|||||

Db 181 YLGEVFKTYNVAVDYITVALLIWNQVGMISIMKGPRLQOAVYIMISALMAVETKY 240

Qy 241 LPEWTAMLLAVISYVDLVAVLCPKGPLMVLVETAOERNETLFPALIVSSYTWMLVNMME 300
|||||

Db 241 LPEWTAMLLAVISYVDLVAVLCPKGPLMVLVETAOERNETLFPALIVSSYTWMLVNMME 300

Qy 301 GDEPQORRYSKSKNAESTERESQDTVAENDDGGFSEMEQORSHLGPHESTPESRAA 360
|||||

Db 301 GDEPQORRYSKSKNAESTERESQDTVAENDDGGFSEMEQORSHLGPHESTPESRAA 360

Qy 361 VOELSSSILAGDEPBERGKLGIDPIFYSVLVKASATASGDMNTTICFVAILIGLCL 420
|||||

Db 361 VOELSSSILAGDEPBERGKLGIDPIFYSVLVKASATASGDMNTTICFVAILIGLCL 420

Qy 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVPFMDOLAFHOPIY 467
|||||

Db 421 TLLLAIFKKALPALPISITFGLVFYFATDYLVPFMDOLAFHOPIY 467

RESULT 23
US-08-706-344C-4
Sequence 4, Application US/08706344C
Patent No. 6248555
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
APPLICANT: WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
TITLE OF INVENTION: Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,344C
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-344C-4

Query Match 43.7%; Score 204; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.4e-186;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRPQNSR 60
|||||

Db 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRPQNSR 60

Qy 61 QVVEODEDEDELTLKYGAKHIVMLFVPVTLICMVVVATISVSFYTRKDGQLIYTPETE 120
|||||

Db 61 QVVEODEDEDELTLKYGAKHIVMLFVPVTLICMVVVATISVSFYTRKDGQLIYTPETE 120

Qy 121 DTEYVQORALHSILNAAMISIVYVMTLLVLYKYRCYKVIHAMLISSLLFFFSFI 180
|||||

Db 121 DTEYVQORALHSILNAAMISIVYVMTLLVLYKYRCYKVIHAMLISSLLFFFSFI 180

Qy 181 YLGEVFKTYNVAVDYITVALLIWN 204
|||||

Db 181 YLGEVFKTYNVAVDYITVALLIWN 204

RESULT 24
US-08-706-344C-28
Sequence 28, Application US/08706344C
Patent No. 6248555
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
APPLICANT: WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
TITLE OF INVENTION: Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,344C
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-344C-28

Query Match 43.7%; Score 204; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.4e-186;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRPQNSR 60
|||||

Db 1 MTELPAPLSTYFQNMQMSDNHLSNTVRSQNDNREROEHNDRRSLGHPPLSNGRPQNSR 60

Qy 61 QVVEODEDEDELTLKYGAKHIVMLFVPVTLICMVVVATISVSFYTRKDGQLIYTPETE 120
|||||

Db 61 QVVEODEDEDELTLKYGAKHIVMLFVPVTLICMVVVATISVSFYTRKDGQLIYTPETE 120

Qy 121 DTEYVQORALHSILNAAMISIVYVMTLLVLYKYRCYKVIHAMLISSLLFFFSFI 180
|||||

Db 121 DTEYVQORALHSILNAAMISIVYVMTLLVLYKYRCYKVIHAMLISSLLFFFSFI 180

Qy 181 YLGEVFKTYNVAVDYITVALLIWN 204
|||||

Db 181 YLGEVFKTYNNAVDTYVALLIWN 204

RESULT 25

US-08-706-344C-30

; Sequence 30, Application US/08706344C

; Patent No. 624855

; GENERAL INFORMATION:

; APPLICANT: MASCO, WILMA

; APPLICANT: TANZI, RUDOLPH

; TITLE OF INVENTION: Genetic Alterations Related To Familial

; TITLE OF INVENTION: Alzheimer's Disease

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/706,344C

; FILING DATE: 30-AUG-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/003,054

; FILING DATE: 31-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0609,4180001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 467 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-706-344C-30

Query Match 43.7%; Score 204; DB 4; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.4e-186;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDREQEHNDRLSLGHPPLSGRPGNSR 60

Db 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDREQEHNDRLSLGHPPLSGRPGNSR 60

QY 61 QVBEDEDEDELTLKYGAKHVIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120

Db 61 QVBEDEDEDELTLKYGAKHVIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120

QY 121 DTEVGOBALSHILNAAMISIVVMTLLVLYRYCKYVIHAWLISSLLLEFFFSFI 180

Db 121 DTEVGOBALSHILNAAMISIVVMTLLVLYRYCKYVIHAWLISSLLLEFFFSFI 180

QY 181 YLGEVFKTYNNAVDTYVALLIWN 204

Db 181 YLGEVFKTYNNAVDTYVALLIWN 204

RESULT 26

US-08-706-344C-32

; Sequence 32, Application US/08706344C

; Patent No. 624855

; GENERAL INFORMATION:

; APPLICANT: TANZI, RUDOLPH

; APPLICANT: MASCO, WILMA

; TITLE OF INVENTION: Genetic Alterations Related To Familial

; TITLE OF INVENTION: Alzheimer's Disease

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/706,344C

; FILING DATE: 30-AUG-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/003,054

; FILING DATE: 31-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0609,4180001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 467 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-706-344C-32

Query Match 43.7%; Score 204; DB 4; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.4e-186;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDREQEHNDRLSLGHPPLSGRPGNSR 60

Db 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDREQEHNDRLSLGHPPLSGRPGNSR 60

QY 61 QVBEDEDEDELTLKYGAKHVIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120

Db 61 QVBEDEDEDELTLKYGAKHVIMLFVPTLCMVVVVATIKSVSYTRKDGOLITPTPE 120

QY 121 DTEVGOBALSHILNAAMISIVVMTLLVLYRYCKYVIHAWLISSLLLEFFFSFI 180

Db 121 DTEVGOBALSHILNAAMISIVVMTLLVLYRYCKYVIHAWLISSLLLEFFFSFI 180

QY 181 YLGEVFKTYNNAVDTYVALLIWN 204

Db 181 YLGEVFKTYNNAVDTYVALLIWN 204

RESULT 27

US-08-788-231A-15

; Sequence 15, Application US/08788231A

; Patent No. 601974

; GENERAL INFORMATION:

; APPLICANT: L'Hernault, Steven W.

; TITLE OF INVENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winer and Sullivan, P.C.

; STREET: 5370 Manhattan Circle, Suite 201

; CITY: Boulder


```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-967-101-4

Query Match                20.8%; Score 97; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 213 IHMKGPLRQOAYLIMISALMALVFYIKYLPENTAMILLAVISYVDLVAVLCPKGPLRMLY 272
Db 213 IHMKGPLRQOAYLIMISALMALVFYIKYLPENTAMILLAVISYVDLVAVLCPKGPLRMLY 272

Oy 273 ETAOERNETLFPALYSSSTMVLMVNAEGDPEAORRV 309
Db 273 ETAOERNETLFPALYSSSTMVLMVNAEGDPEAORRV 309

RESULT 30
US-08-592-541-4
; Sequence 4, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-592-541-4

Query Match                20.8%; Score 97; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 213 IHMKGPLRQOAYLIMISALMALVFYIKYLPENTAMILLAVISYVDLVAVLCPKGPLRMLY 272
Db 213 IHMKGPLRQOAYLIMISALMALVFYIKYLPENTAMILLAVISYVDLVAVLCPKGPLRMLY 272

Oy 273 ETAOERNETLFPALYSSSTMVLMVNAEGDPEAORRV 309
Db 273 ETAOERNETLFPALYSSSTMVLMVNAEGDPEAORRV 309

RESULT 31
US-08-888-077A-17
; Sequence 17, Application US/08888077A
; Patent No. 6020143
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
; STREET: 600 SOUTH AVENUE WEST
; CITY: WESTFIELD
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,077A
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,541
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: PALISI, THOMAS M
; REGISTRATION NUMBER: 36,629
; REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 654-5000
; TELEFAX: (908) 654-7866
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-077A-17

Query Match                20.8%; Score 97; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 213 IHMKGPLRQOAYLIMISALMALVFYIKYLPENTAMILLAVISYVDLVAVLCPKGPLRMLY 272
Db 213 IHMKGPLRQOAYLIMISALMALVFYIKYLPENTAMILLAVISYVDLVAVLCPKGPLRMLY 272

Oy 273 ETAOERNETLFPALYSSSTMVLMVNAEGDPEAORRV 309
Db 273 ETAOERNETLFPALYSSSTMVLMVNAEGDPEAORRV 309
```

RESULT 32
US-09-124-698-4
Sequence 4, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-698-4
Query Match 20.8%; Score 97; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 213 IHMKGPLRLOQAYLIMISALMALVFIRKLPENTAWLLIAVISYDVLAVLCPPKGPLRLV 272
Db 213 IHMKGPLRLOQAYLIMISALMALVFIRKLPENTAWLLIAVISYDVLAVLCPPKGPLRLV 272
QY 273 ETAOERNETLFPALISSTWVLVNMAGDEPAORRV 309
Db 273 ETAOERNETLFPALISSTWVLVNMAGDEPAORRV 309
RESULT 33
US-09-127-480-4
Sequence 4, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-480-4
Query Match 20.8%; Score 97; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 213 IHMKGPLRLOQAYLIMISALMALVFIRKLPENTAWLLIAVISYDVLAVLCPPKGPLRLV 272
Db 213 IHMKGPLRLOQAYLIMISALMALVFIRKLPENTAWLLIAVISYDVLAVLCPPKGPLRLV 272
QY 273 ETAOERNETLFPALISSTWVLVNMAGDEPAORRV 309
Db 273 ETAOERNETLFPALISSTWVLVNMAGDEPAORRV 309
RESULT 34
US-08-496-841C-4
Sequence 4, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-496-841C-4

Query Match 20.8%; Score 97; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 IHMKGPLRQQAYLIMISALMALVFIKYLEPTAWLLIAVISYDVLVAVLCPKGPLRLMV 272
Db 213 IHMKGPLRQQAYLIMISALMALVFIKYLEPTAWLLIAVISYDVLVAVLCPKGPLRLMV 272

Qy 273 ETAOERNETLFPALYSSSTMWLVNMAEGDPEAORRV 309
Db 273 ETAOERNETLFPALYSSSTMWLVNMAEGDPEAORRV 309

RESULT 35
US-08-496-841C-136
Sequence 136, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-08-496-841C-136

Query Match 20.8%; Score 97; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 IHMKGPLRQQAYLIMISALMALVFIKYLEPTAWLLIAVISYDVLVAVLCPKGPLRLMV 272

|||||
Db 213 IHMKGPLRQQAYLIMISALMALVFIKYLEPTAWLLIAVISYDVLVAVLCPKGPLRLMV 272

Qy 273 ETAOERNETLFPALYSSSTMWLVNMAEGDPEAORRV 309
Db 273 ETAOERNETLFPALYSSSTMWLVNMAEGDPEAORRV 309

RESULT 36
US-09-124-523-4
Sequence 4, Application US/09124523
Patent No. 6395960
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-523-4

Query Match 20.8%; Score 97; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2e-84;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 IHMKGPLRQQAYLIMISALMALVFIKYLEPTAWLLIAVISYDVLVAVLCPKGPLRLMV 272
Db 213 IHMKGPLRQQAYLIMISALMALVFIKYLEPTAWLLIAVISYDVLVAVLCPKGPLRLMV 272

Qy 273 ETAOERNETLFPALYSSSTMWLVNMAEGDPEAORRV 309
Db 273 ETAOERNETLFPALYSSSTMWLVNMAEGDPEAORRV 309

RESULT 37
US-08-788-231A-17
Sequence 17, Application US/08788231A
Patent No. 6019974
GENERAL INFORMATION:
APPLICANT: L'Hernault, Steven W.
TITLE OF INVENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND
METHODS

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,231A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,672
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 60-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: YES
US-08-788-231A-17

Query Match 18.0%; Score 84; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. No. 7.9e-72;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 QVQDDEDEDELTKYAKHVMFLFVVTLCMVVYVATISVSFYTRKQGLYTPPTE 120
DB 60 QVQDDEDEDELTKYAKHVMFLFVVTLCMVVYVATISVSFYTRKQGLYTPPTE 119
QY 121 DTEVQGRALHSILNAIMISIV 144
DB 120 DTEVQGRALHSILNAIMISIV 143

RESULT 38
US-08-967-101-138
Sequence 138, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-101-138

Query Match 6.0%; Score 28; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPKGPLRLMVEYTAQERNE 280
DB 183 ISVYDLVAVLCPKGPLRLMVEYTAQERNE 210

RESULT 39
US-08-592-541-138
Sequence 138, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-541-138

Query Match 6.0%; Score 28; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 253 ISVYDLVAVLCRPGPLRMVETAEERNE 280
|||||
Db 183 ISVYDLVAVLCRPGPLRMVETAEERNE 210

RESULT 40

US-09-124-698-138
; Sequence 138, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124.698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592.541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-124-698-138

Query Match 6.0%; Score 28; DB 3; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 253 ISVYDLVAVLCRPGPLRMVETAEERNE 280
|||||
Db 183 ISVYDLVAVLCRPGPLRMVETAEERNE 210

RESULT 41

US-09-127-480-138
; Sequence 138, Application US/09127480
; Patent No. 6194153
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127.480
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7100
; TELEFAX: (617) 248-7000
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-127-480-138

Query Match 6.0%; Score 28; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 253 ISVYDLVAVLCRPGPLRMVETAEERNE 280
|||||
Db 183 ISVYDLVAVLCRPGPLRMVETAEERNE 210

RESULT 42

US-08-496-841C-138
; Sequence 138, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496.841C
; FILING DATE: 28-Jun-1995
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehner, Ph.D.
; REGISTRATION NUMBER: 35,135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237

Thu Feb 6 15:36:10 2003

INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 138:
US-08-496-841C-138

Query Match 6.0%; Score 28; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ISYDVLAVLCPKGPLRLMVLVETAEERNE 280
|||||
DB 183 ISYDVLAVLCPKGPLRLMVLVETAEERNE 210

RESULT 43

US-09-124-523-138
Sequence 138, Application US/09124523
Patent No. 6395960

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-124-523-138

Query Match 6.0%; Score 28; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ISYDVLAVLCPKGPLRLMVLVETAEERNE 280
|||||
DB 183 ISYDVLAVLCPKGPLRLMVLVETAEERNE 210

RESULT 44

US-08-875-972-29
Sequence 29, Application US/08875972
Patent No. 5985564

GENERAL INFORMATION:
APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millita Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173-4799

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,972
FILING DATE: 08-AUG-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan Esq., Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: H095-03PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-972-29

Query Match 6.0%; Score 28; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ISYDVLAVLCPKGPLRLMVLVETAEERNE 280
|||||
DB 259 ISYDVLAVLCPKGPLRLMVLVETAEERNE 286

RESULT 45

US-08-967-101-137
Sequence 137, Application US/08967101
Patent No. 5840540

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-101-137

Query Match 6.0%; Score 28; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPKGPLRMLVETAQERNE 280
Db 259 ISVYDLVAVLCPKGPLRMLVETAQERNE 286

RESULT 46
US-08-592-541-137
Sequence 137, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-541-137

Query Match 6.0%; Score 28; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPKGPLRMLVETAQERNE 280
Db 259 ISVYDLVAVLCPKGPLRMLVETAQERNE 286

RESULT 47
US-08-888-077A-19
Sequence 19, Application US/08888077A
Patent No. 6020143
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-077A-19

Query Match 6.0%; Score 28; DB 3; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPKGPLRMLVETAQERNE 280
Db 259 ISVYDLVAVLCPKGPLRMLVETAQERNE 286

RESULT 48
US-09-124-698-137
Sequence 137, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

```

1 NUMBER OF SEQUENCES: 183
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
4 STREET: High Street Tower - 125 High Street
5 CITY: Boston
6 STATE: Massachusetts
7 COUNTRY: U.S.A.
8 ZIP: 02110
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patentin Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/124,698
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/592,541
21 FILING DATE:
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Pitcher, Edmund R.
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (617) 248-7000
26 TELEFAX: (617) 248-7100
27 INFORMATION FOR SEQ ID NO: 137:
28
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 448 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35
36 US-09-124-698-137
37
38 Query Match 6.0%; Score 28; DB 3; Length 448;
39 Best Local Similarity 100.0%; Pred. No. 1,8e-18;
40 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
41
42 QY 253 ISYDVLVAVLCPKGPLRLVETAGQRNE 280
43 ||||||||||||||||||||||||||||
44 Db 259 ISYDVLVAVLCPKGPLRLVETAGQRNE 286
45
46 RESULT 49
47 US-09-127-480-137
48 Sequence 137, Application US/09127480
49 Patent No. 6194153
50 GENERAL INFORMATION:
51 APPLICANT: ST. GEORGE-HYSLOP, PETER H
52 APPLICANT: KOMMENS, JOHANNA M
53 APPLICANT: FRASER, PAUL E
54 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
55 TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
56 NUMBER OF SEQUENCES: 183
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
59 STREET: High Street Tower - 125 High Street
60 CITY: Boston
61 STATE: Massachusetts
62 COUNTRY: U.S.A.
63 ZIP: 02110
64
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 COMPUTER: IBM PC compatible
68 OPERATING SYSTEM: PC-DOS/MS-DOS
69 SOFTWARE: Patentin Release #1.0, Version #1.30
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER: US/09/127,480
72 FILING DATE:
73 CLASSIFICATION:
74 PRIOR APPLICATION DATA:
75 APPLICATION NUMBER: US/08/592,541
76 FILING DATE:

```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Pitcher, Edmund R.
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 248-7000
: TELEFAX: (617) 248-7100
: INFORMATION FOR SEQ ID NO: 137:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 448 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-127-480-137

Query Match 6.0%; Score 28; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPKGPRLMLVETAEQERNE 280
|||||
Db 259 ISVYDLVAVLCPKGPRLMLVETAEQERNE 286

RESULT 50
US-09-227-725A-2
: Sequence 2, Application US/09227725A
: Patent No. 6383758
: GENERAL INFORMATION:
: APPLICANT: St. George-Hyslop, Peter H.
: APPLICANT: Kommens, Johanna
: APPLICANT: Frisner, Paul E.
: TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
: TITLE OF INVENTION: of use
: FILE REFERENCE: 1034/1P810-US1
: CURRENT APPLICATION NUMBER: US/09/227,725A
: CURRENT FILING DATE: 1999-01-08
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 448
: TYPE: PRT
: ORGANISM: Homo Sapien
:
US-09-227-725A-2

Query Match 6.0%; Score 28; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPKGPRLMLVETAEQERNE 280
|||||
Db 259 ISVYDLVAVLCPKGPRLMLVETAEQERNE 286

Search completed: February 6, 2003, 14:21:24
Job time : 41.1598 secs
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:14:21 : Search time 61.0394 Seconds
(without alignments)
1019.473 Million cell updates/sec

Title: US-09-689-159A-2

Perfect score: 467
Sequence: 1 MTELPAPLSTFYQNQMSQDN.....ATDYLVQPMQQLAFHQFYI 467

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	438	93.8	463	17	AAW05734
2	438	93.8	463	19	AAW05735
3	366	78.4	467	17	AAW05733
4	366	78.4	467	19	AAW05734
5	366	78.4	467	19	AAW05735
6	366	78.4	467	20	AAW05736
7	366	78.4	467	20	AAW05737
8	366	78.4	467	21	AAW05738
9	366	78.4	467	22	AAW05739
10	366	78.4	467	22	AAW05740

11	366	78.4	467	22	AAW05741	Human presenilin (
12	366	78.4	467	23	AAW05742	Presenilin protein
13	366	78.4	467	23	AAW05743	Human presenilin-1
14	366	78.4	467	23	AAW05744	Human mutant prese
15	337	72.2	463	18	AAW11840	Early onset Alzheimer
16	337	72.2	463	19	AAW20854	Human presenilin I
17	337	72.2	463	18	AAW11839	Human early onset
18	309	66.2	429	19	AAW14829	PS1/429 protein.
19	308	66.0	467	17	AAW05752	Presenilin-1-1 C41
20	306	65.5	467	17	AAW05753	Partial AD3 sequen
21	290	62.1	467	17	AAW05754	Presenilin-1-1 L39
22	287	61.5	467	17	AAW05755	Presenilin-1-1 A79
23	284	60.8	467	23	AAW05756	Presenilin-1-1 V82
24	284	60.8	467	23	AAW05757	Human mutant prese
25	282	60.4	467	17	AAW05758	Presenilin-1-1 G38
26	270	57.8	467	17	AAW05759	Presenilin-1-1 V96
27	265	56.7	467	17	AAW05760	Presenilin-1-1 C26
28	265	56.7	467	17	AAW05761	Presenilin-1-1 P26
29	265	56.7	467	17	AAW05762	Presenilin-1-1 E28
30	265	56.7	467	17	AAW05763	Presenilin-1-1 A28
31	265	56.7	467	17	AAW05764	Presenilin-1-1 L28
32	265	56.7	467	17	AAW05765	Presenilin-1-1 Y11
33	265	56.7	467	17	AAW05766	Presenilin-1-1 M13
34	265	56.7	467	17	AAW05767	Presenilin-1-1 I14
35	265	56.7	467	17	AAW05768	Presenilin-1-1 H16
36	265	56.7	467	17	AAW05769	Presenilin-1-1 L17
37	265	56.7	467	17	AAW05770	Presenilin-1-1 G20
38	265	56.7	467	17	AAW05771	Presenilin-1-1 I21
39	265	56.7	467	17	AAW05772	Presenilin-1-1 I23
40	265	56.7	467	17	AAW05773	Presenilin-1-1 A24
41	265	56.7	467	17	AAW05774	Presenilin-1-1 A26
42	265	56.7	467	17	AAW05775	Human S182 gene, P
43	265	56.7	467	17	AAW05776	Human S182 gene, P
44	265	56.7	467	17	AAW05777	Human S182 gene, P
45	265	56.7	467	17	AAW05778	Human S182 gene, P
46	265	56.7	467	17	AAW05779	Human S182 gene, P
47	265	56.7	467	17	AAW05780	Human S182 gene, P
48	265	56.7	467	17	AAW05781	Human S182 gene, P
49	265	56.7	467	17	AAW05782	Human S182 gene, P
50	265	56.7	467	17	AAW05783	Human S182 gene, P
51	265	56.7	467	17	AAW05784	Human S182 gene, P
52	265	56.7	467	17	AAW05785	Human S182 gene, P
53	265	56.7	467	17	AAW05786	Human S182 gene, P
54	265	56.7	467	17	AAW05787	Human S182 gene, P
55	265	56.7	467	17	AAW05788	Human S182 gene, P
56	265	56.7	467	17	AAW05789	Human S182 gene, P
57	265	56.7	467	17	AAW05790	Human S182 gene, P
58	265	56.7	467	17	AAW05791	Human S182 gene, P
59	265	56.7	467	17	AAW05792	Human S182 gene, P
60	265	56.7	467	17	AAW05793	Human S182 gene, P
61	265	56.7	467	17	AAW05794	Human S182 gene, P
62	265	56.7	467	17	AAW05795	Human S182 gene, P
63	265	56.7	467	17	AAW05796	Human S182 gene, P
64	265	56.7	467	17	AAW05797	Human S182 gene, P
65	265	56.7	467	17	AAW05798	Human S182 gene, P
66	265	56.7	467	17	AAW05799	Human S182 gene, P
67	265	56.7	467	17	AAW05800	Human S182 gene, P
68	265	56.7	467	17	AAW05801	Human S182 gene, P
69	265	56.7	467	17	AAW05802	Human S182 gene, P
70	265	56.7	467	17	AAW05803	Human S182 gene, P
71	265	56.7	467	17	AAW05804	Human S182 gene, P
72	265	56.7	467	17	AAW05805	Human S182 gene, P
73	265	56.7	467	17	AAW05806	Human S182 gene, P
74	265	56.7	467	17	AAW05807	Human S182 gene, P
75	265	56.7	467	17	AAW05808	Human S182 gene, P
76	265	56.7	467	17	AAW05809	Human S182 gene, P
77	265	56.7	467	17	AAW05810	Human S182 gene, P
78	265	56.7	467	17	AAW05811	Human S182 gene, P
79	265	56.7	467	17	AAW05812	Human S182 gene, P
80	265	56.7	467	17	AAW05813	Human S182 gene, P
81	265	56.7	467	17	AAW05814	Human S182 gene, P
82	265	56.7	467	17	AAW05815	Human S182 gene, P
83	265	56.7	467	17	AAW05816	Human S182 gene, P

184	28	6.0	359	22	AAW23821	Human EST encoded	157	8	1.7	160	18	AAW11788	Early onset Alzheimer
185	28	6.0	447	17	AAW28508	Full AD/AD3LP seq	158	8	1.7	263	19	AAW54946	Mouse neurogenin 2
186	28	6.0	448	17	AAW05762	Human presenilin-2	159	8	1.7	263	21	AAW70569	Mouse neurogenin 2
187	28	6.0	448	17	AAW05763	Presenilin-2 M339V	160	8	1.7	263	22	AAW60351	Mouse acetal homol
188	28	6.0	448	17	AAW05764	Presenilin-2 M411I	161	8	1.7	263	22	AAW60362	Mouse neurogenin 2
189	28	6.0	448	17	AAW05765	Presenilin-2 I420T	162	8	1.7	263	22	AAW60365	Mouse atonal homol
190	28	6.0	448	18	AAW11321	Human AD4 protein.	163	8	1.7	368	22	AAW61059	Dog P-glycoprotein
191	28	6.0	448	19	AAW23967	Human presenilin-2	164	8	1.7	368	22	AAW60305	Dog P-glycoprotein
192	28	6.0	448	20	AAW23898	Amino acid sequenc	165	8	1.7	498	22	AAW60305	Novel human diagno
193	28	6.0	448	21	AAW23972	Amino acid sequenc	166	8	1.7	519	22	ABW29362	Drosophila melanog
194	28	6.0	448	22	AAW10799	Human presenilin-2	167	8	1.7	1272	21	AAW70596	Rat multidrug resi
195	28	6.0	448	22	AAW63937	Amino acid sequenc	168	8	1.7	1272	21	AAW70597	Rat multidrug resi
196	28	6.0	448	22	AAW05467	Human presenilin (169	8	1.7	1276	21	AAW58189	Murine multidrug r
197	28	6.0	448	23	AAW79417	Human presenilin-2	170	8	1.7	1276	23	AAW79435	Chinese hamster P-
198	28	6.0	448	23	AAW17049	Human mutant prese	171	8	1.7	1276	23	AAW79435	Mouse BCRP protein
199	28	6.0	448	23	AAW17052	Human mutant prese	172	8	1.7	1279	19	AAW80294	Mutated human P-g
100	28	6.0	476	19	AAW20921	Mouse presenilin 1	173	8	1.7	1279	22	AAW81067	Human P-glycoprote
101	25	5.4	33	22	AAW08331	Mouse partial PS-1	174	8	1.7	1279	22	AAW81067	Sequence encoded b
102	24	5.1	414	17	AAW05766	Presenilin-2 delta	175	8	1.7	1280	8	AAW70452	Sequence encoded b
103	24	5.1	448	23	AAW17048	Human mutant prese	176	8	1.7	1280	11	AAW44868	Sequence encoded b
104	24	5.1	448	23	AAW17050	Human mutant prese	177	8	1.7	1280	14	AAW44297	Sequence encoded b
105	23	4.9	448	19	AAW50188	Monoclonal antibod	178	8	1.7	1280	15	AAW63624	Human P-glycoprote
106	23	4.9	47	19	AAW50185	Presenilin-1 fragm	179	8	1.7	1280	18	AAW44073	Human multidrug re
107	23	4.9	124	21	AAW27380	Human presenilin-2	180	8	1.7	1280	19	AAW48997	Wild-type human P
108	22	4.7	22	22	AAW10988	Human presenilin b	181	8	1.7	1280	19	AAW48998	N-terminal single
109	22	4.7	541	22	AAW05767	Presenilin homolog	182	8	1.7	1280	19	AAW48999	C-terminal single
110	22	4.7	541	22	AAW17435	Drosophila melanog	183	8	1.7	1280	19	AAW49000	Human P-glycoprote
111	21	4.5	21	17	AAW05788	Presenilin-1-1 res	184	8	1.7	1280	21	AAW58186	Human wild-type mu
112	20	4.3	21	19	AAW50186	Monoclonal antibod	185	8	1.7	1280	21	AAW58187	Human G185V mutat
113	19	4.1	20	18	AAW34092	Peptide derived fr	186	8	1.7	1280	22	AAW04347	Human multidrug re
114	18	3.9	18	17	AAW05768	Presenilin-1-1 res	187	8	1.7	1280	22	AAW81064	Cynomolgous monke
115	18	3.9	376	18	AAW28506	AD4/AD3LP sequenc	188	8	1.7	1280	22	AAW81066	Human P-glycoprote
116	18	3.9	461	18	AAW14006	Caenorhabditis ele	189	8	1.7	1280	22	AAW81068	Dog P-glycoprote
117	18	3.9	461	18	AAW14007	Caenorhabditis ele	190	8	1.7	1280	22	AAW81068	Human P-glycoprote
118	16	3.4	16	23	ABW07647	Human PS-1 hydrop	191	8	1.7	1280	22	AAW00304	Human MDR1. Homo
119	16	3.4	17	22	AAW12869	Presenilin peptide	192	8	1.7	1280	22	AAW00306	Dog P-glycoprote
120	16	3.4	125	18	AAW11782	Early onset Alzheimer	193	8	1.7	1280	23	AAW24211	Human MDR protein.
121	15	3.2	15	17	AAW05783	Presenilin-1-1 res	194	8	1.7	1280	23	AAW97493	Human P-glycoprote
122	15	3.2	15	21	AAW91072	Keyhole limpet hae	195	8	1.7	1280	23	AAW18964	Human wild type P-
123	15	3.2	16	18	AAW34093	Peptide derived fr	196	8	1.7	1280	23	AAW18965	Human P-gp mutat.
124	15	3.2	16	22	AAW12898	Presenilin peptide	197	8	1.7	1280	23	AAW18966	Human P-gp mutat.
125	15	3.2	16	22	AAW12902	Monoclonal antibod	198	8	1.7	1280	23	AAW18967	Human P-gp mutat.
126	15	3.2	22	19	AAW50187	Arabidopsis thalia	199	8	1.7	1280	23	AAW18968	Human P-gp mutat.
127	15	3.2	294	21	AAW47376	Arabidopsis thalia	200	8	1.7	1280	23	AAW18969	Human P-gp mutat.
128	15	3.2	344	21	AAW47375	Arabidopsis thalia	201	8	1.7	1280	23	AAW18970	Human P-gp mutat.
129	15	3.2	349	21	AAW47374	Arabidopsis thalia	202	8	1.7	1280	23	AAW18971	Human P-gp mutat.
130	15	3.2	355	21	AAW32560	Arabidopsis thalia	203	8	1.7	1280	23	AAW18972	Human P-gp mutat.
131	15	3.2	430	21	AAW32560	Arabidopsis thalia	204	8	1.7	1280	23	AAW18973	Human P-gp mutat.
132	15	3.2	437	21	AAW17559	Arabidopsis thalia	205	8	1.7	1280	23	AAW18974	Human P-gp mutat.
133	15	3.2	437	21	AAW32499	Arabidopsis thalia	206	8	1.7	1280	23	AAW18975	Human P-gp mutat.
134	15	3.2	453	21	AAW17558	Arabidopsis thalia	207	8	1.7	1280	23	AAW18976	Human P-gp mutat.
135	15	3.2	453	21	AAW32498	Arabidopsis thalia	208	8	1.7	1280	23	AAW18977	Human P-gp mutat.
136	14	3.0	14	17	AAW05785	Presenilin-1-1 res	209	8	1.7	1280	23	AAW18978	Human P-gp mutat.
137	11	2.4	11	17	AAW05770	Presenilin-1-1 res	210	8	1.7	1280	23	AAW18979	Human P-gp mutat.
138	11	2.4	11	17	AAW05778	Presenilin-1-1 res	211	8	1.7	1280	23	AAW18980	Human P-gp mutat.
139	11	2.4	11	17	AAW05784	Presenilin-1-1 res	212	8	1.7	1280	23	AAW18997	Human BCRP protein
140	11	2.4	11	17	AAW05786	Presenilin-1-1 res	213	8	1.7	1280	23	AAW07267	Human BCRP protein
141	11	2.4	11	17	AAW05787	Presenilin-1-1 res	214	8	1.7	1280	23	AAW07267	Human BCRP protein
142	11	2.4	87	20	AAW07219	Presenilin/beta-am	215	8	1.7	1281	22	AAW00303	Dog (BCP) P-glycop
143	10	2.1	10	17	AAW05776	Presenilin-1-1 res	216	8	1.7	1281	22	AAW00308	Dog P-glycoprotein
144	10	2.1	10	17	AAW05780	Presenilin-1-1 res	217	8	1.7	1281	22	AAW00309	Dog P-glycoprotein
145	9	1.9	9	17	AAW05782	Presenilin-1-1 res	218	8	1.7	1281	22	AAW00310	Dog P-glycoprotein
146	9	1.9	9	19	AAW50184	Presenilin-1 NT1 e	219	8	1.7	1283	22	AAW81065	Cynomolgous monke
147	8	1.7	8	22	AAW66579	Synthetic peptide	220	8	1.7	2958	22	ABW71368	Drosophila melanog
148	8	1.7	8	22	AAW61341	Recombinant human	221	7	1.5	7	17	AAW05771	Presenilin-1-1 res
149	8	1.7	8	23	AAW99495	Presenilin 1 deriv	222	7	1.5	8	22	AAW66576	Peptide derived fr
150	8	1.7	8	23	ABW06457	Beta-secretase rel	223	7	1.5	8	22	AAW61338	Peptide from proce
151	8	1.7	8	23	AAW75235	Consensus active s	224	7	1.5	8	23	AAW99492	Presenilin 1 deriv
152	8	1.7	19	22	AAW04310	ATP-binding cass	225	7	1.5	8	23	AAW75254	Active site peptid
153	8	1.7	21	18	AAW34052	Human MDR1-P glyco	226	7	1.5	11	17	AAW05807	Presenilin-2 resid
154	8	1.7	75	20	AAW30726	Amino acid sequenc	227	7	1.5	13	21	AAW01687	F151 polypeptide s
155	8	1.7	87	22	AAW74007	Human colon cancer	228	7	1.5	17	21	AAW52037	Human secreted pro
156	8	1.7	126	18	AAW11781	Early onset Alzheimer	229	7	1.5	25	22	ABW32318	Peptide #4969 enco

376	7	1.5	401	23	ABR93450	Herbicidally activ	449	7	1.5	712	18	AAW30749	Rat Y7521 gene pro
377	7	1.5	403	21	AA637514	Arabidopsis thalia	450	7	1.5	714	22	ABG12681	Novel human diagno
378	7	1.5	405	20	AAW04121	Pancreas derived p	451	7	1.5	731	22	ABG12985	Novel human diagno
379	7	1.5	405	20	AAW01601	Protein encoded by	452	7	1.5	731	23	ABR92517	Herbicidally activ
380	7	1.5	405	21	AA637513	Arabidopsis thalia	453	7	1.5	739	22	AA693019	C glutamicum prote
381	7	1.5	405	23	AAE14267	Human Pancreas-der	454	7	1.5	740	19	AAW61533	Human Fas-binding
382	7	1.5	410	21	AAE51721	Human secreted pro	455	7	1.5	740	22	AAU00631	Human death-assoc
383	7	1.5	410	21	AAE51722	Human secreted pro	456	7	1.5	740	22	AAU00631	Human death-assoc
384	7	1.5	411	21	AA639052	Arabidopsis thalia	457	7	1.5	746	21	AAE82742	DNA replication an
385	7	1.5	415	22	ABE52991	Escherichia coli p	458	7	1.5	748	22	ABE57847	Drosophila melanog
386	7	1.5	418	22	AA681186	Mycobacterium tube	459	7	1.5	748	22	AAU34685	E. coli cellular p
387	7	1.5	418	23	ABE61059	Lactobacillus rham	460	7	1.5	748	22	AAU34685	Salmonella typhi c
388	7	1.5	425	22	ABE71352	Arabidopsis thalia	461	7	1.5	765	22	AAU03520	Human protein kina
389	7	1.5	434	21	AAE67240	Human adipophilli-	462	7	1.5	765	23	AAE16275	Human kinase PKIN-
390	7	1.5	438	22	ABE52864	Escherichia coli p	463	7	1.5	774	19	AAW80411	A secreted protein
391	7	1.5	443	21	AA614645	Arabidopsis thalia	464	7	1.5	774	23	ABE61829	Human polypeptide
392	7	1.5	443	22	AAE20005	Arabidopsis 3-keto	465	7	1.5	775	23	AAU93161	Human polypeptide
393	7	1.5	446	21	AA614644	Arabidopsis thalia	466	7	1.5	794	23	AAU93161	Arabidopsis trans
394	7	1.5	447	21	AA637512	Arabidopsis thalia	467	7	1.5	808	22	AAW41031	Human polypeptide
395	7	1.5	449	22	ABE50668	C. elegans UNC-5 p	468	7	1.5	814	22	ABG21977	Human polypeptide
396	7	1.5	451	23	ABE60688	Phaseolin promoter	469	7	1.5	817	22	ABE95119	Novel human diagno
397	7	1.5	452	21	AA605734	Arabidopsis thalia	470	7	1.5	830	23	ABE04808	Human protein sequ
398	7	1.5	456	21	AA605733	Arabidopsis thalia	471	7	1.5	830	23	ABE04810	LDL receptor bindi
399	7	1.5	461	18	AAW19276	Pseudomonas aerugi	472	7	1.5	830	23	ABE04811	LDL receptor bindi
400	7	1.5	477	18	AAW25153	Nsp7524111 restric	473	7	1.5	830	23	ABE04812	LDL receptor bindi
401	7	1.5	478	17	AAE95956	Eukaryotic cell gr	474	7	1.5	830	23	ABE04813	LDL receptor bindi
402	7	1.5	482	21	AAE58366	Anabaena variabil	475	7	1.5	849	23	ABE97265	Novel human protei
403	7	1.5	489	23	ABG64061	Human albumin fusi	476	7	1.5	896	19	AAW41252	Xenopus paraxial p
404	7	1.5	494	19	AAW42394	Pyrococcus furiosu	477	7	1.5	903	20	AAE28713	Deactivated yeast m
405	7	1.5	498	12	AAE13713	PRV glycoprotein g	478	7	1.5	906	20	AAE28702	Yeast multifunctio
406	7	1.5	498	12	AAE13716	Pseudorabies virus	479	7	1.5	906	20	AAE28712	Mutant yeast multi
407	7	1.5	502	22	ABE78823	Pseudorabies virus	480	7	1.5	906	22	AAE20180	Candida tropicalis
408	7	1.5	505	22	AAE01380	Human gene 4 encod	481	7	1.5	906	22	AAE20181	C. tropicalis multi
409	7	1.5	507	22	ABE60080	Human breast cance	482	7	1.5	906	22	AAE20182	C. tropicalis multi
410	7	1.5	512	23	ABP41659	Human ovarian anti	483	7	1.5	906	22	AAE20183	C. tropicalis multi
411	7	1.5	525	21	AAE25294	Eucalyptus grandis	484	7	1.5	938	22	ABE60562	Drosophila melanog
412	7	1.5	527	20	AAE29515	Human lung tumour	485	7	1.5	978	22	ABE59935	Drosophila melanog
413	7	1.5	527	21	AAE44492	Human lung tumour-	486	7	1.5	1022	22	ABE62978	Drosophila melanog
414	7	1.5	527	22	AAE13805	Human lung tumour	487	7	1.5	1024	17	AAW03184	Rice Xa21 (RRK-F)
415	7	1.5	527	22	AAU29284	Human PRO polypept	488	7	1.5	1062	22	ABE71830	Drosophila melanog
416	7	1.5	527	23	AAU7927	Human drug-metabol	489	7	1.5	1134	22	AAU28072	Novel human secret
417	7	1.5	527	23	AAE15434	Human drug-metabol	490	7	1.5	1145	22	ABE62435	Drosophila melanog
418	7	1.5	530	23	AAE52210	Bacillus cellullar dif	491	7	1.5	1149	22	AAW41048	Human polypeptide
419	7	1.5	542	17	AAE90772	Oleosin stearothe	492	7	1.5	1159	22	ABE63460	Drosophila melanog
420	7	1.5	545	20	AAE33830	oleosin-spacer-met	493	7	1.5	1162	21	AAE96255	Kaposi's sarcoma-a
421	7	1.5	545	22	ABE68867	Drosophila melanog	494	7	1.5	1162	21	AAE58500	HHV8 ORF 73 protei
422	7	1.5	545	22	AAU38979	Drosophila G-prote	495	7	1.5	1162	22	AAE62331	Amino acid sequenc
423	7	1.5	559	22	AAE38813	Human polypeptide	496	7	1.5	1162	23	ABE62321	Kaposi's sarcoma-a
424	7	1.5	564	23	ABP40294	Staphylococcus epi	497	7	1.5	1174	22	ABE80539	Shrimp white spot
425	7	1.5	566	21	AAE66641	Membrane-bound pro	498	7	1.5	1245	21	AAE18244	Plasmodium falcipla
426	7	1.5	566	22	AAU29051	Human PRO polypept	499	7	1.5	1263	22	AAE94749	Human protein sequ
427	7	1.5	566	22	AAE65164	Human PRO710 (UNC3	500	7	1.5	1282	22	ABE44552	Human wound healin
428	7	1.5	571	23	ABP39020	Staphylococcus epi	501	7	1.5	1357	21	AAE31776	Arabidopsis thalia
429	7	1.5	580	22	ABE62193	Drosophila melanog	502	7	1.5	1371	22	ABE21216	Novel human diagno
430	7	1.5	585	22	ABE16868	Novel human diagno	503	7	1.5	1406	21	AAE31775	Arabidopsis thalia
431	7	1.5	596	21	AAE39850	Arabidopsis thalia	504	7	1.5	1407	21	AAE31774	Arabidopsis thalia
432	7	1.5	611	22	ABE60610	Drosophila melanog	505	7	1.5	1413	23	AAE21729	Human PKIN-24 prot
433	7	1.5	613	22	ABG22924	Novel human diagno	506	7	1.5	1488	22	AAE10801	Rat TGF-beta Resis
434	7	1.5	616	23	ABE83078	Synoviolin related	507	7	1.5	1489	22	AAE10803	Mouse TGF-beta Res
435	7	1.5	617	22	AAE01355	Human gene 4 encod	508	7	1.5	1490	22	AAE10802	Human TGF-beta Res
436	7	1.5	617	23	ABE83074	Synoviolin amino a	509	7	1.5	1572	18	AAW27160	Mouse receptor ME2
437	7	1.5	617	23	ABE64063	Human albumin fusi	510	7	1.5	1651	23	ABE66725	Human novel polype
438	7	1.5	624	22	ABE70398	Drosophila melanog	511	7	1.5	1675	21	AAE42658	Human OREF ORE2422
439	7	1.5	641	22	AAE23689	Human EST encoded	512	7	1.5	1905	22	ABE59743	Drosophila melanog
440	7	1.5	645	22	AAW40599	Human polypeptide	513	7	1.5	1905	22	AAU38925	Drosophila G-prote
441	7	1.5	659	23	ABE93561	Herbicidally activ	514	7	1.5	1972	19	AAW81171	Human BAZ2-Beta pr
442	7	1.5	664	22	AAW39262	Human polypeptide	515	7	1.5	2047	23	AAU75883	Human adhesion mol
443	7	1.5	671	23	ABE92516	Herbicidally activ	516	7	1.5	2175	22	ABE65698	Drosophila melanog
444	7	1.5	687	22	ABE59384	Drosophila melanog	517	7	1.5	2278	21	AAE53677	Sequence g1/341388
445	7	1.5	689	20	AAE42698	Arabidopsis seed s	518	7	1.5	2281	22	AAW40857	Human polypeptide
446	7	1.5	689	21	AAE01673	F151 protein sequ	519	7	1.5	2380	21	AAE18515	Plasmodium falcipla
447	7	1.5	689	21	AAE57036	Fertilisation-lnde	520	7	1.5	2415	22	ABG20279	Novel human diagno
448	7	1.5	689	22	AAE82455	Arabidopsis seed-s	521	7	1.5	2448	22	AAU36277	Pseudomonas aerugi

522	7	1.5	2458	22	AAU28088	Novel human secret	595	6	1.3	23	20	AAW97865	Human cytokine rec
523	7	1.5	2458	22	AAW39071	Human polypeptide	596	6	1.3	24	18	AAW23485	Antibacterial endo/
524	7	1.5	2647	18	AAW19349	Human filamin. Ho	597	6	1.3	24	18	AAW1884	Nerve cell death i
525	7	1.5	2647	20	AAW33867	Carboxyl terminal	598	6	1.3	25	19	AAW74840	Human secreted pro
526	7	1.5	2707	18	AAW27161	Muscle receptor ME2	599	6	1.3	25	19	AAW11949	Human BPGW peptide
527	7	1.5	2995	19	AAW56643	DNA-dependent prot	600	6	1.3	27	20	AAW02986	Fragment of human
528	7	1.5	3262	21	AAW53675	Mechanical stress	601	6	1.3	28	20	AAW12029	Human 5' EST secre
529	7	1.5	3264	21	AAW53675	Protein 274 sequen	602	6	1.3	28	22	AAW90447	Human immune/haema
530	7	1.5	3960	19	AAW56642	Protein kinase cat	603	6	1.3	28	22	AAW23242	Streptococcus agal
531	7	1.5	4498	22	AAW58595	Drosophila melanog	604	6	1.3	29	21	AAW7381	Catonic antimitro
532	6	1.3	6	17	AAW05774	Presenilin-1-1 res	605	6	1.3	29	21	AAW67381	Human 5' EST relat
533	6	1.3	6	17	AAW05779	Presenilin-1-1 res	606	6	1.3	29	21	AAW65388	Transplant media a
534	6	1.3	6	18	AAW34888	F74 splice mutant	607	6	1.3	30	21	AAW09095	Human 5' EST relat
535	6	1.3	6	18	AAW22378	S182 gene mutation	608	6	1.3	30	23	AAW52234	HCV HepCia segment
536	6	1.3	6	18	AAW22378	S182 gene mutation	609	6	1.3	30	23	AAW84692	HCV HepCia segment
537	6	1.3	6	18	AAW22381	S182 gene mutation	610	6	1.3	31	23	AAW84692	Peptide with growl
538	6	1.3	9	20	AAW97282	Cytotoxic T-cell e	611	6	1.3	32	9	AAW80106	Encoded by Staphyl
539	6	1.3	10	16	AAW82643	HML-1 alpha-E chal	612	6	1.3	32	16	AAW84971	Peptide rII from
540	6	1.3	10	16	AAW82644	HML-1 alpha-E chal	613	6	1.3	34	21	AAW34780	Human secreted pro
541	6	1.3	10	16	AAW82645	HML-1 alpha-E chal	614	6	1.3	34	23	AAW04574	Hepatitis C capsid
542	6	1.3	10	16	AAW82646	HML-1 alpha-E chal	615	6	1.3	35	22	AAW79608	Human protein SBQ
543	6	1.3	10	16	AAW82646	Human CASB765 epit	616	6	1.3	35	22	AAW83655	Human immune/haema
544	6	1.3	12	16	AAW82652	HML-1 alpha-E chal	617	6	1.3	36	21	AAW828719	Human secreted pro
545	6	1.3	12	16	AAW97977	Human peptide #125	618	6	1.3	37	19	AAW75048	Fragment of human
546	6	1.3	12	23	AAW68979	Signature motif #5	619	6	1.3	37	21	AAW33728	Human secreted pro
547	6	1.3	13	22	AAW97978	Human peptide #125	620	6	1.3	37	21	AAW321571	Cone snail alpha-c
548	6	1.3	14	16	AAW82648	HML-1 alpha-E chal	621	6	1.3	38	21	AAW51652	Human secreted pro
549	6	1.3	14	23	AAW67894	Human ADP tryptic	622	6	1.3	39	14	AAW33869	Polyptide p1418
550	6	1.3	15	16	AAW82650	HML-1 alpha-E chal	623	6	1.3	39	21	AAW53975	Human colon cancer
551	6	1.3	15	19	AAW85393	Helper T-cell clas	624	6	1.3	39	22	AAW62649	Novel human diagno
552	6	1.3	15	21	AAW73102	Hepatitis C virus	625	6	1.3	39	22	AAW01102	Human polypeptide
553	6	1.3	15	21	AAW64552	Hepatitis C virus	626	6	1.3	40	12	AAW33352	P1418 HCV antigen
554	6	1.3	15	22	AAW00041	Hepatitis C virus	627	6	1.3	40	21	AAW56574	Arabidopsis thailia
555	6	1.3	15	22	AAW03186	Hepatitis C virus	628	6	1.3	40	22	AAW61618	C glutamylcum prote
556	6	1.3	15	22	AAW03258	Hepatitis C virus	629	6	1.3	41	17	AAW03450	N-acetylglucosamin
557	6	1.3	15	22	AAW03453	Hepatitis C virus	630	6	1.3	41	20	AAW33217	Human beta-catenin
558	6	1.3	15	22	AAW03563	Hepatitis C virus	631	6	1.3	41	20	AAW33232	Human beta-catenin
559	6	1.3	15	22	AAW03648	Hepatitis C virus	632	6	1.3	41	20	AAW11382	Human 5' EST secre
560	6	1.3	15	22	AAW03706	Hepatitis C virus	633	6	1.3	41	21	AAW56118	Human secreted pro
561	6	1.3	15	22	AAW04028	Hepatitis C virus	634	6	1.3	41	21	AAW33935	Human secreted pro
562	6	1.3	15	22	AAW04055	Hepatitis C virus	635	6	1.3	41	22	AAW18597	Human lung antigen
563	6	1.3	15	22	AAW04079	Hepatitis C virus	636	6	1.3	42	22	AAW88741	Secreted protein e
564	6	1.3	15	22	AAW04111	Hepatitis C virus	637	6	1.3	42	22	AAW86591	Novel human connec
565	6	1.3	16	18	AAW25434	Yes SH3 domain bin	638	6	1.3	42	22	AAW50508	Human secreted pro
566	6	1.3	17	19	AAW75144	Human secreted pro	639	6	1.3	42	22	AAW17329	Human nervous syst
567	6	1.3	17	22	AAW22910	Protein #4909 enco	640	6	1.3	42	22	AAW65414	Human brain expres
568	6	1.3	18	10	AAW90023	Human serum albumi	641	6	1.3	42	22	AAW38318	Peptide #12355 enc
569	6	1.3	18	22	AAW29409	Peptide #2060 enco	642	6	1.3	42	23	AAW647105	Human peptide enco
570	6	1.3	18	22	AAW34591	Peptide #2097 enco	643	6	1.3	43	20	AAW88581	Secreted protein e
571	6	1.3	18	22	AAW19997	Protein #1996 enco	644	6	1.3	43	21	AAW58561	Rat somatostatin r
572	6	1.3	18	22	AAW55380	Human brain expres	645	6	1.3	43	21	AAW58562	Mouse somatostatin
573	6	1.3	18	22	AAW67775	Human bone marrow	646	6	1.3	43	21	AAW58563	Human somatostatin
574	6	1.3	18	22	AAW15564	Peptide #2018 enco	647	6	1.3	43	21	AAW64764	Human 5' EST relat
575	6	1.3	18	22	AAW28076	Peptide #2113 enco	648	6	1.3	43	22	AAW47105	Peptide #10108 enc
576	6	1.3	18	22	AAW03328	Peptide #2010 enco	649	6	1.3	43	22	AAW50348	Human secreted pro
577	6	1.3	18	22	AAW37323	Human peptide enco	650	6	1.3	43	22	AAW25970	Protein #7969 enco
578	6	1.3	19	21	AAW34234	Human secreted pep	651	6	1.3	43	22	AAW96018	Human reproductive
579	6	1.3	19	22	AAW22066	Novel human diagno	652	6	1.3	43	22	AAW18866	Human prostate gla
580	6	1.3	19	22	AAW38967	Peptide #6473 enco	653	6	1.3	43	22	AAW63493	Human brain expres
581	6	1.3	19	22	AAW59618	Human bone marrow	654	6	1.3	43	22	AAW63498	Human bone marrow
582	6	1.3	19	22	AAW72191	Human bone marrow	655	6	1.3	43	22	AAW63498	Peptide #10455 enc
583	6	1.3	19	22	AAW32451	Peptide #6488 enco	656	6	1.3	43	23	AAW10092	Human ion channel-
584	6	1.3	19	22	AAW42005	Human peptide enco	657	6	1.3	43	23	AAW45611	Human peptide enco
585	6	1.3	20	16	AAW82651	HML-1 alpha-E chal	658	6	1.3	44	20	AAW13061	Human secreted pro
586	6	1.3	20	21	AAW97375	Chicken Igt Vhl s1	659	6	1.3	44	22	AAW38064	Human secreted pro
587	6	1.3	20	23	AAW85587	Lung tumour protei	660	6	1.3	44	22	AAW33286	Protein #5285 enco
588	6	1.3	20	23	AAW85588	Lung tumour protei	661	6	1.3	44	22	AAW85699	Human brain expres
589	6	1.3	20	23	AAW85589	Chicken Igt Vhl s1	662	6	1.3	44	22	AAW12106	Human bone marrow
590	6	1.3	21	16	AAW82636	HML-1 alpha-E chal	663	6	1.3	44	22	AAW18920	Human 5' EST secre
591	6	1.3	21	22	AAW65831	Murine TANCO 257 s	664	6	1.3	44	22	AAW31467	Peptide #5354 enco
592	6	1.3	21	22	AAW66018	Phage displayed g3	665	6	1.3	44	23	AAW41003	Human peptide enco
593	6	1.3	22	22	AAW03625	Human AZD protein	666	6	1.3	46	20	AAW02778	Human secreted pro
594	6	1.3	22	22	AAW82377	Protein sequence S	667	6	1.3	46	20	AAW12600	Human 5' EST secre

668	6	1.3	46	22	AAM24401	Human EST encoded	741	6	1.3	58	22	AAG73350	Human gene 5-encod
669	6	1.3	46	22	AAU14457	Human novel protei	742	6	1.3	58	22	AAU73386	Human gene 5-encod
670	6	1.3	48	19	AAW75157	Human secreted pro	743	6	1.3	58	23	ABG64205	Human albumin fusi
671	6	1.3	48	22	ABB70642	Drosophila melanog	744	6	1.3	58	23	ABG64206	Human albumin fusi
672	6	1.3	50	20	AAZ52739	Human secreted pro	745	6	1.3	58	23	ABG64209	Human albumin fusi
673	6	1.3	50	22	AAU56573	Proionibacterium	746	6	1.3	59	21	AAU73588	Human peptide enco
674	6	1.3	50	22	AAU62745	Proionibacterium	747	6	1.3	59	22	AAU41209	Arabidopsis thalia
675	6	1.3	50	22	ABB40235	Peptide #7741 enco	748	6	1.3	59	22	AAU82515	Human immunohaema
676	6	1.3	50	22	ABB24665	Protein #664 enco	749	6	1.3	59	22	AAO10963	Human polypeptide
677	6	1.3	50	22	AAU61021	Human brain expres	750	6	1.3	60	20	AAU99073	Human polypeptide
678	6	1.3	50	22	AAU73721	Human bone marrow	751	6	1.3	60	20	AAU88527	Immunoglobulin Iik
679	6	1.3	50	22	AAU73737	Human bone marrow	752	6	1.3	60	22	AAU47728	Fusion of killer t
680	6	1.3	50	22	AAU33908	Human polypeptide	753	6	1.3	61	22	ABG15345	Proionibacterium
681	6	1.3	50	23	ABG43599	Peptide #7945 enco	754	6	1.3	61	22	ABG15347	Novel human diagno
682	6	1.3	50	23	ABP07947	Human peptide enco	755	6	1.3	61	22	AAU14221	Novel human diagno
683	6	1.3	51	15	AAU59858	Human ORFX protein	756	6	1.3	62	16	AAU69526	Human novel protei
684	6	1.3	51	22	AAU14820	Hepatitis C virus	757	6	1.3	62	16	AAU69526	Anti-HCV antibody
685	6	1.3	51	22	ABP02835	Human nervous syst	758	6	1.3	62	16	AAU69531	Anti-HCV antibody
686	6	1.3	52	20	AAU73369	Human ORFX protein	759	6	1.3	62	16	AAU69535	Anti-HCV antibody
687	6	1.3	52	20	AAU73369	Human prostate tum	760	6	1.3	62	22	AAU53228	Proionibacterium
688	6	1.3	53	19	AAU75080	Human secreted pro	761	6	1.3	62	22	AAU67544	Proionibacterium
689	6	1.3	53	21	AAU83376	Human secreted pro	762	6	1.3	62	23	ABP06544	Human ORFX protein
690	6	1.3	53	21	AAU16526	Bacteriophage 77.7	763	6	1.3	63	22	ABU69523	Drosophila melanog
691	6	1.3	53	22	ABU15233	Human nervous syst	764	6	1.3	63	22	AAU67214	Proionibacterium
692	6	1.3	53	22	ABU03171	Human musculoskele	765	6	1.3	63	22	AAU80801	Human haematologic
693	6	1.3	53	23	AAU95379	Human calcium tran	766	6	1.3	63	22	AAU94282	Human reproductive
694	6	1.3	54	20	AAU10870	Amino acid sequenc	767	6	1.3	63	22	AAO13771	Human polypeptide
695	6	1.3	54	21	AAU39049	Human secreted pro	768	6	1.3	64	21	AAU57638	Arabidopsis thalia
696	6	1.3	54	22	ABB30738	Peptide #3389 enco	769	6	1.3	64	22	AAU39438	Proionibacterium
697	6	1.3	54	22	ABB35914	Peptide #420 enco	770	6	1.3	64	22	AAU62362	Proionibacterium
698	6	1.3	54	22	ABB21323	Protein #3322 enco	771	6	1.3	64	22	ABG05340	Novel human diagno
699	6	1.3	54	22	AAU69094	Human brain expres	772	6	1.3	64	23	ABP42478	Human ovarian anti
700	6	1.3	54	22	AAU69094	Human bone marrow	773	6	1.3	64	23	ABP31422	Human ORP395 prote
701	6	1.3	54	22	AAU16932	Peptide #3365 enco	774	6	1.3	65	15	AAU59857	Hepatitis C virus
702	6	1.3	54	22	AAU29417	Peptide #454 enco	775	6	1.3	65	20	AAU12573	Human 5' EST seque
703	6	1.3	54	22	AAU04625	Peptide #307 enco	776	6	1.3	65	21	AAU15090	Human signal pepti
704	6	1.3	54	22	AAU01315	Human gene 6 enco	777	6	1.3	65	21	AAU72332	Human signal pepti
705	6	1.3	55	16	AAU82635	Human peptide enco	778	6	1.3	65	22	AAU57411	Proionibacterium
706	6	1.3	55	22	AAU82635	Human mucosal lym	779	6	1.3	65	22	ABU30691	Peptide #3342 enco
707	6	1.3	55	22	ABB35038	Peptide #2544 enco	780	6	1.3	65	22	ABB35865	Peptide #3371 enco
708	6	1.3	55	22	ABB38298	Peptide #5804 enco	781	6	1.3	65	22	AAU18568	Human lung antigen
709	6	1.3	55	22	ABB23479	Protein #5478 enco	782	6	1.3	65	22	AAU69047	Human bone marrow
710	6	1.3	55	22	AAU58920	Human brain expres	783	6	1.3	65	22	AAU87734	Human immunohaema
711	6	1.3	55	22	AAU71442	Human bone marrow	784	6	1.3	65	22	AAU16884	Peptide #3405 enco
712	6	1.3	55	22	AAU89110	Human immunohaema	785	6	1.3	65	22	AAU29368	Peptide #3405 enco
713	6	1.3	55	22	AAU19095	Peptide #5529 enco	786	6	1.3	65	23	ABG38646	Human peptide enco
714	6	1.3	55	22	AAU28545	Peptide #2582 enco	787	6	1.3	65	23	ABP33298	Human peptide enco
715	6	1.3	55	22	AAU31734	Peptide #5771 enco	788	6	1.3	66	20	AAU00341	Human secreted pro
716	6	1.3	55	23	ABG37755	Human peptide enco	789	6	1.3	66	21	AAU38286	Human secreted pro
717	6	1.3	55	23	ABG41248	Human peptide enco	790	6	1.3	66	21	AAU38290	Human secreted pro
718	6	1.3	55	23	ABP07038	Human ORFX protein	791	6	1.3	67	15	AAU38290	Human ORFX protein
719	6	1.3	56	21	AAU626102	Zea mays protein f	792	6	1.3	67	15	AAU59856	Hepatitis C virus
720	6	1.3	56	22	AAU40524	Proionibacterium	793	6	1.3	68	21	AAU19568	Arabidopsis thalia
721	6	1.3	56	22	ABG25649	Novel human diagno	794	6	1.3	68	21	AAU45680	Arabidopsis thalia
722	6	1.3	56	22	ABU17932	Human nervous syst	795	6	1.3	68	22	AAU61452	Proionibacterium
723	6	1.3	56	22	AAU004488	Human polypeptide	796	6	1.3	68	22	AAU61452	Novel human diagno
724	6	1.3	56	22	AAU77220	Human colon cancer	797	6	1.3	68	22	AAU62849	Human reproductive
725	6	1.3	57	21	ABP32030	Human ORF1003 prot	798	6	1.3	68	23	AAU62849	Human ORFX protein
726	6	1.3	57	21	AAU52114	Human secreted pro	799	6	1.3	69	22	AAU20116	Human polypeptide
727	6	1.3	57	22	ABU41035	Peptide #8541 enco	800	6	1.3	69	22	AAU20116	Human DNA repair a
728	6	1.3	57	22	AAU61890	Human brain expres	801	6	1.3	69	22	AAU32751	Human ORFX protein
729	6	1.3	57	22	AAU74692	Human bone marrow	802	6	1.3	70	22	AAU32751	Novel human secret
730	6	1.3	57	22	AAU606350	Peptide #8845 enco	803	6	1.3	70	22	AAU32751	Human ovarian anti
731	6	1.3	57	22	AAU606350	Human foetal prote	804	6	1.3	71	16	AAU69524	Anti-HCV antibody
732	6	1.3	57	23	ABP03087	Human ORFX protein	805	6	1.3	71	16	AAU69524	Anti-HCV antibody
733	6	1.3	58	22	ABG19930	Streptococcus poly	806	6	1.3	71	16	AAU69524	Anti-HCV antibody
734	6	1.3	58	22	ABU41187	Novel human diagno	807	6	1.3	71	16	AAU69524	Anti-HCV antibody
735	6	1.3	58	22	ABU41187	Peptide #8693 enco	808	6	1.3	71	16	AAU69524	Anti-HCV antibody
736	6	1.3	58	22	ABU41187	Protein #7207 enco	809	6	1.3	71	16	AAU69524	Anti-HCV antibody
737	6	1.3	58	22	AAU74849	Human brain expres	810	6	1.3	71	16	AAU69524	Anti-HCV antibody
738	6	1.3	58	22	AAU74849	Human bone marrow	811	6	1.3	71	16	AAU69524	Anti-HCV antibody
739	6	1.3	58	22	AAU20434	Human immunohaema	812	6	1.3	71	21	AAU19968	Arabidopsis thalia
740	6	1.3	58	22	AAU34966	Peptide #9003 enco	813	6	1.3	71	21	AAU37982	Arabidopsis thalia

814	6	1.3	71	22	ABB44369	Peptide #11875 enc	887	6	1.3	80	22	AAU42555	Protonibacterium
815	6	1.3	71	22	ABR27226	Protein #9225 enco	888	6	1.3	80	22	ABG14485	Novel human diagno
816	6	1.3	71	22	AAW65436	Human brain expres	889	6	1.3	80	22	AAW62596	Human immune/haema
817	6	1.3	71	22	AAW78110	Human bone marrow	890	6	1.3	80	23	AAU87818	Yeast ELO2 partial
818	6	1.3	71	22	AAO11264	Human polypeptide	891	6	1.3	80	23	AAU87819	Yeast ELO2 protein
819	6	1.3	71	22	AAW21991	Peptide #8425 enco	892	6	1.3	81	23	AAU87819	Ovary tissue trans
820	6	1.3	71	22	AAW38338	Peptide #12375 enc	893	6	1.3	81	16	AAAR69523	Anti-HCV antibody
821	6	1.3	71	22	ABG47122	Human peptide enco	894	6	1.3	81	16	AAAR69525	Anti-HCV antibody
822	6	1.3	71	23	ABP01417	Human ORFX protein	895	6	1.3	81	16	AAAR69528	Anti-HCV antibody
823	6	1.3	72	18	AAW28171	Amino acid sequenc	896	6	1.3	81	16	AAAR69538	Anti-HCV antibody
824	6	1.3	72	20	AAV12499	Human 5' EST secre	897	6	1.3	81	16	AAAR69533	Anti-HCV antibody
825	6	1.3	72	21	AAV65676	C. elegans insulin	898	6	1.3	81	17	AAV15430	HCV NS-3 reactive
826	6	1.3	72	21	AAO02219	Human polypeptide	899	6	1.3	81	17	AAV15431	HCV NS-3 reactive
827	6	1.3	73	21	AAU99346	Human PRO831 (UNQ4	900	6	1.3	81	17	AAV15432	HCV NS-3 reactive
828	6	1.3	73	22	AAU49580	Protonibacterium	901	6	1.3	81	17	AAV15433	HCV NS-3 reactive
829	6	1.3	73	22	ABR29349	Peptide #2000 enco	902	6	1.3	81	17	AAV15434	HCV NS-3 reactive
830	6	1.3	73	22	ABR34520	Peptide #2026 enco	903	6	1.3	81	17	AAV15435	HCV NS-3 reactive
831	6	1.3	73	22	ABR19932	Protein #1931 enco	904	6	1.3	81	17	AAV15436	HCV NS-3 reactive
832	6	1.3	73	22	AAW55307	Human brain expres	905	6	1.3	81	17	AAV15437	HCV NS-3 reactive
833	6	1.3	73	22	AAW67706	Human bone marrow	906	6	1.3	81	17	AAV15436	Proctotype peptide
834	6	1.3	73	22	AAW15514	Peptide #1948 enco	907	6	1.3	81	17	AAV15429	HCV NS-3 reactive
835	6	1.3	73	22	AAW24231	Human EST encoded	908	6	1.3	81	23	ABG65108	Human albumin fusi
836	6	1.3	73	22	AAW28005	Peptide #2042 enco	909	6	1.3	81	23	ABG65109	Human albumin fusi
837	6	1.3	73	22	AAW03267	Peptide #1949 enco	910	6	1.3	81	23	ABP03976	Human ORFX protein
838	6	1.3	73	22	AAW06773	Human foetal prote	911	6	1.3	81	23	ABR94023	Human secreted pro
839	6	1.3	73	22	AAW87540	Human PRO831. Hom	912	6	1.3	82	23	ABR94047	Human secreted pro
840	6	1.3	73	22	AAW66095	Protein of the inv	913	6	1.3	82	22	AAW64756	Protonibacterium
841	6	1.3	73	23	ABG37269	Human peptide enco	914	6	1.3	82	22	AAW67679	Human colon cancer
842	6	1.3	74	20	AAW89912	Antigen 3 from clu	915	6	1.3	83	21	AAV58542	Rat somatostatin r
843	6	1.3	74	20	ABP51133	Human ORF4106 prot	916	6	1.3	83	21	AAV58543	Mouse somatostatin
844	6	1.3	75	21	AAW54948	Arabidopsis thalia	917	6	1.3	83	21	AAV58544	Human somatostatin
845	6	1.3	75	22	AAW64148	Protonibacterium	918	6	1.3	83	22	AAW61490	Protonibacterium
846	6	1.3	75	22	ABG11271	Novel human diagno	919	6	1.3	83	22	AAW83245	Human immune/haema
847	6	1.3	75	22	AAO05523	Human polypeptide	920	6	1.3	83	22	AAO09891	Human polypeptide
848	6	1.3	75	22	AAO12191	Human secreted pro	921	6	1.3	83	23	ABG40606	Human peptide enco
849	6	1.3	76	21	AAW01738	Protonibacterium	922	6	1.3	84	16	AAAR69530	Anti-HCV antibody
850	6	1.3	76	22	AAU58988	Peptide #9346 enco	923	6	1.3	84	17	AAV15443	HCV NS-3 reactive
851	6	1.3	76	22	ABR41840	Human brain expres	924	6	1.3	84	22	AAU41307	Protonibacterium
852	6	1.3	76	22	AAW62713	Human bone marrow	925	6	1.3	84	22	AAU67297	Protonibacterium
853	6	1.3	76	22	AAW75531	Human bone marrow	926	6	1.3	84	22	ABG21779	Novel human diagno
854	6	1.3	76	22	AAO13858	Human polypeptide	927	6	1.3	84	22	ABG24914	Novel human diagno
855	6	1.3	76	22	AAW56388	Peptide #9675 enco	928	6	1.3	84	22	AAW51246	Mouse amino acid s
856	6	1.3	76	23	AAU91254	Nucleic acid selec	929	6	1.3	84	23	ABP30853	Streptococcus poly
857	6	1.3	77	14	AAW49399	p270 polypeptide.	930	6	1.3	85	21	AAW41874	Arabidopsis thalia
858	6	1.3	77	17	AAV15428	HCV NS-3 reactive	931	6	1.3	85	21	AAW52520	Arabidopsis thalia
859	6	1.3	77	17	AAW87560	Tomato p270 cDNA-e	932	6	1.3	85	22	AAW46176	Protonibacterium
860	6	1.3	77	18	AAW08365	Tomato ovary-speci	933	6	1.3	85	22	ABG06213	Novel human diagno
861	6	1.3	77	22	ABG06203	Novel human diagno	934	6	1.3	85	22	ABR17157	Human nervous syst
862	6	1.3	77	22	ABG06427	Novel human diagno	935	6	1.3	85	22	AAW60686	Human reproductive
863	6	1.3	77	22	AAW87596	Human immune/haema	936	6	1.3	85	23	AAU81757	Partial mouse clk-
864	6	1.3	77	23	ABR48184	Listeria monocytog	937	6	1.3	86	22	AAU56810	Protonibacterium
865	6	1.3	78	19	AAW69195	Precursor sequence	938	6	1.3	86	22	ABR15822	Human nervous syst
866	6	1.3	78	21	AAW32697	Eucalyptus grandis	939	6	1.3	88	23	AAU49349	Protonibacterium
867	6	1.3	78	22	ABR32134	Peptide #4785 enco	940	6	1.3	88	23	ABP34746	Human ORFX191 prot
868	6	1.3	78	22	ABR37385	Peptide #4891 enco	941	6	1.3	89	10	AAW2025	Sequence encoded i
869	6	1.3	78	22	ABR22675	Protein #4674 enco	942	6	1.3	89	21	AAW11334	Arabidopsis thalia
870	6	1.3	78	22	AAW58069	Human brain expres	943	6	1.3	89	22	ABG06199	Novel human diagno
871	6	1.3	78	22	AAW70512	Human bone marrow	944	6	1.3	89	22	ABG14499	Novel human diagno
872	6	1.3	78	22	AAW18348	Peptide #4782 enco	945	6	1.3	89	22	ABG22646	Novel human diagno
873	6	1.3	78	22	AAW25353	Human protein sequ	946	6	1.3	89	22	ABG26397	Novel human diagno
874	6	1.3	78	22	AAW30833	Peptide #4870 enco	947	6	1.3	89	22	ABR44016	Peptide #11522 enc
875	6	1.3	78	22	AAW05955	Peptide #4637 enco	948	6	1.3	89	22	ABR26922	Protein #8921 enco
876	6	1.3	78	23	ABG40156	Human peptide enco	949	6	1.3	89	22	AAW65031	Human brain expres
877	6	1.3	79	15	AAW59834	Hepatitis C virus	950	6	1.3	89	22	AAW77746	Human bone marrow
878	6	1.3	79	19	AAW75173	Human secreted pro	951	6	1.3	89	22	AAW21657	Peptide #8091 enco
879	6	1.3	79	21	AAW58924	Breast and ovarian	952	6	1.3	89	22	AAW37960	Peptide #11997 enc
880	6	1.3	79	22	AAW23229	Human digestive sy	953	6	1.3	89	22	AAW46512	S. plisteinaespiral
881	6	1.3	79	22	AAO13703	Human polypeptide	954	6	1.3	89	23	ABG466774	Human peptide enco
882	6	1.3	79	22	AAW31305	Human gene 19-enco	955	6	1.3	89	23	ABW55012	Lactococcus lactis
883	6	1.3	79	23	ABG63472	Human albumin fusi	956	6	1.3	90	15	AAW39835	Hepatitis C virus
884	6	1.3	79	23	ABG47307	Human peptide enco	957	6	1.3	90	20	AAW38406	Human secreted pro
885	6	1.3	79	23	ABP05686	Human ORFX protein	958	6	1.3	90	21	AAW02157	Human secreted pro
886	6	1.3	80	16	AAW74230	HCV antigenic NS3	959	6	1.3	90	23	ABP11487	Human ORFX protein

960	6	1.3	91	18	AAW27796	Iron (III) dicitra
961	6	1.3	91	21	AAW16784	Bacteriophage Dp-1
962	6	1.3	91	21	AAW13333	Aradidopsis thalia
963	6	1.3	91	22	AAW98937	Human excretory re
964	6	1.3	91	22	ABR03894	Human musculoskele
965	6	1.3	91	22	AAW42652	Human kidney relat
966	6	1.3	92	20	AAV13124	Human secreted pro
967	6	1.3	92	21	AAW34735	Human secreted pro
968	6	1.3	92	21	AAW60105	Aradidopsis thalia
969	6	1.3	92	21	AAW69209	Amino acid sequenc
970	6	1.3	92	22	AAW63023	Propionibacterium
971	6	1.3	92	22	AAW65867	Propionibacterium
972	6	1.3	92	22	AAW31014	Novel human secret
973	6	1.3	92	22	AAW89224	Human immune/haema
974	6	1.3	93	16	AAW69529	Anti-HCV antibody
975	6	1.3	93	16	AAW69534	Anti-HCV antibody
976	6	1.3	93	22	ABG18825	Novel human diagno
977	6	1.3	94	21	AAW32851	Eucalyptus grandis
978	6	1.3	94	23	ABW78910	Tumour necrosis fa
979	6	1.3	94	23	AAW49145	Human immune/haema
980	6	1.3	95	22	AAW82228	Human immune/haema
981	6	1.3	96	20	AAW40019	Peptide sequence d
982	6	1.3	96	21	AAW34178	Zea mays protein f
983	6	1.3	96	22	ABW70664	Drosophila melanog
984	6	1.3	96	22	ABW17878	Human nervous syst
985	6	1.3	96	22	AAW02114	Human polypeptide
986	6	1.3	96	22	AAW06006	Human polypeptide
987	6	1.3	96	23	ABR08519	Human ORF protein
988	6	1.3	97	11	AAW05246	Amino acid sequenc
989	6	1.3	98	19	AAW37384	Hepatitis C virus
990	6	1.3	98	21	AAW15079	Arabidopsis thalia
991	6	1.3	98	21	AAW00199	Human secreted pro
992	6	1.3	98	23	ABW47340	Listeria monocytog
993	6	1.3	99	21	AAW60104	Arabidopsis thalia
994	6	1.3	99	21	AAW73378	HTM clone 1646005
995	6	1.3	99	23	ABW66956	Schizosaccharomyce
996	6	1.3	100	22	ABG11267	Novel human diagno
997	6	1.3	100	22	AAW04053	Human polypeptide
998	6	1.3	100	23	ABW57523	Cyclin-dependent k
999	6	1.3	101	21	AAW34177	Zea mays protein f
1000	6	1.3	101	21	AAW00200	Human secreted pro

ALIGNMENTS

RESULT 1

AAW05734 standard; Protein: 463 AA.

AAW05734:

23-JUL-1997 (first entry)

Presenilin-1-2.

Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;

depression; antibody; gene expression modulator; therapy.

Homo sapiens.

WO9634099-A2.

31-OCT-1996.

29-APR-1996; 96WO-CA00263.

31-JUL-1995; 95US-0509359.

28-APR-1995; 95US-0431048.

28-JUN-1995; 95US-0496841.

(HSCR-) HSC RES & DEV LP.

PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX Fraser PE, Rommens JM, St George-Hyslop PH;
XX WPI, 1996-497631/49.
DR N-PSDB; AAT40029.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 2; Page 132-134; 178pp; English.
XX
CC AAW05733 and AAW05734 represent the two different forms of wild type
CC human presenilin-1 (PS-1). This form of presenilin-1 results from
CC alternate splicing of the genomic DNA sequence. AAW05762 represents the
CC coding sequence for wild type human PS-2. The presenilins are a family
CC of highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding these sequences can be used for diagnosis of these
CC diseases. These proteins, or vectors that express them or containing
CC antisense sequences, antibodies selective for mutant forms of these
CC proteins (such as AAW05736) and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are useful
CC as models for drug screening. The antibodies can also be used e.g. for
CC affinity purification and in immunoassays.
XX
XX
SQ Sequence 463 AA;

Query Match 93.8%; Score 438; DB 17; Length 463;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	30	NDNREOHNDRLSLGHPEPLSNGRQVSGQVVEODEEDELTLKYGAHVIMLFVPV	89
DB	26	NDNREOHNDRLSLGHPEPLSNGRQVSGQVVEODEEDELTLKYGAHVIMLFVPV	85
QY	90	TLCMVVVAATIKSVSFTRKDGQILYPTFEDTETVGORLHSLINAAIMISIVVMTIL	149
DB	86	TLCMVVVAATIKSVSFTRKDGQILYPTFEDTETVGORLHSLINAAIMISIVVMTIL	145
QY	150	LVLVLYKRCYKVIHAWLILSSLLLEFFSFYLGVEFKTVNAVADYITVALTIMNLGVG	209
DB	146	LVLVLYKRCYKVIHAWLILSSLLLEFFSFYLGVEFKTVNAVADYITVALTIMNLGVG	205
QY	210	MISIHMKGPLRLOQATYIMISALMAVFTYLPDWTAMLLAVISYDLVAVLCPRGPLR	269
DB	206	MISIHMKGPLRLOQATYIMISALMAVFTYLPDWTAMLLAVISYDLVAVLCPRGPLR	265
QY	270	MLVETAOERNETLEFPALITYSTWVWLVNNAEGDPEAQRKSKSKNAESTERESODTYA	329
DB	266	MLVETAOERNETLEFPALITYSTWVWLVNNAEGDPEAQRKSKSKNAESTERESODTYA	325
QY	330	ENDDGFSEEMEAQRSHLQPHRSTPESRAAVQELSSILAGEDPBERGVKGLGDFTFY	389
DB	326	ENDDGFSEEMEAQRSHLQPHRSTPESRAAVQELSSILAGEDPBERGVKGLGDFTFY	385
QY	390	SVLVGKASATASGDWNTTACFAVAILGLCTLLLAIRKALPALPISTFGLVTFEAT	449
DB	386	SVLVGKASATASGDWNTTACFAVAILGLCTLLLAIRKALPALPISTFGLVTFEAT	445
QY	450	DYLVOPFMQLAFHOFYI 467	
DB	446	DYLVOPFMQLAFHOFYI 463	

RESULT 2

AAW23965 standard; Protein: 463 AA.

AAW23965:

XX 20-JUL-1998 (first entry)
DT
XX
DE Human presenilin-1.
XX
KW Presenilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;
KW cerebral haemorrhage; schizophrenia; depression; epilepsy;
KW mental retardation; diagnosis; therapy; transgenic animal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 177 /note= "Phe117Ser mutation site (Claim 1)"
FT MISC-difference 439 /note= "Ile439Val mutation site (Claim 1)"
FT MISC-difference 253 /note= "Asp2537Ala mutation site, associated with
FT MISC-difference 254..286 residue 254-286 deletion (Claim 1)"
FT MISC-difference 254..286 /note= "residue 254-286 deletion mutant, associated
FT with Asp253Ala mutation (Claim 1)"
XX
XX WO9801549-A2.
PD 15-JAN-1998.
XX
XX 04-JUL-1997: 97WO-CA00475.
XX
XX 02-JAN-1997: 97US-0034590.
PR 05-JUL-1996: 96US-0021673.
PR 12-JUL-1996: 96US-0021700.
PR 08-NOV-1996: 96US-0029895.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX
XX WPI: 1998-286355/25.
DR N-PSDB: AAV04667.
XX
XX New isolated mutant presenilin-1 genes - useful for developing
PT products for use in detection, diagnosis and therapy of Alzheimer's
PT disease and for drug screening
XX
XX Claim 1; Page 185-186; 238pp; English.
XX
XX This polypeptide comprises human presenilin-1 (hps1). Its amino
CC acid sequence was deduced from an isolated cDNA clone (see AAV04667).
CC Another hps1 sequence (see AAW23964) results from alternative
CC splicing of the hps1 mRNA transcript. A murine PS1 homologue (see
CC AAW23966) and a human presenilin-2 protein (see AAW23967) are also
CC provided. Mutations in the PS-1 and PS-2 genes are linked to the
CC development in humans of forms of familial Alzheimer's disease
CC (FAD) and may be causative of other disorders, e.g. cognitive,
CC intellectual, neurological or physiological disorders such as
CC cerebral haemorrhage, schizophrenia, depression, mental retardation
CC and epilepsy. Use of the nucleic acids and proteins comprising or
CC derived from the presenilins is made in screening and diagnosing
CC FAD, identifying and developing therapeutics for treatment of FAD,
CC and in producing cell lines and transgenic animals useful as models
CC of FAD. Methods for identifying substances that bind to, or
CC modulate the activity of a presenilin protein, and methods for
CC identifying substances that affect the interaction of a
CC presenilin-interacting protein with a presenilin protein are also
CC disclosed.
XX
XX Sequence 463 AA;
SO

QY 30 NDNREROEHNDRRSLGHEPEPLSNRPOGNSRQVVEODEEDELTLKYGAKHVMLEFVPV 89
DB 26 NDNREROEHNDRRSLGHEPEPLSNRPOGNSRQVVEODEEDELTLKYGAKHVMLEFVPV 85
QY 90 TLCAVVVVATIKSVSFYTRKDGQILYPTEDTETVQGRALSHLMAIMISVIVMTIL 149
DB 86 TLCAVVVVATIKSVSFYTRKDGQILYPTEDTETVQGRALSHLMAIMISVIVMTIL 145
QY 150 LVLYKRYRCYVHHAMLISSLLLFPSFTYLGVEPFTYVAVDYTVALLINLGVV 209
DB 146 LVLYKRYRCYVHHAMLISSLLLFPSFTYLGVEPFTYVAVDYTVALLINLGVV 205
QY 210 MISIHMKGPLRLOOAYLIMISALMALVFIKLPENTAMLIAVISYDLVAVLCPKPLR 269
DB 206 MISIHMKGPLRLOOAYLIMISALMALVFIKLPENTAMLIAVISYDLVAVLCPKPLR 265
QY 270 MLVETAEERNETLPPALISSTMYLVNMAEGDEPAQRVSKNSKYNMAESTERESQDTVA 329
DB 266 MLVETAEERNETLPPALISSTMYLVNMAEGDEPAQRVSKNSKYNMAESTERESQDTVA 325
QY 330 ENDDGGESEWEAQRDSHLGPHRSTPESRAVQELSSILAGEDEEERGVLGLGDFIFY 389
DB 326 ENDDGGESEWEAQRDSHLGPHRSTPESRAVQELSSILAGEDEEERGVLGLGDFIFY 385
QY 390 SVLVGKASATASGDMNTIACEVAITLIGCLTLTLTLAIFKKALPALPISITFGVFPAT 449
DB 386 SVLVGKASATASGDMNTIACEVAITLIGCLTLTLTLAIFKKALPALPISITFGVFPAT 445
QY 450 DYLVQPFMDQLAFHQFYI 467
DB 446 DYLVQPFMDQLAFHQFYI 463

RESULT 3
AAW05733 standard; Protein: 467 AA.
XX
XX AAW05733:
AC
XX 23-JUL-1997 (first entry)
DT
XX
XX Presenilin-1-1.
DE
XX
XX Presenilin-1; human; hps1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy.
XX
XX Homo sapiens.
OS
XX
XX WO9634099-A2.
PN
XX 31-OCT-1996.
PD
XX
XX 29-APR-1996: 96WO-CA00263.
PF
XX
XX 31-JUL-1985: 95US-0509359.
PR 28-APR-1985: 95US-0431048.
PR 28-JUN-1995: 95US-0496841.
XX
XX (HSCR-) HSC RES & DEV LP.
XX PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
XX Fraser PE, Rommens JM, St George-Hyslop PH;
PI
XX
XX WPI: 1996-497631/49.
DR N-PSDB: AAT40028.
XX
XX New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
XX Claim 2; Page 128-130; 178pp; English.
PS

CC AAM05733 and AAM05734 represent the two different forms of wild type
CC human presenilin-1 (PS-1). The form represented by AAM05734 results from
CC alternate splicing of the genomic DNA sequence. AAM05762 represents the
CC coding sequence for wild type human PS-2. The presenilins are a family
CC of highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding these sequences can be used for diagnosis of these
CC diseases. These proteins, or vectors that express them or containing
CC antisense sequences, antibodies selective for mutant forms of these
CC proteins (such as AAM05736) and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are useful
CC as models for drug screening. The antibodies can also be used e.g. for
CC affinity purification and in immunoassays.

XX Sequence 467 AA;

Query Match 78.4%; Score 366; DB 17; Length 467;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTEPALSTFQNAQMSDNLSTVRSQDNRRQCHNDRRSIGHPPLSNGRPGNSR 60
DB 1 MTEPALSTFQNAQMSDNLSTVRSQDNRRQCHNDRRSIGHPPLSNGRPGNSR 60
QY 61 QVVEDEDEDEBELTKGAKHVIMLFVPTLCMVVVATIKSVSEFYRKQGLYTPETE 120
DB 61 QVVEDEDEDEBELTKGAKHVIMLFVPTLCMVVVATIKSVSEFYRKQGLYTPETE 120
QY 121 DTEVGGRALHSILNAAIMTSIVVMTLLVLVYKRCYVIAHMLISLLLFPSFI 180
DB 121 DTEVGGRALHSILNAAIMTSIVVMTLLVLVYKRCYVIAHMLISLLLFPSFI 180
QY 181 YLGEVFTYVAVDYITVALLINMLGVVGMSTHMKGPLRLOQAYLIMISALAVPTKY 240
DB 181 YLGEVFTYVAVDYITVALLINMLGVVGMSTHMKGPLRLOQAYLIMISALAVPTKY 240
QY 241 LPEWTAMLIIVISVYVVLVLCPKGPLRMIVETAQERNETLPALYSSMWLVMAE 300
DB 241 LPEWTAMLIIVISVYVVLVLCPKGPLRMIVETAQERNETLPALYSSMWLVMAE 300
QY 301 GDPPEAQRVSKNSKYNAESTERESQDTVAENDDGFSEWEAQRDSHLGRSTPESRAA 360
DB 301 GDPPEAQRVSKNSKYNAESTERESQDTVAENDDGFSEWEAQRDSHLGRSTPESRAA 360
QY 361 VOELSSSILAGEPEEGVNLGLGDFTFYSVLVKASATASGDMNTTIACFVALIGLCL 420
DB 361 VOELSSSILAGEPEEGVNLGLGDFTFYSVLVKASATASGDMNTTIACFVALIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVYFATDYLVOPFMDOLAFOFYI 467
DB 421 TLLLLAIFKKALPALPISITFGVYFATDYLVOPFMDOLAFOFYI 467

RESULT 4
AAM23964
ID AAM23964 standard; Protein; 467 AA.

XX AAM23964;

XX 20-JUL-1998 (first entry)

XX Human presenilin-1.

XX Presenilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;

XX cerebral haemorrhage; schizophrenia; depression; epilepsy;

XX mental retardation; diagnosis; therapy; transgenic animal.

OS Homo sapiens.
XX
FH Key Location/Qualifiers

FT Domain 82..100
FT /label= TM1
FT /note= "transmembrane domain 1"
FT Domain 101..132
FT /label= TM1-2
FT /note= "hydrophilic loop"
FT Domain 133..154
FT /label= TM2
FT /note= "transmembrane domain 2"
FT Domain 155..163
FT /label= TM2-3
FT /note= "hydrophilic loop"
FT Domain 164..183
FT /label= TM3
FT /note= "transmembrane domain 3"
FT Domain 184..194
FT /label= TM3-4
FT /note= "hydrophilic loop"
FT Domain 195..212
FT /label= TM4
FT /note= "transmembrane domain 4"
FT Domain 213..220
FT /label= TM4-5
FT /note= "hydrophilic loop"
FT Domain 221..238
FT /label= TM5
FT /note= "transmembrane domain 5"
FT Domain 239..243
FT /label= TM5-6
FT /note= "hydrophilic loop"
FT Domain 244..262
FT /label= TM6
FT /note= "transmembrane domain 6"
FT Domain 263..407
FT /label= TM6-7
FT /note= "hydrophilic loop"
FT Domain 408..428
FT /label= TM8
FT /note= "transmembrane domain 8"
FT Misc-difference 177
FT /note= "Phe117Ser mutation site (Claim 1)"
FT Misc-difference 439
FT /note= "Ile439Val mutation site (Claim 1)"
FT Misc-difference 257
FT /note= "Asp257Ala mutation site, associated with
FT residue 258-290 deletion (Claim 1)"
FT Misc-difference 258..290
FT /note= "residue 258-290 deletion mutant, associated
FT with Asp257Ala mutation (Claim 1)"
FT Misc-difference 143
FT /note= "Ile143Thr mutation site (Claim 18)"
FT Misc-difference 146
FT /note= "Met146Leu mutation site (Claim 18)"
FT Misc-difference 171
FT /note= "Leu171Pro mutation site (Claim 18)"
FT Misc-difference 260
FT /note= "Ala260Val mutation site (Claim 18)"
FT Misc-difference 263
FT /note= "Cys263Arg mutation site (Claim 18)"
FT Misc-difference 264
FT /note= "Pro264Leu mutation site (Claim 18)"
FT Misc-difference 267
FT /note= "Pro267Ser mutation site (Claim 18)"
FT Misc-difference 280
FT /note= "Glu280Ala mutation site (Claim 18)"
FT Misc-difference 280
FT /note= "Glu280Gly mutation site (Claim 18)"
FT Misc-difference 285
FT /note= "Ala285Val mutation site (Claim 18)"
FT Misc-difference 286
FT /note= "Leu286Val mutation site (Claim 18)"
FT Misc-difference 322
FT /note= "Leu322Val mutation site (Claim 18)"

FT	Misc-difference	392	/note-	"Leu32Val mutation site (Claim 18)"
FT	Misc-difference	410	/note-	"Cys410Tyr mutation site (Claim 18)"
FT	Misc-difference	79	/note-	"Ala79Xaa mutation site"
FT	Misc-difference	82	/note-	"Val82Leu mutation site"
FT	Misc-difference	96	/note-	"Val96Phe mutation site"
FT	Misc-difference	115	/note-	"Tyr115His mutation site"
FT	Misc-difference	139	/note-	"Met139Thr mutation site"
FT	Misc-difference	139	/note-	"Met139Val mutation site"
FT	Misc-difference	146	/note-	"Met146Val mutation site"
FT	Misc-difference	163	/note-	"His163Arg mutation site"
FT	Misc-difference	163	/note-	"His163Tyr mutation site"
FT	Misc-difference	209	/note-	"Gly209Val mutation site"
FT	Misc-difference	211	/note-	"Ile211Thr mutation site"
FT	Misc-difference	231	/note-	"Ala231Thr mutation site"
FT	Misc-difference	246	/note-	"Ala246Glu mutation site"
FT	Misc-difference	291..319	/note-	"residue 291-319 deletion site"
FT	Misc-difference	384	/note-	"Gly384Ala mutation site"
FT	Misc-difference	26..29	/note-	"residue 26-29 deletion, resulting from alternative splicing"
PN	WO9801549-A2.			
PD	15-JAN-1998.			
XX				
PF	04-JUL-1997:	97WO-CA00475.		
XX				
PR	02-JAN-1997:	97US-0034590.		
PR	05-JUL-1996:	96US-0021673.		
PR	12-JUL-1996:	96US-0021700.		
PR	08-NOV-1996:	96US-0028855.		
XX				
PA	(HSCR-) HSC RES & DEV LP.			
PA	(UTOR) UNIV TORONTO GOVERNING COUNCIL.			
PI	Fraser PE, Rommens JM, St George-Hyslop PH:			
XX				
DR	WPI: 1998-286355/25.			
DR	N-PSDB: AAV04666.			
XX				
PT	New isolated mutant presenilin-1 genes - useful for developing			
PT	products for use in detection, diagnosis and therapy of Alzheimer's			
PT	disease and for drug screening			
XX				
PS	Claim 1: Page 180-182; 238pp: English.			
XX				
CC	This polypeptide comprises human, presenilin-1 (hps1). Its amino			
CC	acid sequence was deduced from an isolated cDNA clone (see AAV04666)			
CC	Another hps1 sequence (see AAW23965) results from alternative			
CC	splicing of the hps1 mRNA transcript. A murine PS1 homologue (see			
CC	AAW23966) and a human presenilin-2 protein (see AAW23967) are also			
CC	provided. Mutations in the PS-1 and PS-2 genes are linked to the			
CC	development in humans of forms of familial Alzheimer's disease			
CC	(FAD) and may be causative of other disorders, e.g. cognitive,			
CC	intellectual, neurological or physiological disorders such as			
CC	cerebral haemorrhage, schizophrenia, depression, mental retardation			

	Query Match	78.4%	Score 366	DB 19	Length 467	
	Best Local Similarity	99.8%	Pred. No. 0			
	Matches 466	Conservative 0	Mismatches 1	Indels 0	Gaps 0	
QY	1 MTELPAPLSYFONAMSEDNHLSNVRSONDRKOEHRDRSLGHPPLSGRPOGNSR	60				
Db	1 MTELPAPLSYFONAMSEDNHLSNVRSONDRKOEHRDRSLGHPPLSGRPOGNSR	60				
QY	61 QVEODEDEDELTLYGAKHVIMLFVPTLCMVVVVATIKSFYTRKDGULITYPTE	120				
Db	61 QVEODEDEDELTLYGAKHVIMLFVPTLCMVVVVATIKSFYTRKDGULITYPTE	120				
QY	121 DTEYGGORALHSILNAAIMISYIVMTLLVLYRYCKYVTHAMLISSLLPFPSFI	180				
Db	121 DTEYGGORALHSILNAAIMISYIVMTLLVLYRYCKYVTHAMLISSLLPFPSFI	180				
QY	181 YLGEVFKTYNNAVDITYALLIMNLGVGMISIHMKGPRLQOAVLIMISALMALVFITY	240				
Db	181 YLGEVFKTYNNAVDITYALLIMNLGVGMISIHMKGPRLQOAVLIMISALMALVFITY	240				
QY	241 LPEWTAMILIAVISYVDLVAVLCPRKPLRLMETAOERNETLFPALISSTWMLVNNAE	300				
Db	241 LPEWTAMILIAVISYVDLVAVLCPRKPLRLMETAOERNETLFPALISSTWMLVNNAE	300				
QY	301 GDPKQRRYSKSKSTNAESTERESODTYAENDDGFSEMEQORSHLCPHRSPESSRA	360				
Db	301 GDPKQRRYSKSKSTNAESTERESODTYAENDDGFSEMEQORSHLCPHRSPESSRA	360				
QY	361 VOELSSSLIAGDPEERGKLGIGDFIFSVLVGRASATASGDMWTTTACFALLIGLCL	420				
Db	361 VOELSSSLIAGDPEERGKLGIGDFIFSVLVGRASATASGDMWTTTACFALLIGLCL	420				
QY	421 TLLLLAIFKKALPALPISITTEGLVFVFATDYLVOFPMDLAFHQEYI	467				
Db	421 TLLLLAIFKKALPALPISITTEGLVFVFATDYLVOFPMDLAFHQEYI	467				
RESULT 5						
AAW41430						
ID	AAW41430 standard; Protein: 467 AA.					
XX	AAW41430;					
XX	04-JUN-1998 (first entry)					
XX	PS1/467 protein.					
XX	Presentin peptide; PS1/429; immunogen; immune response; PS1 gene;					
KW	Alzheimer's disease; mitochondrial pathology; neurodegeneration;					
KW	apoptosis; PS1/467.					
XX	Homo sapiens.					
XX	W09746678.1.					
XX	11-DEC-1997.					
XX	03-JUN-1997; 9XWO-US09272.					
XX	18-JUL-1996; 96US-0683315.					
XX	06-JUN-1996; 96US-0659296.					

XX (FARB) BAYER CORP.
 PA
 XX Chisholm JC, Davis JN, Drache B;
 PI
 XX WPI: 1998-042186/04.
 DR
 XX N-PSDB: AAVI7358.
 DR
 XX
 PT DNA encoding presenilin peptide PS1/429 and its analogues - useful
 PT for diagnosis and treatment of Alzheimer's disease
 XX
 PS Claim 7; Fig 2; 77pp: English.
 XX
 CC This sequence is the PS1/467 presenilin peptide. This sequence is
 CC specifically stated as not being in the nucleic acid of the invention,
 CC which encodes the PS1/429 presenilin peptide PS1/429 (II). Cells
 CC transformed with the DNA are used to produce recombinant (II) and
 CC analogues, useful e.g. as immunogens for generating an immune response
 CC against PS1/429. (II) is a new product of the PS1 gene, mutations in
 CC which cause Alzheimer's disease (AD). The nucleic acids are generally
 CC useful as probes for detection and quantification of PS1/429,
 CC particularly for diagnosis of AD, especially the target sequences that
 CC hybridise with probes are isolated for sequencing. Antibodies (Ab) can
 CC also be diagnosed at the protein level using Ab as immunoassay reagents.
 CC Ab can also be used to identify epitopes and for affinity purification of
 CC peptides. Antisense nucleic acid may also be used to regulate expression
 CC of the PS1/429 gene, and both nucleic acids and peptides are useful as
 CC size markers in electrophoresis, chromatography etc. The transgenic
 CC animals are used as models for AD, e.g. for testing drugs. Regulators of
 CC the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases
 CC involving mitochondrial pathology, apoptosis and neurodegeneration.
 CC Typical regulators are antisense sequences, ribozymes, aptamers,
 CC synthetic or natural compounds. (II) may also be used to target other
 CC coding sequences to particular cellular locations.
 CC
 XX Sequence 467 AA:
 SQ
 Query Match 78.4%; Score 366; DB 19; Length 467;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
 ID AAY24419
 XX AAY24419 standard; Protein: 467 AA.
 XX
 AC AAY24419;
 XX
 DT 23-SEP-1999 (first entry)
 XX
 DE Human presenilin-1.
 XX
 KW Presenilin-1; mutation; gene mutant animal; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN W0934670-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 07-JAN-1999; 99WO-JP00015.
 XX
 PR 08-JAN-1998; 98JP-0002191.
 XX
 PA (DAUC) DAII CHI PHARM CO LTD.
 XX
 PI Takeda J, Takeda M;
 XX
 DR WPI: 1999-430307/36.
 DR
 DR N-PSDB: AAX90184.
 XX
 PT Mutant presenilin-1 gene-introduced animals, useful as model animals
 PT for study of Alzheimer's diseases in human and screening substances
 PT for prevention and/or treatment of the diseases
 XX
 PS Disclosure: Page 51-52; 64pp: Japanese.
 PS
 CC The present invention describes a gene mutant animal having a non-human
 CC mutant presenilin gene. The mutant presenilin gene causes amino acid
 CC substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139,
 CC 143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269,
 CC 280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding
 CC N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by
 CC replacing isoleucine of position 213 by another amino-acid especially
 CC threonine. The gene mutant animals e.g. mice can be used as model
 CC animals for the study of human Alzheimer's diseases and to screen and
 CC evaluate substances as candidates for prevention and/or therapy of
 CC Alzheimer's diseases in patients. They can over-produce amyloid
 CC beta protein in the hippocampus earlier. Such animals are being
 CC pathologically close to human patients with Alzheimer's diseases. The
 CC present sequence represents human presenilin-1, as given in the present
 CC invention.
 XX
 SQ Sequence 467 AA:
 Query Match 78.4%; Score 366; DB 20; Length 467;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Db 181 YLGEVFKTYNNAVDTITVALTIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIRY 240
Oy 241 LPETWAMILLAVISYVDLVAVLCPRKPLRMVETAOERNEITLFPALITSSTWMLVNNAE 300
Db 241 LPETWAMILLAVISYVDLVAVLCPRKPLRMVETAOERNEITLFPALITSSTWMLVNNAE 300
Oy 301 GDPENQRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
Db 301 GDPENQRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
Oy 361 VOELSSSTILAGEDPERGVKLGIDFIFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
Db 361 VOELSSSTILAGEDPERGVKLGIDFIFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
Oy 421 TLLLAIFKKALPALPISITFGLVFYFANDYLVOPMDLAFHOFYI 467
Db 421 TLLLAIFKKALPALPISITFGLVFYFANDYLVOPMDLAFHOFYI 467

RESULT 7
AAY23897
ID AAY23897 standard; protein: 467 AA.
AC AAY23897;
DT 27-SEP-1999 (first entry)
DE Amino acid sequence of the wild type human presenilin 1 (PS1) protein.
KW Human; presenilin 1; PS1; presenilin-binding protein; interacting domain;
KW presenilin allele; Alzheimer's disease; senile dementia;
KW psychiatric disease; schizophrenia; depression; neurological disease;
KW stroke; cerebral haemorrhage.
XX Homo sapiens.
OS
XX MO9935501-A1.
XX 15-JUL-1999.
XX 08-JAN-1999; 99WO-CA00018.
XX 09-JAN-1998; 98US-0070948.
XX (UNOR ) UNIV TORONTO GOVERNING COUNCIL.
XX Fraser PE, St George-Hyslop PH;
XX MPI, 1999-419410/35.
XX Identifying substances that alter presenilin interactions, useful
XX for screening individuals for presenilin alleles associated with
XX Alzheimer's disease - useful for diagnosis of Alzheimer's disease
XX disclosure; Page 34-36; 40pp; English.
XX The present sequence represents wild type human presenilin 1 (PS1)
XX protein. The specification describes a method for identifying substances
XX that alter the interaction of a presenilin with a presenilin-binding
XX protein. The method comprises contacting the interacting domain of a
XX presenilin protein to a presenilin-binding protein in the presence of
XX a test substance, and measuring the interaction of the presenilin and
XX the presenilin-binding protein. The method can be used to screen
XX individuals for presenilin alleles associated with Alzheimer's disease
XX and related disorders, such as senile dementia's, psychiatric diseases
XX such as schizophrenia and depression, and neurological disease, such as
XX stroke and cerebral haemorrhage.
XX Sequence 467 AA:
Query Match 78.4%; Score 366; DB 20; Length 467;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 MTELPAPLSTYFONAMSDNHLNSTRVSONDREROEHNDRSLGHPRLSNGRPOGNSR 60
Db 1 MTELPAPLSTYFONAMSDNHLNSTRVSONDREROEHNDRSLGHPRLSNGRPOGNSR 60
Oy 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMNVVAVTAKSVSFYTRKDGQLITPFTL 120
Db 61 QVEODEEDELTLKYGAKHVMLEFVPTLCMNVVAVTAKSVSFYTRKDGQLITPFTL 120
Oy 121 DTEYGORALHSILAAIMISYVMTLLVLYRYCKYVHAMLISSLLLEFFSFT 180
Db 121 DTEYGORALHSILAAIMISYVMTLLVLYRYCKYVHAMLISSLLLEFFSFT 180
Oy 181 YLGEVFKTYNNAVDTITVALTIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIRY 240
Db 181 YLGEVFKTYNNAVDTITVALTIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIRY 240
Oy 241 LPETWAMILLAVISYVDLVAVLCPRKPLRMVETAOERNEITLFPALITSSTWMLVNNAE 300
Db 241 LPETWAMILLAVISYVDLVAVLCPRKPLRMVETAOERNEITLFPALITSSTWMLVNNAE 300
Oy 301 GDPENQRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
Db 301 GDPENQRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRDSHLGPHRSTPESRAA 360
Oy 361 VOELSSSTILAGEDPERGVKLGIDFIFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
Db 361 VOELSSSTILAGEDPERGVKLGIDFIFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
Oy 421 TLLLAIFKKALPALPISITFGLVFYFANDYLVOPMDLAFHOFYI 467
Db 421 TLLLAIFKKALPALPISITFGLVFYFANDYLVOPMDLAFHOFYI 467

RESULT 8
AAB07971
ID AAB07971 standard; protein: 467 AA.
AC AAB07971;
DT 14-NOV-2000 (first entry)
DE Amino acid sequence of human presenilin I polypeptide.
KW Human; presenilin; PS1; PS2; nerve cell growth; nerve damage; hNPRAP;
KW neural plakophilin related armadillo protein; Alzheimer's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; stroke;
KW multiple sclerosis; ischemia; stroke; neural paropathy; sciatic crush;
KW motor neuron disease; peripheral neuropathy; neuropathy; diabetes;
KW spinal cord injury; facial nerve crush.
XX Homo sapiens.
OS
XX WO200047615-A2.
XX 17-AUG-2000.
XX 11-FEB-2000; 2000WO-CA00126.
XX 12-FEB-1998; 99US-0119835.
XX (UNOR ) UNIV TORONTO GOVERNING COUNCIL.
XX St George-Hyslop PH, Fraser PE;
XX MPI, 2000-524531/47.
XX Stimulation of nerve cell growth using human Neural Plakophilin Related
XX Armadillo Protein (hNPRAP) polypeptide, useful for the treatment of
XX diseases such as Alzheimer's, Parkinson's, and stroke -
XX disclosure; Page 19-20; 33pp; English.

```

CC The present sequence represents a human presenilin 1 (PS1) polypeptide.
CC Human Neural Plakophilin Related Armadillo protein (hNPRAP) polypeptide
CC is known to interact with PSI and PS2. The specification describes a
CC method for stimulating the growth of nerve cells, comprising contacting
CC them with hNPRAP. The hNPRAP polypeptide and polynucleotide are useful
CC for treating nerve damage caused by a variety of diseases or physical
CC traumas, including Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis (ALS), multiple sclerosis, stroke, ischemia associated
CC with stroke, neural paropathy, motor neuron diseases, sciatic crush,
CC peripheral neuropathy, neuropathy associated with diabetes, spinal cord
CC injuries and facial nerve crush.

SO Sequence 467 AA:

Query Match 78.4%; Score 366; DB 21; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYQNAQMSQNDNLSTVRSQNDNRROEHNDRRSLGHEPLSNGRPQNSR 60
DB 1 MTELPAPLSTYQNAQMSQNDNLSTVRSQNDNRROEHNDRRSLGHEPLSNGRPQNSR 60
QY 61 QVDEDEDEDELTKYGAHVIMLEFVPTLCMVVVAATIKSVSFYRKDGQLYTPPTE 120
DB 61 QVDEDEDEDELTKYGAHVIMLEFVPTLCMVVVAATIKSVSFYRKDGQLYTPPTE 120
QY 121 DTEVVGORALHSILNAIMISVIYVMTLLVLYKYRCYKVIHAMLIISSLLFFFSFI 180
DB 121 DTEVVGORALHSILNAIMISVIYVMTLLVLYKYRCYKVIHAMLIISSLLFFFSFI 180
QY 181 YLGEVFTYNAVDYITVALLIMNLGVVGMISIHMKGRLQQAYLIMISALMALVFIKY 240
DB 181 YLGEVFTYNAVDYITVALLIMNLGVVGMISIHMKGRLQQAYLIMISALMALVFIKY 240
QY 241 LPEWTAMLILAVISVYDVAVLCRPGRLRMVETAQERNETLFPALIISSMTWLVNMAE 300
DB 241 LPEWTAMLILAVISVYDVAVLCRPGRLRMVETAQERNETLFPALIISSMTWLVNMAE 300
QY 301 GDPAQRVRSKNSKYNAESTERESQDTVAENDDGFSEMEQAORDSHLGRSTPESRAA 360
DB 301 GDPAQRVRSKNSKYNAESTERESQDTVAENDDGFSEMEQAORDSHLGRSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVAIIIGLCL 420
DB 361 VOELSSSILAGEDPEERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVAIIIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVYFATDYLVOFPMDQLAFHOFTY 467
DB 421 TLLLLAIFKKALPALPISITFGVYFATDYLVOFPMDQLAFHOFTY 467

RESULT 9
AAE10798 ID AAE10798 standard; Protein; 467 AA.

AC AAE10798;

DT 18-DEC-2001 (first entry)

DE Human presenilin-1 (PS-1) protein.

XX Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy;
KW neurodegenerative disease; Alzheimer's disease; nootropic; prophylaxis;
KW neuronal disorder; cognitive disorder.

OS Homo sapiens.

PN WO200167097-A2.

PD 13-SEP-2001.

PF 09-MAR-2001; 2001WO-GB01059.

XX

PR 10-MAR-2000; 2000GB-0005895.

PA (GLAXO) GLAXO GROUP LTD.

PI Hale RS, Rowley A, Blackstock W;

DR WPI; 2001-589954/66.

DR N-PSDB; AAD18120.

PT Identifying presenilin or catenin p120 activity modulator useful for
PT modulating presenilin-catenin p120 interaction and thus for treating
PT cognitive disorder e.g., Alzheimer's disease comprises enhancing
PT cognitive function

XX Example 1; Page 41-42; 48pp; English.

CC The invention relates to a method for identifying modulators of
CC presenilin and catenin p120. Modulators of catenin p120 and presenilin
CC are useful for the treatment and prophylaxis of disorders that is
CC responsive to modulation of presenilin/catenin p120 activity. In
CC particular, neuronal disorders such as cognitive disorders and
CC neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNAs
CC are useful for identifying mutations in catenin p120 genes.
CC Identification of such mutations assist in the diagnosis of or
CC susceptibility to Alzheimer's or other conditions associated with
CC presenilin and in assessing the physiology of such disorders. Catenin
CC p120 DNAs are also used in hybridisation studies to monitor expression of
CC expression. The present sequence is human presenilin-1 (PS-1) protein.

XX Sequence 467 AA:

Query Match 78.4%; Score 366; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYQNAQMSQNDNLSTVRSQNDNRROEHNDRRSLGHEPLSNGRPQNSR 60
DB 1 MTELPAPLSTYQNAQMSQNDNLSTVRSQNDNRROEHNDRRSLGHEPLSNGRPQNSR 60
QY 61 QVDEDEDEDELTKYGAHVIMLEFVPTLCMVVVAATIKSVSFYRKDGQLYTPPTE 120
DB 61 QVDEDEDEDELTKYGAHVIMLEFVPTLCMVVVAATIKSVSFYRKDGQLYTPPTE 120
QY 121 DTEVVGORALHSILNAIMISVIYVMTLLVLYKYRCYKVIHAMLIISSLLFFFSFI 180
DB 121 DTEVVGORALHSILNAIMISVIYVMTLLVLYKYRCYKVIHAMLIISSLLFFFSFI 180
QY 181 YLGEVFTYNAVDYITVALLIMNLGVVGMISIHMKGRLQQAYLIMISALMALVFIKY 240
DB 181 YLGEVFTYNAVDYITVALLIMNLGVVGMISIHMKGRLQQAYLIMISALMALVFIKY 240
QY 241 LPEWTAMLILAVISVYDVAVLCRPGRLRMVETAQERNETLFPALIISSMTWLVNMAE 300
DB 241 LPEWTAMLILAVISVYDVAVLCRPGRLRMVETAQERNETLFPALIISSMTWLVNMAE 300
QY 301 GDPAQRVRSKNSKYNAESTERESQDTVAENDDGFSEMEQAORDSHLGRSTPESRAA 360
DB 301 GDPAQRVRSKNSKYNAESTERESQDTVAENDDGFSEMEQAORDSHLGRSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVAIIIGLCL 420
DB 361 VOELSSSILAGEDPEERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVAIIIGLCL 420
QY 421 TLLLLAIFKKALPALPISITFGVYFATDYLVOFPMDQLAFHOFTY 467
DB 421 TLLLLAIFKKALPALPISITFGVYFATDYLVOFPMDQLAFHOFTY 467

RESULT 10

AAAG63936 ID AAG63936 standard; Protein; 467 AA.

XX

```

AC AAG63936;
XX
XX 29-OCT-2001 (first entry)
DT
DE Amino acid sequence of human presenilin 1.
XX
XX KIAA0253; presenilin; Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX WO200167109-A1.
XX
XX 13-SEP-2001.
XX
XX 09-MAR-2001; 2001WO-GB01057.
XX
XX 10-MAR-2000; 2000GB-0005894.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Hale RS, Rowley A, Blackstock W,
XX
XX WPI: 2001-522960/57.
XX
XX N-PSDB; AAH74993.
XX
XX
XX Identifying a modulator of presenilin function by determining the
XX ability of presenilin to bind to a KIAA0253 polypeptide in the presence
XX and absence of a test compound, useful in the treatment or prophylaxis
XX of Alzheimer's disease -
XX
XX Disclosure: Page 40-41; 48pp; English.
XX
XX The present sequence represents human presenilin 1. KIAA0253 binds to
XX presenilin. The specification describes a method of identifying a
XX modulator of presenilin function or KIAA0253 function. The method
XX comprises determining presenilin activity or KIAA0253 activity
XX in the presence and absence of a test compound, where presenilin
XX activity is determined by its ability to bind to KIAA0253. A modulator
XX of presenilin or KIAA0253 polypeptide is useful in the manufacture of
XX a medicament for the treatment or prophylaxis of Alzheimer's disease.
XX The KIAA0253 polynucleotide and KIAA0253 polypeptide are useful in the
XX treatment, prophylaxis or diagnosis of Alzheimer's disease.
XX
XX Sequence 467 AA:
SQ
Query Match 78.4%; Score 366; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MTELPAPISTYFQNAOMSEDNHLSNTVRSQNDNRROEHNDRSLGHPPLSGRPGNSR 60
DB 1 MTELPAPISTYFQNAOMSEDNHLSNTVRSQNDNRROEHNDRSLGHPPLSGRPGNSR 60
OY 61 QVEDDEDEDEDELTLYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKDGOLITPTPE 120
DB 61 QVEDDEDEDEDELTLYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKDGOLITPTPE 120
OY 121 DTEYTGQRALHSILNAAMISIVVMTILVLYKRCYVHAMLIISLLFFFSFI 180
DB 121 DTEYTGQRALHSILNAAMISIVVMTILVLYKRCYVHAMLIISLLFFFSFI 180
OY 122 DTEYTGQRALHSILNAAMISIVVMTILVLYKRCYVHAMLIISLLFFFSFI 180
DB 122 DTEYTGQRALHSILNAAMISIVVMTILVLYKRCYVHAMLIISLLFFFSFI 180
OY 181 YGVEFKTVNAVADITVALLIMNGVGMISIHMKGPLRLOAVLIMISALMALVEFIY 240
DB 181 YGVEFKTVNAVADITVALLIMNGVGMISIHMKGPLRLOAVLIMISALMALVEFIY 240
OY 181 YGVEFKTVNAVADITVALLIMNGVGMISIHMKGPLRLOAVLIMISALMALVEFIY 240
DB 181 YGVEFKTVNAVADITVALLIMNGVGMISIHMKGPLRLOAVLIMISALMALVEFIY 240
OY 241 LPEMTAMLIIVSYVDLAVLCPRGPLMELVETAQERNETLEPALIYSSVTWMLVNAE 300
DB 241 LPEMTAMLIIVSYVDLAVLCPRGPLMELVETAQERNETLEPALIYSSVTWMLVNAE 300
OY 301 GPPEAQRVRSKSKYNAESTERESQDTVAENDGCFSEMEQRDSHLCGRHSTPESRAA 360
DB 301 GPPEAQRVRSKSKYNAESTERESQDTVAENDGCFSEMEQRDSHLCGRHSTPESRAA 360

```

```

OY 361 VOELSSSILAGEDPEERGKVLGLGDFIFPSYLVGKASATASGDMWTTTACFAVAILGLCL 420
DB 361 VOELSSSILAGEDPEERGKVLGLGDFIFPSYLVGKASATASGDMWTTTACFAVAILGLCL 420
OY 421 TLLLAIFKKALPALPISTIFGLVFFPATDYLVQPFMDLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISTIFGLVFFPATDYLVQPFMDLAFHQFYI 467
RESULT 11
AAE05466
ID AAE05466 standard; Protein; 467 AA.
XX
XX AAE05466;
AC
XX 24-SEP-2001 (first entry)
DT
XX
XX Human presenilin (PS1) protein.
DE
XX
XX Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
XX NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
XX peripheral neuropathy; motorneuron disorder; neurodegenerative disorder;
XX Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
XX Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
XX nerve deafness; Alzheimer's disease; epilepsy.
XX
XX Homo sapiens.
XX
XX WO200151671-A2.
XX
XX 19-JUL-2001.
XX
XX 08-JAN-2001; 2001WO-US00526.
XX
XX 10-JAN-2000; 2000US-0175200.
XX
XX 04-JAN-2001; 2001US-0754949.
XX
XX (SCTO-) SCTOS INC.
XX
XX McCarthy J, Cordell B;
XX
XX WPI: 2001-451872/48.
XX
XX N-PSDB; AAE05466.
XX
XX Identifying inhibitors of neuronal degeneration useful for treating
XX e.g. Alzheimer's disease, by determining the ability of a compound to
XX induce nuclear factor kappa B activation, with the involvement of
XX presenilin or Par-4 -
XX
XX Claim 4; Page 60-61; 66pp; English.
XX
XX The invention relates to human Par-4 protein, presenilin protein (PS1
XX and PS2) and their corresponding DNA molecules. The invention also
XX relates to a method for identifying inhibitors of neuronal degeneration,
XX comprising cotransfecting eukaryotic host cells expressing presenilin
XX (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct,
XX exposing the cotransfected cells to a candidate molecule and monitoring
XX the ability of the candidate molecule to induce NF-kappa B activation.
XX Presenilin proteins participate in nuclear factor kappa B (NF-kappa B)
XX signalling and activation. The inhibitors of neuronal degeneration
XX are useful for treating neurodegenerative disorders such as Alzheimer's
XX disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
XX chorea, Down's syndrome, nerve deafness, Meniere's disease and also for
XX treating peripheral neuropathies, motorneuron disorders such as
XX amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions
XX involving spinal muscular atrophy and paralysis. The present sequence
XX is human presenilin (PS1) protein.
XX
XX Sequence 467 AA:
SQ
Query Match 78.4%; Score 366; DB 22; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 MTELPAPLSTYFONAMQMSDNHLSNTVRSQNDNRREROEHNDRRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSTYFONAMQMSDNHLSNTVRSQNDNRREROEHNDRRSLGHPPLSNGRPOGNSR 60
OY 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMVVVAATIKSVSFYTRKDQOLIYTPETE 120
DB 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMVVVAATIKSVSFYTRKDQOLIYTPETE 120
OY 121 DTEYVGORALSHILNAALIMISIVVMTLLVLYKRYCKYIHAMLISSLLFFESFI 180
DB 121 DTEYVGORALSHILNAALIMISIVVMTLLVLYKRYCKYIHAMLISSLLFFESFI 180
OY 181 YLGEVFKTYNNAVDTYVALLIWNLGVGVMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
DB 181 YLGEVFKTYNNAVDTYVALLIWNLGVGVMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
OY 241 LPEMTAWILILAVISYVDLVAALCPKGPLRMLVETAOERNEITLFPALIISSITWMLVYNAE 300
DB 241 LPEMTAWILILAVISYVDLVAALCPKGPLRMLVETAOERNEITLFPALIISSITWMLVYNAE 300
OY 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEMEAOQSDSHLGPHRSTPESRAA 360
DB 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEMEAOQSDSHLGPHRSTPESRAA 360
OY 361 VOELSSSTILAGEDPEERGVKLGDFITFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
DB 361 VOELSSSTILAGEDPEERGVKLGDFITFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
OY 421 TLLLLAIFKKALPALPISITFGVLVFPATDYLVOFMDQLAFHOFYI 467
DB 421 TLLLLAIFKKALPALPISITFGVLVFPATDYLVOFMDQLAFHOFYI 467

RESULT 12
AA018049
ID AA018049 standard; Protein: 467 AA.
XX AA018049:
XX 02-SEP-2002 (first entry)
XX Presentilin protein.
XX Sel-12; presentilin; neuronal disorder; familial Alzheimer's disease;
XX amyloid precursor protein; APP.
XX Unidentified.
XX OS
XX US6376239-B1.
XX PN
XX 23-APR-2002.
XX PD
XX 04-APR-1997; 97US-0832867.
XX PF
XX 04-APR-1997; 97US-0832867.
XX PR
XX (ELG-) ELGGENE GMBH.
XX PA
XX
XX PI
XX Baumeister R;
XX
XX WPI; 2002-478281/51.
XX DR
XX N-PSDB; AAL47323.
XX
XX Isolated DNA molecule comprising promoter of the sel-12 gene from
XX Caenorhabditis elegans operably linked to heterologous gene, directs
XX expression in neural cells and is useful to develop drugs to treat
XX neuronal disorders.
XX
XX Claim 2; Fig 4; 78pp; English.
XX
XX The present invention relates to DNA molecules comprising the promoter of
XX the sel-12 gene from Caenorhabditis elegans operably linked to a

```

```

CC heterologous DNA sequence encoding a protein of interest. The sequence
CC can be used to develop drugs for the treatment, prevention or delay of a
CC neuronal disorder. In particular, the neuronal disorder may be familial
CC Alzheimer's disease. The present sequence is a presentilin protein
CC described in the exemplification of the invention.
XX
XX Sequence 467 AA:
XX
XX Query Match 78.4%; Score 366; DB 23; Length 467;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 MTELPAPLSTYFONAMQMSDNHLSNTVRSQNDNRREROEHNDRRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSTYFONAMQMSDNHLSNTVRSQNDNRREROEHNDRRSLGHPPLSNGRPOGNSR 60
OY 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMVVVAATIKSVSFYTRKDQOLIYTPETE 120
DB 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMVVVAATIKSVSFYTRKDQOLIYTPETE 120
OY 121 DTEYVGORALSHILNAALIMISIVVMTLLVLYKRYCKYIHAMLISSLLFFESFI 180
DB 121 DTEYVGORALSHILNAALIMISIVVMTLLVLYKRYCKYIHAMLISSLLFFESFI 180
OY 181 YLGEVFKTYNNAVDTYVALLIWNLGVGVMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
DB 181 YLGEVFKTYNNAVDTYVALLIWNLGVGVMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
OY 241 LPEMTAWILILAVISYVDLVAALCPKGPLRMLVETAOERNEITLFPALIISSITWMLVYNAE 300
DB 241 LPEMTAWILILAVISYVDLVAALCPKGPLRMLVETAOERNEITLFPALIISSITWMLVYNAE 300
OY 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEMEAOQSDSHLGPHRSTPESRAA 360
DB 301 GDPFAORRVSKNSKYNAESTERESQDTVAENDDGFSEMEAOQSDSHLGPHRSTPESRAA 360
OY 361 VOELSSSTILAGEDPEERGVKLGDFITFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
DB 361 VOELSSSTILAGEDPEERGVKLGDFITFYSVLVGKASATASGDMNTTACFVAAILIGLCL 420
OY 421 TLLLLAIFKKALPALPISITFGVLVFPATDYLVOFMDQLAFHOFYI 467
DB 421 TLLLLAIFKKALPALPISITFGVLVFPATDYLVOFMDQLAFHOFYI 467

RESULT 13
AA079416
ID AA079416 standard; protein: 467 AA.
XX AA079416:
XX
XX 02-JUL-2002 (first entry)
XX Human presentilin-1, PS-1.
XX
XX Human; integrin-linked kinase; ILK; presentilin-1; protein kinase B; PKB;
XX gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;
XX neuroprotective; cytosstatic; cancer.
XX
XX Homo sapiens.
XX
XX WO200222862-A2.
XX PN
XX 23-MAR-2002.
XX PD
XX 12-SEP-2001; 2001WO-GB04094.
XX PF
XX 12-SEP-2001; 2000GB-0022333.
XX PR
XX (GLAX ) GLAXO GROUP LTD.
XX PA
XX
XX PI
XX Hiles ID, Ellis C;
XX

```


DR WPI: 2002-351896/38.

XX Identifying agent that modulates interaction between integrin-linked
PT kinase and presenilin-1, useful for treating Alzheimer's disease, and
PT Identifying agent that modulates protein kinase B or gamma secretase
PS activity

XX Disclosure: Page 43-45; 53pp; English.

XX The invention relates to identifying an agent modulating interaction
CC between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising
CC providing ILK, PS1 or their functional variants, as first and second
CC components respectively, contacting the components in the presence of
CC a test agent under conditions that in absence of the agent would
CC permit the components to interact and determining whether the agent is
CC capable of modulating the interaction between the components. Also
CC included are the method above where the components are protein kinase
CC beta (PKB), gamma secretase or their functional variants, test kits
CC for carrying out the methods and an agent identified by the methods.
CC The methods are used for identifying an agent that modulates
CC interaction between ILK and PS1, or PKB or gamma-secretase. The agent has
CC therapeutic applications in treating humans or animals, for treating a
CC host suffering from a condition associated with an interaction between
CC ILK and PS1, activity of PKB, activity of gamma-secretase, apoptosis,
CC cancer and Alzheimer's disease. The agent is also useful for
CC manufacturing a medicament for use in treatment of the above mentioned
CC conditions. The present sequence represents human presenilin-1, PS-1.

XX Sequence 467 AA:

Query Match 78.4%; Score 366; DB 23; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPPLSGRPOGNSR 60
DB 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPPLSGRPOGNSR 60

QY 61 QVVEDDEDEDELTKYGAHHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120
DB 61 QVVEDDEDEDELTKYGAHHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120

QY 121 DTEYVGORALHSILNAAMISYIVVMTLLVLYRYRCYKVYHAWLIISLLLEFFFSPT 180
DB 121 DTEYVGORALHSILNAAMISYIVVMTLLVLYRYRCYKVYHAWLIISLLLEFFFSPT 180

QY 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVFYKY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVFYKY 240

QY 241 LPEMTAMILLANYSYVDVAVLCPRGRLMLETAEORNETLFPALITYSSSTVWMLVNAE 300
DB 241 LPEMTAMILLANYSYVDVAVLCPRGRLMLETAEORNETLFPALITYSSSTVWMLVNAE 300

QY 301 GDPENQRRYSKSKYNAESTERESQDTVAENDGCFSEEMEAQRSHLCPHRSPTESRAA 360
DB 301 GDPENQRRYSKSKYNAESTERESQDTVAENDGCFSEEMEAQRSHLCPHRSPTESRAA 360

QY 361 VOELSSSILAGEDPERGVKGLGDFIFYSVLVGKASATASGDMWTTTACFVAIIIGLCL 420
DB 361 VOELSSSILAGEDPERGVKGLGDFIFYSVLVGKASATASGDMWTTTACFVAIIIGLCL 420

QY 421 TLLLLAIFKALPALPISTTRGLVYFPAFTDYVOPFMOLAHOFYI 467
DB 421 TLLLLAIFKALPALPISTTRGLVYFPAFTDYVOPFMOLAHOFYI 467

RESULT 14
AAE17051
ID AAE17051 standard; Protein; 467 AA.
XX AAE17051;
XX

PT 18-APR-2002 (first entry)

XX Human mutant presenilin 1 (PS1) wild type protein.

XX Human; presenilin 1; PS1; amyloid precursor protein; APP; drug screening;
XX Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
XX Huntington's disease; amyotrophic lateral sclerosis; Picks disease;
XX head injury disease; frontal lobe dementia; cerebellar degeneration;
XX ischaemic injury; schizophrenia.

XX Homo sapiens.

XX WO200202601-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US16508.

XX 30-JUN-2000; 2000US-215345P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Carter DB, Tomasselli AG;

XX WPI: 2002-140082/18.

PT Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT useful for screening of drugs for treating pathologies associated with
PT aberrant amyloid precursor protein processing, such as Alzheimer's
PT disease

XX Disclosure: Fig 1; 80pp; English.

XX The invention relates to mutant presenilin 1 (PS1) and presenilin 2
XX (PS2) polypeptides. Presenilin are involved in the processing of amyloid
XX precursor protein (APP) from which major amyloidogenic peptides are
XX cleaved. Mutant presenilins are useful for identifying agents that
XX modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
XX presenilin is also useful as a target for screening drugs useful in the
XX treatment of pathologies associated with aberrant amyloid precursor
XX protein processing, such as Alzheimer's disease, Parkinson's disease,
XX multiple sclerosis, Huntington's disease, amyotrophic lateral sclerosis,
XX head injury disease, Picks disease, frontal lobe dementia, cerebellar
XX degeneration, stroke, ischemic injury and schizophrenia. A transgenic
XX non-human animal is useful for analysing the interaction between APP and
XX mutant presenilin-processing protease in vivo, and for screening anti-
XX Alzheimer's disease drugs in vivo. A transgenic non-human
XX animal is useful for analysing the interaction between APP and mutant
XX presenilin-processing protease in vivo, and for screening anti-
XX Alzheimer's disease drugs in vivo. The present sequence is human
XX PS1 wild type protein.

XX Sequence 467 AA:

Query Match 78.4%; Score 366; DB 23; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPPLSGRPOGNSR 60
DB 1 MTELPAPLSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPPLSGRPOGNSR 60

QY 61 QVVEDDEDEDELTKYGAHHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120
DB 61 QVVEDDEDEDELTKYGAHHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120

QY 121 DTEYVGORALHSILNAAMISYIVVMTLLVLYRYRCYKVYHAWLIISLLLEFFFSPT 180
DB 121 DTEYVGORALHSILNAAMISYIVVMTLLVLYRYRCYKVYHAWLIISLLLEFFFSPT 180

QY 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVFYKY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNGVGMISIHMKGPLRLOQAYLIMISALMALVFYKY 240

```

OY 241 LPENTAMILAVISYVDLVAVLCPKGPLMLVETAQERNETLFPALISSTWVWLVNNAE 300
DB 241 LPENTAMILAVISYVDLVAVLCPKGPLMLVETAQERNETLFPALISSTWVWLVNNAE 300
OY 301 GDPKQRRVSKNSKYNASTEREODTYVAENDDGFSEEMKQDRSHLGPFRSTPESRAA 360
DB 301 GDPKQRRVSKNSKYNASTEREODTYVAENDDGFSEEMKQDRSHLGPFRSTPESRAA 360
OY 361 VOELSSSILAGEDPERGKVLGDFIFYSVLVYKASATASGDMNTTITACFVALIGLCL 420
DB 361 VOELSSSILAGEDPERGKVLGDFIFYSVLVYKASATASGDMNTTITACFVALIGLCL 420
OY 421 TLLLAIFKKALPALPISITFGLVFFATDYLVPFMDQLAFHOEYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYLVPFMDQLAFHOEYI 467

RESULT 15
AAW11840
ID AAW11840 standard; Protein; 463 AA.
AC AAW11840;
XX
XX 07-MAY-1997 (first entry)
DE Early onset Alzheimer's disease (EOAD) splice variant polypeptide.
XX
XX Early onset Alzheimer's disease; EOAD; neurodegenerative disease;
XX diagnosis; therapy; inhibitor; antagonist; antibody.
XX
XX Homo sapiens.
XX
XX MO9703086-A1.
XX
XX 30-JUN-1997.
XX
XX 26-JUN-1996; 96WO-US11064.
XX
XX 18-JUL-1995; 95US-0001501.
XX 13-JUL-1995; 95US-0001142.
XX
XX (UYSF-) UNIV SOUTH FLORIDA.
XX
XX Hardy JA.
XX
XX WPI: 1997-118980/11.
XX N-PSDB; AAT59536.
XX
XX Early onset Alzheimer's disease gene - useful for diagnosing a
XX pre-disposition to Alzheimer's disease
XX
XX Disclosure; Fig 2; 44pp; English.
XX
XX A 463-amino acid polypeptide (AAW11840) is the product of a full-
XX length cDNA (AAT59536) of an early onset Alzheimer's disease (EOAD)
XX splice variant gene. A 467-amino acid polypeptide (AAW11839) is the
XX product of a full-length cDNA (AAT59535) of the EOAD gene. The 2
XX polypeptides can be produced in transformed host cells and used to
XX raise antibodies, or to identify antagonist/inhibitor cpds. useful
XX in the treatment of Alzheimer's disease, esp. EOAD.
XX
XX Sequence 463 AA;
XX
Query Match 72.2%; Score 337; DB 18; Length 463;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 30 NDNEROEHDNRSLGHPPELSNGRPOGNSROYVODEDEDELTKYGAKHVIMLFVPV 89
DB 26 NDNEROEHDNRSLGHPPELSNGRPOGNSROYVODEDEDELTKYGAKHVIMLFVPV 85
C* 90 TLCAVVVAATIKSVSFYTRKGQILYPTEDTETVGORALHSLINAAIMISVIVMTIL 149

```

```

DB 86 TLCAVVVAATIKSVSFYTRKGQILYPTEDTETVGORALHSLINAAIMISVIVMTIL 145
OY 150 LVLYKYKCYVIAHAWLITSSLLFFPSFYLGVEPFTVAVADYITVALLINNLGVG 209
DB 146 LVLYKYKCYVIAHAWLITSSLLFFPSFYLGVEPFTVAVADYITVALLINNLGVG 205
OY 210 MISHMKGPRLQOAYLIMISALMALVFIKYLPEMTAMLIYVSYDLVAVLCPKGPLR 269
DB 206 MISHMKGPRLQOAYLIMISALMALVFIKYLPEMTAMLIYVSYDLVAVLCPKGPLR 265
OY 270 MLVETAQERNETLFPALISSTWVWLVNNAEGDEPAQRRVSKNSKYNASTEREODTYVA 329
DB 266 MLVETAQERNETLFPALISSTWVWLVNNAEGDEPAQRRVSKNSKYNASTEREODTYVA 325
OY 330 ENDDGGESEEMKQDRSHLGPFRSTPESRAVQELSSSILAGEDPERGKVLGDFIFY 389
DB 326 ENDDGGESEEMKQDRSHLGPFRSTPESRAVQELSSSILAGEDPERGKVLGDFIFY 385
OY 390 SVLVKASATASGDMNTTITACFVALIGLCLTLLLAIFKKALPALPISITFGLVFFAT 449
DB 386 SVLVKASATASGDMNTTITACFVALIGLCLTLLLAIFKKALPALPISITFGLVFFAT 445
OY 450 DYLVQPFMDQLAFHOEYI 467
DB 446 DYLVQPFMDQLAFHOEYI 463

RESULT 16
AAV20854
ID AAV20854 standard; Protein; 463 AA.
AC AAV20854;
XX
XX 22-JUL-1999 (first entry)
DE Human presenilin 1 wild type protein fragment.
XX
XX Human: beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
XX frameshift mutation; age-related disease; neurodegenerative disorder;
XX Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
XX Huntington's disease; multiple sclerosis; alcoholic liver disease;
XX diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
XX ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
XX neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
XX glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
XX bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
XX high mobility group protein-C; neuroendocrine specific protein A.
XX
XX Homo sapiens.
XX
XX MO9845328-A2.
XX
XX 15-OCT-1998.
XX
XX 02-APR-1998; 98WO-IB00705.
XX
XX 10-APR-1997; 97US-0043163.
XX
XX (UYUT-) RIJSDUNIV UTRECHT.
XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
XX Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX WPI: 1998-609901/51.
XX N-PSDB; AAX75761.
XX
XX Diagnosing disease by detecting frameshift mutations in RNA or
XX corresponding protein mutations - used to diagnose cancer and
XX neurological diseases, particularly Alzheimer's disease, and also
XX for treatment and prevention with specific ribozymes or wild-type
XX RNA

```

XX PS Disclosure: Figure 10: 258bp: English.

CC CC This invention describes a novel method for the diagnosis of a disease

CC CC caused by, or associated with, an RNA molecule that has a frameshift

CC CC mutation. The method is used to diagnose age-related diseases, especially

CC CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's

CC CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,

CC CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II

CC CC and many others listed) or susceptibility to these disorders. The method

CC CC allows a definitive diagnosis of Alzheimer's disease in living patients,

CC CC at an early stage. It is based on the observation that disease may be

CC CC caused by mutations in RNA rather than DNA. The invention describes the

CC CC use of neuronal system RNA molecules, specifically proteins including

CC CC beta-amyloid precursor protein (beta-Ap), the microtubule associated

CC CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule

CC CC associated protein 2 (Map2), neurofilament-L, neurofilament-M,

CC CC neurofilament-F, presenilin 1, presenilin II, glial fibrillary acidic

CC CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma

CC CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group

CC CC protein-C (HMGp-C) and neuroendocrine specific protein A.

XX SQ Sequence 463 AA:

Query Match 72.2%; Score 337; DB 19; Length 463;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NDNREOEHNDRSLGHPPLSNGRPOGNSROVVEODEEDELTKYGAHVIMLEFV 89

DB 26 NDNREOEHNDRSLGHPPLSNGRPOGNSROVVEODEEDELTKYGAHVIMLEFV 85

QY 90 TLGMVVVATIKSVSYFTRKDGOLITPTEDTEYVGOALHSILNAAIMISIVVMTL 149

DB 86 TLGMVVVATIKSVSYFTRKDGOLITPTEDTEYVGOALHSILNAAIMISIVVMTL 145

QY 150 LVLYKRYCYKIYHAWLIISLLEFFSFYLGVEFKYNNVAVDYITVALLIMNGVVG 209

DB 146 LVLYKRYCYKIYHAWLIISLLEFFSFYLGVEFKYNNVAVDYITVALLIMNGVVG 205

QY 210 MISIHKKGLRLQOAVLIMISALMALVFITKYLEPENTAMILAVISYVDLVAVLCPRGPIR 269

DB 206 MISIHKKGLRLQOAVLIMISALMALVFITKYLEPENTAMILAVISYVDLVAVLCPRGPIR 265

QY 270 MLVETAQERNETLFPALIVSSTVWMLVNNAEQDPEAQRVSKSKYNAESTERESODTVA 329

DB 266 MLVETAQERNETLFPALIVSSTVWMLVNNAEQDPEAQRVSKSKYNAESTERESODTVA 325

QY 330 ENDDGSESEWEAQRDSSLGPHRSTPESRAAVOELSSILAGEDPERGVKLGIDFIFY 389

DB 326 ENDDGSESEWEAQRDSSLGPHRSTPESRAAVOELSSILAGEDPERGVKLGIDFIFY 385

QY 390 SYLVGKASATASGDWNTTACFAVALIGCLTLLLAIFKKALPALPISITGVLVYFAT 449

DB 386 SYLVGKASATASGDWNTTACFAVALIGCLTLLLAIFKKALPALPISITGVLVYFAT 445

QY 450 DYLVOPFMDQLAFHOFYI 467

DB 446 DYLVOPFMDQLAFHOFYI 463

RESULT 17

AAW11839

ID AAW11839 standard; Protein: 467 AA.

XX AC AAW11839;

XX DT 07-MAY-1997 (first entry)

XX DE Human early onset Alzheimer's disease (EOAD) polypeptide.

KW Early Onset Alzheimer's disease; EOAD; neurodegenerative disease;

KW diagnosis: therapy; inhibitor; antagonist; antibody.

XX OS Homo sapiens.

XX PS

XX Key Location/Qualifiers

FT Misc-difference 26..29

FT

XX W09703086-A1.

XX 30-JAN-1997.

XX 26-JUN-1996; 96MO-US11064.

XX 18-JUL-1995; 95US-0001501.

XX 13-JUL-1995; 95US-0001142.

XX (UYSE-) UNITV SOUTH FLORIDA.

XX Hardy JA;

XX WPI, 1997-118980/11.

XX N-PSDB: AAT59535.

XX

XX Early Onset Alzheimer's disease gene - useful for diagnosing a

XX pre-disposition to Alzheimer's disease

XX Disclosure: Fig 1: 44pp: English.

XX

XX A 467-amino acid polypeptide (AAW11839) is the product of a

XX full-length cDNA (AAT59535) of the early onset Alzheimer's disease

XX (EOAD) gene. A 463-amino acid polypeptide (AAW11840) is the

XX product of another full-length cDNA (AAT59535) of an EOAD splice

XX variant gene. The 2 polypeptides can be produced in transformed

XX host cells and used to raise antibodies, or to identify

XX antagonist/inhibitor cpds., useful in the treatment of Alzheimer's

XX disease, esp. EOAD.

XX SQ Sequence 467 AA:

Query Match 72.2%; Score 337; DB 18; Length 467;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 30 NDNREOEHNDRSLGHPPLSNGRPOGNSROVVEODEEDELTKYGAHVIMLEFV 89

DB 30 NDNREOEHNDRSLGHPPLSNGRPOGNSROVVEODEEDELTKYGAHVIMLEFV 89

QY 90 TLGMVVVATIKSVSYFTRKDGOLITPTEDTEYVGOALHSILNAAIMISIVVMTL 149

DB 90 TLGMVVVATIKSVSYFTRKDGOLITPTEDTEYVGOALHSILNAAIMISIVVMTL 149

QY 150 LVLYKRYCYKIYHAWLIISLLEFFSFYLGVEFKYNNVAVDYITVALLIMNGVVG 209

DB 150 LVLYKRYCYKIYHAWLIISLLEFFSFYLGVEFKYNNVAVDYITVALLIMNGVVG 209

QY 210 MISIHKKGLRLQOAVLIMISALMALVFITKYLEPENTAMILAVISYVDLVAVLCPRGPIR 269

DB 210 MISIHKKGLRLQOAVLIMISALMALVFITKYLEPENTAMILAVISYVDLVAVLCPRGPIR 269

QY 270 MLVETAQERNETLFPALIVSSTVWMLVNNAEQDPEAQRVSKSKYNAESTERESODTVA 329

DB 270 MLVETAQERNETLFPALIVSSTVWMLVNNAEQDPEAQRVSKSKYNAESTERESODTVA 329

QY 330 ENDDGSESEWEAQRDSSLGPHRSTPESRAAVOELSSILAGEDPERGVKLGIDFIFY 389

DB 330 ENDDGSESEWEAQRDSSLGPHRSTPESRAAVOELSSILAGEDPERGVKLGIDFIFY 389

QY 390 SYLVGKASATASGDWNTTACFAVALIGCLTLLLAIFKKALPALPISITGVLVYFAT 449

DB 390 SYLVGKASATASGDWNTTACFAVALIGCLTLLLAIFKKALPALPISITGVLVYFAT 449

QY 450 DYLVOPFMDQLAFHOFYI 467

DB 446 DYLVOPFMDQLAFHOFYI 463

Db 450 DYLVQPFMDQLAFHQFYI 467

RESULT 18
AAW05759 standard; Protein; 429 AA.

AC AAW05759 standard; Protein; 429 AA.

DE 04-JUN-1998 (first entry)

PS1/429 protein.

Presentin peptide; PS1/429; immunogen; immune response; PS1 gene; Alzheimer's disease; mitochondrial pathology; neurodegeneration; apoptosis.

Homo sapiens.

009746678-A1.

11-DEC-1997.

03-JUN-1997; 97WO-US09272.

18-JUL-1996; 96US-0683315.

06-JUN-1996; 96US-0659296.

(FARB) BAYER CORP.

Chisholm JC, Davis JN, Drache B.

WPI: 1998-042186/04.

N-PSDB; AAW17357.

DNA encoding presentin peptide PS1/429 and its analogues - useful for diagnosis and treatment of Alzheimer's disease

Claim 24; Fig 1; 77pp; English.

This sequence is the PS1/429 presentin peptide (II) of the invention. Cells transformed with the DNA are used to produce recombinant (II) and analogues, useful e.g. as immunogens for generating an immune response against PS1/429. (II) is a new product of the PS1 gene, mutations in which cause Alzheimer's disease (AD). The nucleic acids are generally useful as probes for detection and quantification of PS1/429, particularly for diagnosis of AD, especially the target sequences that hybridise with probes are isolated for sequencing. Antibodies (Ab) can also be diagnosed at the protein level using Ab as immunoassay reagents. Ab can also be used to identify epitopes and for affinity purification of peptides. Antisense nucleic acid may also be used to regulate expression of the PS1/429 gene, and both nucleic acids and peptides are useful as size markers in electrophoresis, chromatography etc. The transgenic animals are used as models for AD, e.g. for testing drugs. Regulators of the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases involving mitochondrial pathology, apoptosis and neurodegeneration. Typical regulators are antisense sequences, ribozymes, aptamers, synthetic or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations.

Sequence 429 AA:

Query Match 66.2%; Score 309; DB 19; Length 429;
Best Local Similarity 99.8%; Pred. No. 1.6e-266;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

58 NSROVVEDEDEDELTKYGAHVIMLVPTLCMVVATIKSVSFTKKDQLIYTP 117
|||||
20 NSRQVVEDEDEDELTKYGAHVIMLVPTLCMVVATIKSVSFTKKDQLIYTP 79
|||||
118 FTEDTEYVGRALHSILMAIMISYIVMTLLVLYVKRYKIYHAWLLISLLLEFF 177
|||||
80 FTEDTEYVGRALHSILMAIMISYIVMTLLVLYVKRYKIYHAWLLISLLLEFF 139

QY 178 SEIYLGEVEFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVF 237
|||||
DB 140 SPIYLGVEFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRLQOAVLIMISALMALVF 199
|||||

QY 238 IKYLPENTAMLLAVISYVDLVAVLCPKGPLMLVETAOERNETLFPALLIYSTWMLVN 297
|||||
DB 200 IKYLPENTAMLLAVISYVDLVAVLCPKGPLMLVETAOERNETLFPALLIYSTWMLVN 259
|||||

QY 298 MAEGDPEAORRYSKSKYNAESTEREODTYAENDGGFSEEMQARSHLCPHSTPES 357
|||||
DB 260 MAEGDPEAORRYSKSKYNAESTEREODTYAENDGGFSEEMQARSHLCPHSTPES 319
|||||

QY 358 RAAVDELSSSILAGEDEPERGKLGIDFIFYSVLVGRASATASGDMWTJTACFVALILG 417
|||||
DB 320 RAAVDELSSSILAGEDEPERGKLGIDFIFYSVLVGRASATASGDMWTJTACFVALILG 379
|||||

QY 418 LCLTLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
|||||
DB 380 LCLTLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 429
|||||

RESULT 19
AAW05759 standard; Protein; 467 AA.

AAW05759; 96US-0683315.

23-JUL-1997 (first entry)

Presentin-1-1 C410Y mutation.

Presentin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutin.

Homo sapiens.

Key Location/Qualifiers
Modified-site 410 /label=C410Y

WC9634099-A2.

31-DEC-1996.

29-APR-1996; 96WO-CA00263.

31-JUL-1995; 95US-0509359.

28-APR-1995; 95US-0431048.

28-JUN-1995; 95US-0496841.

(HSCR-) HSC RES & DEV LP.
(UTOR) UNIV TORONTO GOVERNING COUNCIL.

Fraser PE, Rommens JM, St George-Hyslop PH;
WPI: 1996-497631/49.

New presentin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.

Claim 3; Page -: 178pp; English.

AAW05736-W05760 represent mutated versions of the human presentin-1-1 protein (see AAW05734 for wild type sequence). AAW05734 represents a different wild type form of presentin-1 that results from alternate splicing of the genomic DNA sequence. The presentins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in

CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

SO Sequence 467 AA:

Query Match 66.0%; Score 308; DB 17; Length 467;
 Best Local Similarity 99.8%; Pred. No. 1.7e-295;
 Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPELPAFLYFQNAQSENNHLSNTYRSQNDNREHNDKRLGPEPLSNRPGNSR 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MPELPAFLYFQNAQSENNHLSNTYRSQNDNREHNDKRLGPEPLSNRPGNSR 60
 QY 61 QVEODEEDELTKYGAHVIMLFVPYTLCAVVVATIKSVFTRKDGOLITPTE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 QVEODEEDELTKYGAHVIMLFVPYTLCAVVVATIKSVFTRKDGOLITPTE 120
 QY 121 DTEVGORALHSLNAAIMISVIVMTLLVLYKRYCYKVIHAWLISSLLFFESFI 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 DTEVGORALHSLNAAIMISVIVMTLLVLYKRYCYKVIHAWLISSLLFFESFI 180
 QY 181 YLGEVKTYNVADYITVALLINLGVGMISIHMKGPLRLQOAYLIMSALMAVFIKY 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 YLGEVKTYNVADYITVALLINLGVGMISIHMKGPLRLQOAYLIMSALMAVFIKY 240
 QY 241 LPEWTAMLLIAVISYDLVAVLCRPGRLMLVETAOERNETLFPALISSTMYLVNMAE 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 LPEWTAMLLIAVISYDLVAVLCRPGRLMLVETAOERNETLFPALISSTMYLVNMAE 300
 QY 301 GDEPAORVSKNSKYNAESTERESQDTVAENDGCFSEMEAOARDSHLGHRSTPESRAA 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 GDEPAORVSKNSKYNAESTERESQDTVAENDGCFSEMEAOARDSHLGHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGMWNTTIA 409
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGMWNTTIA 409

RESULT 20

AAW28507
 ID AAW28507 standard; Protein: 407 AA.

AC AAW28507;

DT 07-DEC-1997 (first entry)

XX Partial AD3 sequence.

XX AD3: AD4/AD3LP; Alzheimer's disease; chromosome; missegregation;

KW presentin; inhibitor; AD; trisomy 21.

XX Homo sapiens.

XX Location/Qualifiers

FT key 86 /label= mutation

FT MISC-difference 103 /note= "M -> L"

FT MISC-difference 186 /label= mutation

FT MISC-difference 226 /note= "A -> E"

FT MISC-difference 350 /label= mutation

FT MISC-difference 350 /label= mutation

/note= "C -> Y"

FR W09107213-A2.

PN 27-FEB-1997.

PD 15-AUG-1996; 96WO-US1314.

PF 16-AUG-1995; 95US-0002448.

PR (HARD) HARVARD COLLEGE.

PA Li J, Potter H;

DR WPI: 1997-165297/15.

DR N-PSDB: AAT87402.

PT Identifying genes which cause chromosome missegregation - useful for

PT identifying causes of and treatments for diseases, e.g. Alzheimer's

PS disclosure; Fig 1; 77pp; English.

CC Identifying genes which cause improper chromosome segregation,
 CC screening for inhibitors of chromosome missegregation and processes
 CC caused by genes encoding chromosome missegregation promoters
 CC was exemplified using Alzheimer's disease. The sequences
 CC given in Aat87401 to Aat87426 can be used in the above methods.
 CC The five mutations indicated in the Features table cosegregate
 CC with early-onset familial Alzheimer's disease. It is predicted
 CC that these mutations result in increased levels of cells with
 CC trisomy 21 in carriers of the mutation compared with non-carriers.

SO Sequence 407 AA:

Query Match 65.5%; Score 306; DB 18; Length 407;
 Best Local Similarity 99.8%; Pred. No. 1.4e-293;
 Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 61 QVEODEEDELTKYGAHVIMLFVPYTLCAVVVATIKSVFTRKDGOLITPTE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 QVEODEEDELTKYGAHVIMLFVPYTLCAVVVATIKSVFTRKDGOLITPTE 60
 QY 121 DTEVGORALHSLNAAIMISVIVMTLLVLYKRYCYKVIHAWLISSLLFFESFI 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 DTEVGORALHSLNAAIMISVIVMTLLVLYKRYCYKVIHAWLISSLLFFESFI 120
 QY 181 YLGEVKTYNVADYITVALLINLGVGMISIHMKGPLRLQOAYLIMSALMAVFIKY 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 YLGEVKTYNVADYITVALLINLGVGMISIHMKGPLRLQOAYLIMSALMAVFIKY 180
 QY 241 LPEWTAMLLIAVISYDLVAVLCRPGRLMLVETAOERNETLFPALISSTMYLVNMAE 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 LPEWTAMLLIAVISYDLVAVLCRPGRLMLVETAOERNETLFPALISSTMYLVNMAE 240
 QY 301 GDEPAORVSKNSKYNAESTERESQDTVAENDGCFSEMEAOARDSHLGHRSTPESRAA 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 GDEPAORVSKNSKYNAESTERESQDTVAENDGCFSEMEAOARDSHLGHRSTPESRAA 300
 QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGMWNTTIA 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGMWNTTIA 360
 QY 421 TLLLLAIFKKALPALPISITFGVLFVATDYLVOPFDOLAFOFYI 467
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 TLLLLAIFKKALPALPISITFGVLFVATDYLVOPFDOLAFOFYI 407

RESULT 21

AAW05758
 ID AAW05758 standard; Protein: 467 AA.

AC AAW05758;

```

XX 23-JUL-1997 (first entry)
DT
XX
DE Presenilin-1 L392V mutation.
XX
KW Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; muten.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 392
FT /label= L392V
XX
XX WO9634099-A2.
XX
XX 31-OCT-1996.
XX
XX 29-APR-1996; 96WO-CA00263.
XX
XX 31-JUL-1995; 95US-0509359.
XX 28-APR-1995; 95US-0431048.
XX 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RBS & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX WPI: 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
XX Claim 3; Page -: 178pp; English.
XX
XX AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAW05734 for wild type sequence). AAW05734 represents a
CC different wild type form of presenilin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presenilins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common structural hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC useful as models for drug screening. The antibodies can also be used e.g.
CC for affinity purification and in immunoassays.
XX
XX Sequence 467 AA:
XX
XX Query Match 62.1%; Score 290; DB 17; Length 467;
XX Best Local Similarity 99.7%; Pred. No. 1e-277;
XX Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MTELPAPISTFONQMSQEDNHLSTNVRSONDREROEHNDRLSLGPEPLSGRPOGNSR 60
XX |
XX 1 MTELPAPISTFONQMSQEDNHLSTNVRSONDREROEHNDRLSLGPEPLSGRPOGNSR 60
XX |
XX 61 QVVEDEDEDELTLTKYGAHYIMLFVPTLCMVVVAITIKSVSYTRKDGILITPTPE 120
XX |
XX 61 QVVEDEDEDELTLTKYGAHYIMLFVPTLCMVVVAITIKSVSYTRKDGILITPTPE 120
XX |
XX 121 DTEYVGOARLHSLNAAIMISIVVMTILVLYKYRCYKVIHAWLISSLLLEFFFSFI 180
XX |
XX 121 DTEYVGOARLHSLNAAIMISIVVMTILVLYKYRCYKVIHAWLISSLLLEFFFSFI 180
XX |
XX 181 YLGEVFETYNVAVDYITVALLIWNLGVGVMISIHMKGPLRLQOAYLIMISALMALVFIRY 240
XX |

```

```

DB 181 YLGEVFETYNVAVDYITVALLIWNLGVGVMISIHMKGPLRLQOAYLIMISALMALVFIRY 240
XX |
XX 241 LPEWTAMLILAVISYVDIAVAIVLCPPRLMLVETAOERNETLEFPALITYSTWMLVNMAE 300
XX |
XX 241 LPEWTAMLILAVISYVDIAVAIVLCPPRLMLVETAOERNETLEFPALITYSTWMLVNMAE 300
XX |
XX 301 GPPEAORRVSKNSKYNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
XX |
XX 301 GPPEAORRVSKNSKYNAESTERESODTVAENDDGFSEMEAROSHLGPHRSTPESRAA 360
XX |
XX 361 VOELSSIIAGDDPEERGVKLGIDFIYFSV 391
XX |
XX 361 VOELSSIIAGDDPEERGVKLGIDFIYFSV 391
XX |
XX
XX RESULT 22
XX AAW05736
XX ID AAW05736 standard; Protein; 467 AA.
XX
XX AAW05736;
XX
XX AC
XX AC
XX 23-JUL-1997 (first entry)
XX
XX Presenilin-1 A79X mutation.
XX
XX Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
XX familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
XX depression; antibody; gene expression modulator; therapy; muten.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 79
XX /label= A79X
XX /note= "X = unspecified amino acid"
XX
XX WO9634099-A2.
XX
XX 31-OCT-1996.
XX
XX 29-APR-1996; 96WO-CA00263.
XX
XX 31-JUL-1995; 95US-0509359.
XX 28-APR-1995; 95US-0431048.
XX 28-JUN-1995; 95US-0496841.
XX
XX (HSCR-) HSC RBS & DEV LP.
XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
XX Fraser PE, Rommens JM, St George-Hyslop PH;
XX WPI: 1996-497631/49.
XX
XX New presenilin genes - useful for diagnosis, therapy and drug
XX screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
XX Claim 3; Page -: 178pp; English.
XX
XX AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAW05734 for wild type sequence). AAW05734 represents a
CC different wild type form of presenilin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presenilins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common structural hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are

```

CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 61.5%; Score 287; DB 17; Length 467;
 Best Local Similarity 99.7%; Pred. No. 9.5e-275;
 Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 80 KHVIMFVVTLCMVVAVTIKSVSYTRKDDQILYPTPEDETEYVGORALHSILNAIM 139
 DB 80 KHVIMFVVTLCMVVAVTIKSVSYTRKDDQILYPTPEDETEYVGORALHSILNAIM 139
 OY 140 ISIVVMTLLVLYKYRCYKVIHAWLIISLILFFSFYIYGEVFKYNNVADYITVA 199
 DB 140 ISIVVMTLLVLYKYRCYKVIHAWLIISLILFFSFYIYGEVFKYNNVADYITVA 199
 OY 200 LLIWNLGVGMISIHMKGPLRLQOAVLIMISALMALVFTKYLPEWTAMLIAVISYDLY 259
 DB 200 LLIWNLGVGMISIHMKGPLRLQOAVLIMISALMALVFTKYLPEWTAMLIAVISYDLY 259
 OY 260 AVLCPRGLRMLVETAOERNTLFPALIVSSTWVLVNAEGDPEAQRVSKSKNAES 319
 DB 260 AVLCPRGLRMLVETAOERNTLFPALIVSSTWVLVNAEGDPEAQRVSKSKNAES 319
 OY 320 TERESQDTVAENDDGFSEMEQORDSHLGPHRSTPESRAAVOELSSILAGDPERGV 379
 DB 320 TERESQDTVAENDDGFSEMEQORDSHLGPHRSTPESRAAVOELSSILAGDPERGV 379
 OY 380 KLGIDGFIFYSVLVGRASATASGDMWTTIACFVAIILIGLCTLLLAIFKKALPALPIST 439
 DB 380 KLGIDGFIFYSVLVGRASATASGDMWTTIACFVAIILIGLCTLLLAIFKKALPALPIST 439
 OY 440 TEGVYFATDYLVOPFMDQAFHQFYI 467
 DB 440 TEGVYFATDYLVOPFMDQAFHQFYI 467

RESULT 23

AA05737
 ID AA05737 standard; Protein; 467 AA.

XX AA05737;
 XX
 DT 23-JUL-1997 (first entry)
 XX

DE Presentin-1-1 V82L mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; muten1.

XX Homo sapiens.

OS
 XX
 FT Key Location/Qualifiers
 FT Modified-site 82
 FT /label= V82L

XX W09634099-a2.
 XX

PD 31-OCT-1996.
 XX

PF 29-APR-1996; 96MO-CA00263.
 XX

PR 31-JUL-1995; 95US-0509359.
 PR 28-APR-1995; 95US-0431048.
 PR 28-JUN-1995; 95US-0496841.

XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX Fraser PE, Rommens JM, St George-Hyslop PH;
 PI

DR WPI; 1996-497631/49.

XX New presentin genes - useful for diagnosis, therapy and drug
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.

XX Claim 3; Page -; 178pp; English.

PS AAM05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 60.8%; Score 284; DB 17; Length 467;
 Best Local Similarity 99.7%; Pred. No. 8.8e-272;
 Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 83 IMFVPTLCMVVAVTIKSVSYTRKDDQILYPTPEDETEYVGORALHSILNAIMISV 142
 DB 83 IMFVPTLCMVVAVTIKSVSYTRKDDQILYPTPEDETEYVGORALHSILNAIMISV 142
 OY 143 IYVMTLLVLYKYRCYKVIHAWLIISLILFFSFYIYGEVFKYNNVADYITVALLI 202
 DB 143 IYVMTLLVLYKYRCYKVIHAWLIISLILFFSFYIYGEVFKYNNVADYITVALLI 202
 OY 203 WNLGVGMISIHMKGPLRLQOAVLIMISALMALVFTKYLPEWTAMLIAVISYDLYAVL 262
 DB 203 WNLGVGMISIHMKGPLRLQOAVLIMISALMALVFTKYLPEWTAMLIAVISYDLYAVL 262
 OY 263 CPKGPLRMLVETAOERNTLFPALIVSSTWVLVNAEGDPEAQRVSKSKNAESTER 322
 DB 263 CPKGPLRMLVETAOERNTLFPALIVSSTWVLVNAEGDPEAQRVSKSKNAESTER 322
 OY 323 ESQDTVAENDDGFSEMEQORDSHLGPHRSTPESRAAVOELSSILAGDPERGVKLG 382
 DB 323 ESQDTVAENDDGFSEMEQORDSHLGPHRSTPESRAAVOELSSILAGDPERGVKLG 382
 OY 383 LSGDIFYSVLVGRASATASGDMWTTIACFVAIILIGLCTLLLAIFKKALPALPISTFG 442
 DB 383 LSGDIFYSVLVGRASATASGDMWTTIACFVAIILIGLCTLLLAIFKKALPALPISTFG 442
 OY 443 LVFYFATDYLVOPFMDQAFHQFYI 467
 DB 443 LVFYFATDYLVOPFMDQAFHQFYI 467

RESULT 24

AAE17046
 ID AAE17046 standard; Protein; 467 AA.

XX AAE17046;
 XX

DT 18-APR-2002 (first entry)
 XX

DE Human mutant presentin 1 (ps1) protein #2.

KW Human; presentin 1; PS1; amyloid precursor protein; APP; drug screening;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
 KW Huntington's disease; amyotrophic lateral sclerosis; Pick's disease;
 KW head injury disease; frontal lobe dementia; cerebral degeneration;

```

KW | ischaemic injury; schizophrenia; mutant; mutein.
XX |
OS | Homo sapiens.
XX | Synthetic.
FH | /key Location/Qualifiers
FT | /note= "Encoded by GTGCTGTG"
FT | /label= "Unknown"
FT | /note= "Wild type Phe substituted with Xaa; Encoded
FT | by NNN"
FT | /label= "Unknown"
FT | /note= "Wild type Ile substituted with Xaa; Encoded
FT | by NNN"
PN | WO200202601-A2.
XX |
XX | 10-JAN-2002.
XX |
XX | 29-JUN-2001; 2001WO-US16508.
XX |
XX | 30-JUN-2000; 2000US-215345P.
XX |
XX | (PHNA ) PHARMACIA & UPJOHN CO.
XX |
XX | Carter DB, Tomasselli AG;
XX |
XX | WPT: 2002-140082/18.
XX | N-PSDB; AAD27444.
XX |
XX | Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
XX | useful for screening of drugs for treating pathologies associated with
XX | aberrant amyloid precursor protein processing, such as Alzheimer's
XX | disease -
XX |
XX | Claim 15; Page 68-70; 80pp; English.
XX |
XX | The invention relates to mutant presenilin 1 (PS1) and presenilin 2
XX | (PS2) polypeptides. Presenilin are involved in the processing of amyloid
XX | precursor protein (APP) from which major amyloidogenic peptides are
XX | cleaved. Mutant presenilins are useful for identifying agents that
XX | modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
XX | presenilin is also useful as a target for screening drugs useful in the
XX | treatment of pathologies associated with aberrant amyloid precursor
XX | protein processing, such as Alzheimer's disease, Parkinson's disease,
XX | multiple sclerosis, Huntington's disease, amyotrophic lateral sclerosis,
XX | head injury disease, Pick's disease, frontal lobe dementia, cerebellar
XX | degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
XX | non-human animal is useful for analysing the interaction between APP and
XX | mutant presenilin-processing protease in vivo, and for screening anti-
XX | Alzheimer's disease drugs in vivo. A transgenic non-human
XX | animal is useful for analysing the interaction between APP and mutant
XX | presenilin-processing protease in vivo, and for screening anti-
XX | Alzheimer's disease drugs in vivo. The present sequence is human
XX | mutant PS1 protein.
XX |
XX | Sequence 467 AA;
XX |
XX | Query Match 60.8%; Score 284; DB 23; Length 467;
XX | Best Local Similarity 99.7%; Pred. No. 8.8e-272;
XX | Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX |
QY | 1 MTELPAPLSTYQNMQMSDNHLSTNVRSONNREQENDRSLGHPPLNSNGRQGSNR 60
DB | 1 MTELPAPLSTYQNMQMSDNHLSTNVRSONNREQENDRSLGHPPLNSNGRQGSNR 60
QY | 61 QVEDDEDEDELTKYGAHKVIMLFVPTLCMVVVVATIKSVSPYTRKQDOLITPTPE 120
DB | 61 QVEDDEDEDELTKYGAHKVIMLFVPTLCMVVVVATIKSVSPYTRKQDOLITPTPE 120
QY | 121 DTEVGGQRALHSLINAAIMISVIVMTLLVLYKRYCKYIHAWLITSSDLLLFFFSFI 180
DB | 121 DTEVGGQRALHSLINAAIMISVIVMTLLVLYKRYCKYIHAWLITSSDLLLFFFSFI 180

```

```

DB | 121 DTEVGGQRALHSLINAAIMISVIVMTLLVLYKRYCKYIHAWLITSSDLLLFFFSFI 180
QY | 181 YGGEVFKTYNNAVDTITVALIWMIGVGMISIHMKGPLRLQOAVLIMISALMAVFIRY 240
DB | 181 YGGEVFKTYNNAVDTITVALIWMIGVGMISIHMKGPLRLQOAVLIMISALMAVFIRY 240
QY | 241 LPEWTAMLILAVISYDVAVCLCPKPLMLVETAOERNETLFPALITSSITWMLVNNAE 300
DB | 241 LPEWTAMLILAVISYDVAVCLCPKPLMLVETAOERNETLFPALITSSITWMLVNNAE 300
QY | 301 GDPFAQRVSKNSKYNAESTEREODTVAENDGFSFEEMEAQRDSHLGPHRSTPESRAA 360
DB | 301 GDPFAQRVSKNSKYNAESTEREODTVAENDGFSFEEMEAQRDSHLGPHRSTPESRAA 360
QY | 361 VOELSSSILAGDPPERGYKLGLD 385
DB | 361 VOELSSSILAGDPPERGYKLGLD 385

RESULT 25
AAW05757
ID | AAW05757 standard; Protein; 467 AA.
XX |
XX | AAW05757;
XX |
XX | 23-JUL-1997 (first entry)
XX |
XX | Presenilin-1-1 G384A mutation.
XX |
XX | Presenilin-1; human; hPS1-1; hPS1-2; integral membrane protein; AD;
XX | familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
XX | depression; antibody; gene expression modulator; therapy; mutein.
XX |
XX | Homo sapiens.
XX |
XX | Key Location/Qualifiers
XX | Modified-site 384 /label= G384A
XX |
XX | WO9634099-A2.
XX |
XX | 31-OCT-1996.
XX |
XX | 29-APR-1996; 96WO-CA00263.
XX |
XX | 31-JUL-1995; 95US-0509359.
XX | 28-APR-1995; 95US-0431048.
XX | 28-JUN-1995; 95US-0496841.
XX |
XX | (HSCR-) HSC RES & DEV LP.
XX | (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX |
XX | Fraser PE, Rommens JM, St George-Hyslop PH;
XX | WPT: 1996-497631/49.
XX |
XX | New presenilin genes - useful for diagnosis, therapy and drug
XX | screening of familial Alzheimer's disease, cerebral disorders, etc.
XX |
XX | Claim 3; Page -, 178pp; English.
XX |
XX | AAW05736-W05760 represent mutated versions of the human presenilin-1-1
XX | protein (see AAW05733 for wild type sequence). AAW05734 represents a
XX | different wild type form of presenilin-1 that results from alternate
XX | splicing of the genomic DNA sequence. The presenilins are a family of
XX | highly conserved integral membrane proteins with a common structural
XX | motif, common alternate splicing patterns, and common mutational hot
XX | spot regions. Mutations in PS genes are implicated in familial
XX | Alzheimer's disease (AD) and possibly other diseases such as cerebral
XX | haemorrhage, schizophrenia, depression etc., so detection of mutations in
XX | the DNA encoding the wild type sequences can be used for diagnosis of
XX | these diseases. The wild type proteins, or vectors that express them or

```


CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA;

Query Match 60.4%; Score 282; DB 17; Length 467;
 Best Local Similarity 99.7%; Pred. No. 8.4e-270;
 Matches 382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSPFQNMQMSDNHLSNTVRSQNDNRERQEHNDKRSGLGHPPLSGNRPGQNSR 60
 DB 1 MTELPAPLSPFQNMQMSDNHLSNTVRSQNDNRERQEHNDKRSGLGHPPLSGNRPGQNSR 60
 QY 61 QVEDDEDEDELTKYAKAHVIMLFVVTLCMNVVAVATIKSVSYTRKDGOLITPTPE 120
 DB 61 QVEDDEDEDELTKYAKAHVIMLFVVTLCMNVVAVATIKSVSYTRKDGOLITPTPE 120
 QY 121 DTEYGOBALHSILMAAIMISIVVMTLLVLYKRCYKVIHAWLIISLILFFFSFI 180
 DB 121 DTEYGOBALHSILMAAIMISIVVMTLLVLYKRCYKVIHAWLIISLILFFFSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLIMNLGVGMISIHMKGPLRQOAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNLGVGMISIHMKGPLRQOAVLIMISALMALVFIKY 240
 QY 241 LPERTAMILAVISYDVAVLCPRGLRLMLETQERNETLFPALITSSIMVWLVNMAE 300
 DB 241 LPERTAMILAVISYDVAVLCPRGLRLMLETQERNETLFPALITSSIMVWLVNMAE 300
 QY 301 GPPEQRKRVSKSKYNAESTERESODTVAENDDGFSEEMEQRDSHLGPHRSTPESRA 360
 DB 301 GPPEQRKRVSKSKYNAESTERESODTVAENDDGFSEEMEQRDSHLGPHRSTPESRA 360
 QY 361 VOELSSSILAGEDPEERGVKGL 383
 DB 361 VOELSSSILAGEDPEERGVKGL 383

RESULT 26
 AAM05738
 ID AAM05738 standard; Protein; 467 AA.

XX AAM05738;

XX 23-JUL-1997 (first entry)

XX Presentin-1-1 V96F mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;

KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 depression; antibody; gene expression modulator; therapy; muten.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 96 /label= V96F

XX MO9634099-A2.

XX 31-OCT-1996.

XX 29-APR-1996; 96WO-CA00263.

XX 31-JUL-1995; 95US-0509359.

XX 28-APR-1995; 95US-0431048.

XX 28-JUN-1995; 95US-0496841.

XX (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX Fraser PE, Rommens JM, St George-Hyslop PH;
 PI WPI: 1996-497631/49.

XX New presentin genes - useful for diagnosis, therapy and drug
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.

XX Claim 3; Page -: 178pp; English.

CC AAM05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA;

Query Match 57.8%; Score 270; DB 17; Length 467;
 Best Local Similarity 99.7%; Pred. No. 6.1e-258;
 Matches 370; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 97 VATIKSVSYTRKDGOLITPTPTEDTEYGOBALHSILMAAIMISIVVMTLLVLYKY 156
 DB 97 VATIKSVSYTRKDGOLITPTPTEDTEYGOBALHSILMAAIMISIVVMTLLVLYKY 156
 QY 157 RCYKVIHAWLIISLILFFFSFIYLGVEFKTYNAVDYITVALLIMNLGVGMISIHMK 216
 DB 157 RCYKVIHAWLIISLILFFFSFIYLGVEFKTYNAVDYITVALLIMNLGVGMISIHMK 216
 QY 217 GPLRQOAVLIMISALMALVFIKYLPENTAMILAVISYDVAVLCPRGLRLMLETQ 276
 DB 217 GPLRQOAVLIMISALMALVFIKYLPENTAMILAVISYDVAVLCPRGLRLMLETQ 276
 QY 277 ERNETLFPALITSSIMVWLVNMAEGDPEAQRRVSKSKYNAESTERESODTVAENDDGF 336
 DB 277 ERNETLFPALITSSIMVWLVNMAEGDPEAQRRVSKSKYNAESTERESODTVAENDDGF 336
 QY 337 SEEMEQRDSHLGPHRSTPESRAVOELSSSILAGEDPEERGVKGLGPFITYSVLYGKA 396
 DB 337 SEEMEQRDSHLGPHRSTPESRAVOELSSSILAGEDPEERGVKGLGPFITYSVLYGKA 396
 QY 397 SATASGDWNTTIACFVAILIGLCTLLTLAIFKKALPALPISITGLVFFATDYLVOPE 456
 DB 397 SATASGDWNTTIACFVAILIGLCTLLTLAIFKKALPALPISITGLVFFATDYLVOPE 456
 QY 457 MDQLAFHQFYI 467
 DB 457 MDQLAFHQFYI 467

RESULT 27

AAM05750
 ID AAM05750 standard; Protein; 467 AA.

XX AAM05750;

XX 23-JUL-1997 (first entry)

XX Presentin-1-1 C263R mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;

```

KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KM depression; antibody; gene expression modulator; therapy; muten.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 263
FT /label=C263R
XX
PN W09634099-A2.
XX
PD 31-OCT-1996.
XX
PE 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
DR WPI; 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 3; Page -: 178pp; English.
XX
CC AAM05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAM05734 for wild type sequence). AAM05734 represents a
CC different wild type form of presenilin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presenilins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are
CC useful as models for drug screening. The antibodies can also be used e.g.
CC for affinity purification and in immunoassays.
XX
SQ Sequence 467 AA;
Query Match 56.7%; Score 265; DB 17; Length 467;
Best Local Similarity 99.6%; Pred. No. 5.3e-253;
Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 MTELPAPLSTYFQNAQMSQEDNHLSTNVSQNDNRRERQEHNDRRSLGHPPLSNGRPQNSR 60
DB 1 MTELPAPLSTYFQNAQMSQEDNHLSTNVSQNDNRRERQEHNDRRSLGHPPLSNGRPQNSR 60
OY 61 QVNEBODEEDELTLKYGAKIVIMLFVPTLCMVVVAATIKSVSFYTRKQQLTYPTTE 120
DB 61 QVNEBODEEDELTLKYGAKIVIMLFVPTLCMVVVAATIKSVSFYTRKQQLTYPTTE 120
OY 121 DTEVVGQRALSHINAAIMISIVVMTILLVLKRYGQYKIHMLIISLLFFPSFI 180
DB 121 DTEVVGQRALSHINAAIMISIVVMTILLVLKRYGQYKIHMLIISLLFFPSFI 180
OY 181 YLGEVFQYVNAVVDYITVALLINMLGVVGMISIMHKGPLRLQQAYLIMISALMLVETIKY 240
DB 181 YLGEVFQYVNAVVDYITVALLINMLGVVGMISIMHKGPLRLQQAYLIMISALMLVETIKY 240
OY 241 LPEWTAAVLIAVISVYDLVAVLCRKGPLRMIVTAQERNELFPALLIYSSIMVWLVMAE 300
DB 241 LPEWTAAVLIAVISVYDLVAVLCRKGPLRMIVTAQERNELFPALLIYSSIMVWLVMAE 300

```

```

OY 301 GDPEAQRVSKNSKYNAESTERESODTVAENDDGGFSEWEAQRDSHLGPHRSPESRAA 360
DB 301 GDPEAQRVSKNSKYNAESTERESODTVAENDDGGFSEWEAQRDSHLGPHRSPESRAA 360
OY 361 VOELSSSILAGEDPERGVKLGIDFIFYSVLVGKASATASGDMWNTTACFAVILIGLCL 420
DB 361 VOELSSSILAGEDPERGVKLGIDFIFYSVLVGKASATASGDMWNTTACFAVILIGLCL 420
OY 421 TLLLAIFRKALPALPISITFGIVFYFATDYLNQPFMQLAFFHOFYI 467
DB 421 TLLLAIFRKALPALPISITFGIVFYFATDYLNQPFMQLAFFHOFYI 467

RESULT 28
AAM05751
ID AAM05751 standard; Protein: 467 AA.
XX
AC AAM05751;
XX
DT 23-JUL-1997 (first entry)
XX
DE Presenilin-1-1 P264L mutation.
XX
KM Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KM familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KM depression; antibody; gene expression modulator; therapy; muten.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 264
FT /label= p264L
XX
PN W09634099-A2.
XX
PD 31-OCT-1996.
XX
PE 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
DR WPI; 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 3; Page -: 178pp; English.
XX
CC AAM05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAM05734 for wild type sequence). AAM05734 represents a
CC different wild type form of presenilin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presenilins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are
CC useful as models for drug screening. The antibodies can also be used e.g.
CC for affinity purification and in immunoassays.
XX

```

SQ Sequence 467 AA:

56.7%; Score 265; DB 17; Length 467;

Query Match Best Local Similarity 99.6%; Pred. No. 5.3e-253;

Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSQNDNREROEHNDRLSLGHPPLSLNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSQNDNREROEHNDRLSLGHPPLSLNGRPOGNSR 60
 OY 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMNVVAVATIKSVSFYTRKDGQILITPTE 120
 DB 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMNVVAVATIKSVSFYTRKDGQILITPTE 120
 OY 121 DTEVGORALHSILNAAMISIVVMTILLVLYKRCYKVHAWLISSLLLEFFSFI 180
 DB 121 DTEVGORALHSILNAAMISIVVMTILLVLYKRCYKVHAWLISSLLLEFFSFI 180
 OY 181 YLGEVFKTYNNAVDYITVAALLIWNLGVMGMSIHKMGPRLQOAYLIMSALMALVFITY 240
 DB 181 YLGEVFKTYNNAVDYITVAALLIWNLGVMGMSIHKMGPRLQOAYLIMSALMALVFITY 240
 OY 241 LPEWTAMILAVISYVDLVAVLCPRGSLRMIVETAQERNETLFPALISSTWMLVNNAE 300
 DB 241 LPEWTAMILAVISYVDLVAVLCPRGSLRMIVETAQERNETLFPALISSTWMLVNNAE 300
 OY 301 GDPFAQRVSKSKYNAESTERESODTYVAENDDGFSEMEQORSHLGPHRSTPESRAA 360
 DB 301 GDPFAQRVSKSKYNAESTERESODTYVAENDDGFSEMEQORSHLGPHRSTPESRAA 360
 OY 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 OY 421 TLLLAIFKKALPALPISITTEGLVFFPATDYLVQPFMDLAFHOEYI 467
 DB 421 TLLLAIFKKALPALPISITTEGLVFFPATDYLVQPFMDLAFHOEYI 467

RESULT 29

AAW05752 AAW05752 standard; Protein; 467 AA.

AC AAW05752;

DT 23-JUL-1997 (first entry)

DE Presentin-1-1 P267S mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; muten.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Modified-site 267

FT FT /label= P267S

XX W09634099-A2.

XX 31-OCT-1996.

XX 29-APR-1996; 96WO-CA00263.

XX 31-JUL-1995; 95US-0509359.

XX 28-APR-1995; 95US-0431048.

XX 28-JUN-1995; 95US-0496841.

XX (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 XX Fraser PE, Rommens JM, St George-Hyslop PH;

XX WPI: 1996-497631/49.

DR New presentin genes - useful for diagnosis, therapy and drug
 XX screening of familial Alzheimer's disease, cerebral disorders, etc.
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.

XX Claim 3; Page -; 178pp; English.

CC AAW05736-005760 represent mutated versions of the human presentin-1-1
 CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

SQ Sequence 467 AA:

56.7%; Score 265; DB 17; Length 467;

Query Match Best Local Similarity 99.6%; Pred. No. 5.3e-253;

Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSQNDNREROEHNDRLSLGHPPLSLNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSQNDNREROEHNDRLSLGHPPLSLNGRPOGNSR 60
 OY 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMNVVAVATIKSVSFYTRKDGQILITPTE 120
 DB 61 QVVEDDEDEDELTKYGAKHVIMLFVPTLCMNVVAVATIKSVSFYTRKDGQILITPTE 120
 OY 121 DTEVGORALHSILNAAMISIVVMTILLVLYKRCYKVHAWLISSLLLEFFSFI 180
 DB 121 DTEVGORALHSILNAAMISIVVMTILLVLYKRCYKVHAWLISSLLLEFFSFI 180
 OY 181 YLGEVFKTYNNAVDYITVAALLIWNLGVMGMSIHKMGPRLQOAYLIMSALMALVFITY 240
 DB 181 YLGEVFKTYNNAVDYITVAALLIWNLGVMGMSIHKMGPRLQOAYLIMSALMALVFITY 240
 OY 241 LPEWTAMILAVISYVDLVAVLCPRGSLRMIVETAQERNETLFPALISSTWMLVNNAE 300
 DB 241 LPEWTAMILAVISYVDLVAVLCPRGSLRMIVETAQERNETLFPALISSTWMLVNNAE 300
 OY 301 GDPFAQRVSKSKYNAESTERESODTYVAENDDGFSEMEQORSHLGPHRSTPESRAA 360
 DB 301 GDPFAQRVSKSKYNAESTERESODTYVAENDDGFSEMEQORSHLGPHRSTPESRAA 360
 OY 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 OY 421 TLLLAIFKKALPALPISITTEGLVFFPATDYLVQPFMDLAFHOEYI 467
 DB 421 TLLLAIFKKALPALPISITTEGLVFFPATDYLVQPFMDLAFHOEYI 467

RESULT 30

AAW05753 AAW05753 standard; Protein; 467 AA.

AC AAW05753;

DT 23-JUL-1997 (first entry)

DE Presentin-1-1 E280A/G mutation.

XX Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; muten.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 280
 FT /label= E280X
 FT /note= "X = Ala, Gly"
 XX

W09634099-A2.

31-OCT-1996.

29-APR-1996: 96WC-CA00263.

31-JUL-1995: 95US-0509359.

28-APR-1995: 95US-0431048.

28-JUN-1995: 95US-0496841.

(HSCR-) HSC RES & DEV LP.

(UTOR) UNIV TORONTO GOVERNING COUNCIL.

Fraser PE, Rommens JM, St George-Hyslop PH;

WPI: 1996-497631/49.

New presenilin genes - useful for diagnosis, therapy and drug

screening of familial Alzheimer's disease, cerebral disorders, etc.

Claim 3; Page -: 178pp; English.

AAW05736-W05760 represent mutated versions of the human presenilin-1-1
 protein (see AAW05733 for wild type sequence). AAW05734 represents a
 different wild type form of presenilin-1 that results from alternate
 splicing of the genomic DNA sequence. The presenilins are a family of
 highly conserved integral membrane proteins with a common structural
 motif, common alternate splicing patterns, and common mutational hot
 spot regions. Mutations in PS genes are implicated in familial
 Alzheimer's disease (AD) and possibly other diseases such as cerebral
 haemorrhage, schizophrenia, depression etc., so detection of mutations in
 the DNA encoding the wild type sequences can be used for diagnosis of
 these diseases. The wild type proteins, or vectors that express them or
 containing antisense sequences, antibodies selective for these mutant
 forms of the proteins and modulators of PS gene expression are
 potentially useful for treatment of AD etc. Transgenic animals are
 useful as models for drug screening. The antibodies can also be used e.g.
 for affinity purification and in immunoassays.

Sequence 467 AA:

Query Match 56.7%; Score 265; DB 17; Length 467;

Best Local Similarity 99.6%; Pred. No. 5; 3e-253;

Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MTELPAPLSTFONAKMSDNHLSNTRSONDNREORHNDNRSGHEPPLNSGPGNSR 60

1 MTELPAPLSTFONAKMSDNHLSNTRSONDNREORHNDNRSGHEPPLNSGPGNSR 60

61 QVVEODEDEDELTKYGAHVIMLEFVPLVCWVVVATIKSYFYRKDGQILYPTFE 120

61 QVVEODEDEDELTKYGAHVIMLEFVPLVCWVVVATIKSYFYRKDGQILYPTFE 120

121 DTEVGORALHSLNAIMISVYVMTLLVLYLKRKYVIAHAWLITSLLLFFPSFI 180

121 DTEVGORALHSLNAIMISVYVMTLLVLYLKRKYVIAHAWLITSLLLFFPSFI 180

181 YLGEVFTYVAVDYITVALINLGVGMISIMHGKPLDQAYLIMLSALMAVPIKY 240

181 YLGEVFTYVAVDYITVALINLGVGMISIMHGKPLDQAYLIMLSALMAVPIKY 240

QY 241 LPEWTAMLLIAVISYDVLAVLCPKPLRLMLVETAQERNETLPALIIYSTVMVLVNNAE 300
 DB 241 LPEWTAMLLIAVISYDVLAVLCPKPLRLMLVETAQERNETLPALIIYSTVMVLVNNAE 300
 QY 301 GDPFAQRVSKNSKYNASTERESQDTVAENDCGFSEWFAQDLSHLCPRSTPESRAA 360
 DB 301 GDPFAQRVSKNSKYNASTERESQDTVAENDCGFSEWFAQDLSHLCPRSTPESRAA 360
 QY 361 VOELSSSTILAGEDPEERGVKLGDFIFYSLVGKASATASGDMNTIACPVAILIGICT 420
 DB 361 VOELSSSTILAGEDPEERGVKLGDFIFYSLVGKASATASGDMNTIACPVAILIGICT 420
 QY 421 TLLLLAIFKKALPALPISITFGVFEATDYLVQPFMDOLAFHOYI 467
 DB 421 TLLLLAIFKKALPALPISITFGVFEATDYLVQPFMDOLAFHOYI 467

RESULT 31
 AAW05754
 ID AAW05754 standard; Protein: 467 AA.

XX AAW05754.

23-JUL-1997 (first entry)

Presenilin-1-1 A285V mutation.

Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;

familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;

depression; antibody; gene expression modulator; therapy; muten.

Homo sapiens.

Key Location/Qualifiers

FT Modified-site 285

FT /label= A285V

W09634099-A2.

31-OCT-1996.

29-APR-1996: 96WC-CA00263.

31-JUL-1995: 95US-0509359.

28-APR-1995: 95US-0431048.

28-JUN-1995: 95US-0496841.

(HSCR-) HSC RES & DEV LP.

(UTOR) UNIV TORONTO GOVERNING COUNCIL.

Fraser PE, Rommens JM, St George-Hyslop PH;

WPI: 1996-497631/49.

New presenilin genes - useful for diagnosis, therapy and drug

screening of familial Alzheimer's disease, cerebral disorders, etc.

Claim 3; Page -: 178pp; English.

AAW05736-W05760 represent mutated versions of the human presenilin-1-1
 protein (see AAW05733 for wild type sequence). AAW05734 represents a
 different wild type form of presenilin-1 that results from alternate
 splicing of the genomic DNA sequence. The presenilins are a family of
 highly conserved integral membrane proteins with a common structural
 motif, common alternate splicing patterns, and common mutational hot
 spot regions. Mutations in PS genes are implicated in familial
 Alzheimer's disease (AD) and possibly other diseases such as cerebral
 haemorrhage, schizophrenia, depression etc., so detection of mutations in
 the DNA encoding the wild type sequences can be used for diagnosis of
 these diseases. The wild type proteins, or vectors that express them or
 containing antisense sequences, antibodies selective for these mutant
 forms of the proteins and modulators of PS gene expression are
 potentially useful for treatment of AD etc. Transgenic animals are

CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

SO Sequence 467 AA:

Query Match

56.7%; Score 265; DB 17; Length 467;

Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDREHNDRLSLGHPPLSGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDREHNDRLSLGHPPLSGRPGNSR 60
 QY 61 QVDEDEDEDELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTKRDGLITPTPE 120
 DB 61 QVDEDEDEDELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTKRDGLITPTPE 120
 QY 121 DTEYGORALSHILNAIMISIVVMTLLVLYKRCYKVHAWLISSLLFFFSFI 180
 DB 121 DTEYGORALSHILNAIMISIVVMTLLVLYKRCYKVHAWLISSLLFFFSFI 180
 QY 181 YLGEVFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFITY 240
 DB 181 YLGEVFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFITY 240
 QY 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNETLFPALIVSSSTVWMLVNAE 300
 DB 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNETLFPALIVSSSTVWMLVNAE 300
 QY 301 GDPEAQRVSKSKYNAESTERESQDTVAENDGGFSEMEQRDRLGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKSKYNAESTERESQDTVAENDGGFSEMEQRDRLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPERGVKGLGDFITYSVLVKASATASDWMNTTACFAVAILIGLCL 420
 DB 361 VOELSSSILAGEDPERGVKGLGDFITYSVLVKASATASDWMNTTACFAVAILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVYFATDYLVOPFMOLAHOFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVYFATDYLVOPFMOLAHOFYI 467

RESULT 32

AAW05755 ID AAW05755 standard; Protein: 467 AA.

AC AAW05755:

XX 23-JUL-1997 (first entry)

XX Presentin-1-1 L286V mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;

KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; muten.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 286
 FT Label= L286V

XX MO9634099-A2.

XX 31-OCT-1996.

XX 29-APR-1996; 96WO-CA00263.

XX 31-JUL-1995; 95US-0509359.

XX 28-APR-1995; 95US-0431048.
 XX 28-JUN-1995; 95US-0496841.

XX (HSCR-) HSC RES & DEV LP.

PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

PI Fraser PE, Rommens JM, St George-Hyslop PH;

DR WPI: 1996-497631/49.

PT New presentin genes - useful for diagnosis, therapy and drug
 screening of familial Alzheimer's disease, cerebral disorders, etc.

PS Claim 3; Page -: 178pp; English.

AAW05736-W05760 represent mutated versions of the human presentin-1-1
 protein (see AAW05733 for wild type sequence). AAW05734 represents a
 different wild type form of presentin-1 that results from alternate
 splicing of the genomic DNA sequence. The presentins are a family of
 highly conserved integral membrane proteins with a common structural
 motif, common alternate splicing patterns, and common mutational hot
 spot regions. Mutations in PS genes are implicated in familial
 Alzheimer's disease (AD) and possibly other diseases such as cerebral
 haemorrhage, schizophrenia, depression etc., so detection of mutations in
 the DNA encoding the wild type sequences can be used for diagnosis of
 these diseases. The wild type proteins, or vectors that express them or
 containing antisense sequences, antibodies selective for these mutant
 forms of the proteins and modulators of PS gene expression are
 potentially useful for treatment of AD etc. Transgenic animals are
 useful as models for drug screening. The antibodies can also be used e.g.
 for affinity purification and in immunoassays.

SO Sequence 467 AA:

Query Match

56.7%; Score 265; DB 17; Length 467;

Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDREHNDRLSLGHPPLSGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDREHNDRLSLGHPPLSGRPGNSR 60
 QY 61 QVDEDEDEDELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTKRDGLITPTPE 120
 DB 61 QVDEDEDEDELTKYGAKHVIMLFVPTLCMVVAVATIKSVSYTKRDGLITPTPE 120
 QY 121 DTEYGORALSHILNAIMISIVVMTLLVLYKRCYKVHAWLISSLLFFFSFI 180
 DB 121 DTEYGORALSHILNAIMISIVVMTLLVLYKRCYKVHAWLISSLLFFFSFI 180
 QY 181 YLGEVFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFITY 240
 DB 181 YLGEVFKTYNNAVDTITVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVFITY 240
 QY 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNETLFPALIVSSSTVWMLVNAE 300
 DB 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNETLFPALIVSSSTVWMLVNAE 300
 QY 301 GDPEAQRVSKSKYNAESTERESQDTVAENDGGFSEMEQRDRLGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKSKYNAESTERESQDTVAENDGGFSEMEQRDRLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPERGVKGLGDFITYSVLVKASATASDWMNTTACFAVAILIGLCL 420
 DB 361 VOELSSSILAGEDPERGVKGLGDFITYSVLVKASATASDWMNTTACFAVAILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVYFATDYLVOPFMOLAHOFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVYFATDYLVOPFMOLAHOFYI 467

RESULT 33

AAW05739 ID AAW05739 standard; Protein: 467 AA.

XX AAW05739;

```

DT 23-JUL-1997 (first entry)
XX
DE Presentin-1-1 Y115H mutation.
XX
KW Presentin-1: human; hps1-1; hps1-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; mutain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 115
FT /label= Y115H
XX
PN MO9634099-A2.
XX
PD 31-OCT-1996.
XX
PE 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX
DR WPI; 1996-497631/49.
XX
PT New presentin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
XX
PS Claim 3; Page -: 178pp; English.
XX
CC AAM05736-W05760 represent mutated versions of the human presentin-1-1
CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
CC different wild type form of presentin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presentins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are
CC useful as models for drug screening. The antibodies can also be used e.g.
CC for affinity purification and in immunoassays.
XX
XX
SQ Sequence 467 AA:

```

Query Match 56.7%; Score 265; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MTELPAPLSTYQNMQSEEDNLSTVRSQNDNRERHNDNRSGHPEPLSNGRPOGNSR 60
DB 1 MTELPAPLSTYQNMQSEEDNLSTVRSQNDNRERHNDNRSGHPEPLSNGRPOGNSR 60
QY 61 QVVEDEDEDEELTKGAKHVMLEFVPTLCMVVVVATIKSVFYTRKQGLTYRPFTE 120
DB 61 QVVEDEDEDEELTKGAKHVMLEFVPTLCMVVVVATIKSVFYTRKQGLTYRPFTE 120
QY 121 DTEVGORALHSIIMAAIMSVIVMTLLVLYKRCYKVIHAWLTISSLLFFPSFI 180
DB 121 DTEVGORALHSIIMAAIMSVIVMTLLVLYKRCYKVIHAWLTISSLLFFPSFI 180
QY 181 YLGEVFTYNAVVDYITVALLIMNGVVGMIISHWKGPLRLQQAYLIMISALMALVFIRY 240
DB 181 YLGEVFTYNAVVDYITVALLIMNGVVGMIISHWKGPLRLQQAYLIMISALMALVFIRY 240

```

```

DB 181 YLGEVFTYNAVVDYITVALLIMNGVVGMIISHWKGPLRLQQAYLIMISALMALVFIRY 240
QY 241 LPENTAMILLIAVISYDVAVLCPKGPLRMLVETAOENETLFPALITSSPMVLVNNAE 300
DB 241 LPENTAMILLIAVISYDVAVLCPKGPLRMLVETAOENETLFPALITSSPMVLVNNAE 300
QY 301 GDPFAQRVRSKNSKYNAESTERESODTVAENDDGFSEMEQAQDSHLGPHRSTPESRAA 360
DB 301 GDPFAQRVRSKNSKYNAESTERESODTVAENDDGFSEMEQAQDSHLGPHRSTPESRAA 360
QY 361 VOELSSSTIAGEDEPERKVLGLDFTYSLVYKASATAGDWNNTIACVALLIGLCL 420
DB 361 VOELSSSTIAGEDEPERKVLGLDFTYSLVYKASATAGDWNNTIACVALLIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGVFPATDYLVOPFMDQLAFHOEYI 467
DB 421 TLLLAIFKKALPALPISITFGVFPATDYLVOPFMDQLAFHOEYI 467

```

RESULT 34
 AAM05740
 ID AAM05740 standard; Protein: 467 AA.
 XX
 AC AAM05740;
 XX
 DT 23-JUL-1997 (first entry)
 XX
 DE Presentin-1-1 M139T/V mutation.
 XX
 KW Presentin-1: human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; mutain.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 139
 FT /label= M139X
 FT /note= "X = Thr, Val"
 XX
 PN WO9634099-A2.
 XX
 PD 31-OCT-1996.
 XX
 PE 29-APR-1996; 96WO-CA00263.
 XX
 PR 31-JUL-1995; 95US-0509359.
 PR 28-APR-1995; 95US-0431048.
 PR 28-JUN-1995; 95US-0496841.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 XX
 PI Fraser PE, Rommens JM, St George-Hyslop PH;
 XX
 DR WPI; 1996-497631/49.
 XX
 PT New presentin genes - useful for diagnosis, therapy and drug
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.
 XX
 PS Claim 3; Page -: 178pp; English.
 XX
 CC AAM05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or

CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 56.7%; Score 265; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQEHNDRLSLGHPPLSGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQEHNDRLSLGHPPLSGRPOGNSR 60
 QY 61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVVVATIKSVSFYTRKDGLITPTPE 120
 DB 61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVVVATIKSVSFYTRKDGLITPTPE 120
 QY 121 DRETGORALHSILNAAIMISYVMTLLVLYKRCYKHYHAWLITSLLEFFSFI 180
 DB 121 DRETGORALHSILNAAIXISYVMTLLVLYKRCYKHYHAWLITSLLEFFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIHMKGPLRLOQAVLIMSALMAVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIHMKGPLRLOQAVLIMSALMAVFIKY 240
 QY 241 LPEWTAMLILAVISYDLAVLCPRKPLRLMVELTAOERNETLFPALITYSTWMLVMAE 300
 DB 241 LPEWTAMLILAVISYDLAVLCPRKPLRLMVELTAOERNETLFPALITYSTWMLVMAE 300
 QY 301 GDPEAQRVSKSKYNAESTERESODTVAENDGCFSEMEARQDSHLGPHRSTPESRA 360
 DB 301 GDPEAQRVSKSKYNAESTERESODTVAENDGCFSEMEARQDSHLGPHRSTPESRA 360
 QY 361 VOELSSILAGDPBERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 DB 361 VOELSSILAGDPBERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISTFGLVFFATDYLVOPMDLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISTFGLVFFATDYLVOPMDLAFHQFYI 467

RESULT 35

AAW05741 ID AAW05741 standard; Protein: 467 AA.

XX AAW05741:

XX 23-JUL-1997 (first entry)

XX Presentin-1-1 I143T mutation.

XX Presentin-1: human; hps1-1; hps1-2; PS-2: integral membrane protein; AD;

XX familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;

XX depression; antibody; gene expression modulator; therapy; muten.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 143 /label= I143T

XX W09634099-A2.

XX 31-OCT-1996.

XX 29-APR-1996; 96WO-CA00263.

XX 31-JUL-1995; 95US-0509359.

XX 28-APR-1995; 95US-0431048.

PR 28-JUN-1995; 95US-0496841.

XX (HSCR-) HSC RES & DEV LP.

PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX Fraser PE, Rommens JM, St George-Hyslop PH;

XX WPI: 1996-497631/49.

XX New presentin genes - useful for diagnosis, therapy and drug

XX screening of familial Alzheimer's disease, cerebral disorders, etc.

XX Claim 3; Page -: 178pp; English.

CC AAW05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 56.7%; Score 265; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQEHNDRLSLGHPPLSGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQEHNDRLSLGHPPLSGRPOGNSR 60
 QY 61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVVVATIKSVSFYTRKDGLITPTPE 120
 DB 61 QVEDDEDEDEDELTLYKGAHVIMLFVPTLCMVVVVATIKSVSFYTRKDGLITPTPE 120
 QY 121 DRETGORALHSILNAAIMISYVMTLLVLYKRCYKHYHAWLITSLLEFFSFI 180
 DB 121 DRETGORALHSILNAAIXISYVMTLLVLYKRCYKHYHAWLITSLLEFFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIHMKGPLRLOQAVLIMSALMAVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALIMNLGVGMISIHMKGPLRLOQAVLIMSALMAVFIKY 240
 QY 241 LPEWTAMLILAVISYDLAVLCPRKPLRLMVELTAOERNETLFPALITYSTWMLVMAE 300
 DB 241 LPEWTAMLILAVISYDLAVLCPRKPLRLMVELTAOERNETLFPALITYSTWMLVMAE 300
 QY 301 GDPEAQRVSKSKYNAESTERESODTVAENDGCFSEMEARQDSHLGPHRSTPESRA 360
 DB 301 GDPEAQRVSKSKYNAESTERESODTVAENDGCFSEMEARQDSHLGPHRSTPESRA 360
 QY 361 VOELSSILAGDPBERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 DB 361 VOELSSILAGDPBERGVKLGDFIFYSVLVGKASATASGDMWTTTACFAVAILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISTFGLVFFATDYLVOPMDLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISTFGLVFFATDYLVOPMDLAFHQFYI 467

RESULT 36

AAW05742 ID AAW05742 standard; Protein: 467 AA.

XX		
AC		AAM05742;
XX		
DT		23-JUL-1997 (first entry)
XX		
DE		Presenilin-1 M146L/V mutation.
XX		
KM		Presentin-1; human; hpsl-1; hpsl-2; PS-2; integral membrane protein; AD
KW		familial Alzheimer's disease; cerebral hemorrhage; schizophrenia;
RN		'depression; antibody; gene expression modulator; therapy; muten.
OS		Homo sapiens.
XX		
FH		Key Location/Qualifiers
FT		Modified-site 146
FT		/label= M146X
FT		/note= "X = Leu, Val"
XX		
PX		M0963409-A2.
PD		
XX		31-OCT-1996.
PF		
XX		29-APR-1996; 96MO-CA00263.
PR		
XX		31-JUL-1995; 95US-0509359.
PR		28-APR-1995; 95US-0431048.
XX		28-JUN-1995; 95US-0496841.
PA		(HSCR-) HSC RES & DEV LP.
PA		(UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX		
PI		Fraser PE, Kommens JM, St George-Hyslop PH;
XX		WPJ; 1996-497631/49.
DR		
XX		
PT		New presenilin genes - useful for diagnosis, therapy and drug
PT		screening of familial Alzheimer's disease, cerebral disorders, etc.
XX		
PS		Claim 3; Page -: 178pp; English.
XX		
CC		AAM05736-M05760 represent mutated versions of the human presenilin-1-1
CC		protein (see AAM05733 for wild type sequence). AAM05734 represents a
CC		different wild type form of presenilin-1 that results from alternate
CC		splicing of the genomic DNA sequence. The presenilins are a family of
CC		highly conserved integral membrane proteins with a common structural
CC		motif, common alternate splicing patterns, and common mutational hot
CC		spot regions. Mutations in PS genes are implicated in familial
CC		Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC		hemorrhage, schizophrenia, depression etc., so detection of mutations
CC		in the DNA encoding the wild type sequences can be used for diagnosis of
CC		these diseases. The wild type proteins, or vectors that express them or
CC		containing antisense sequences, antibodies selective for these mutant
CC		forms of the proteins and modulators of PS gene expression are
CC		potentially useful for treatment of AD etc. Transgenic animals are
CC		useful as models for drug screening. The antibodies can also be used e.g
CC		for affinity purification and in immunoassays.
XX		
CC		
SQ		Sequence 467 AA:
Query Match		56.7%; Score 265; DB 17; Length 467;
Best Local Similarity		99.6%; Pred. No. 5.3e-253;
Matches 465; Conservative		0; Mismatches 2; Indels 0; Gaps 0
OY		1 MTELPALSLSFQNAKMSNDNLNTFRSONDNREGRHNDRLSLGHPLEPLSGRFGNSR 60
DB		1 MTELPALSLSFQNAKMSNDNLNTFRSONDNREGRHNDRLSLGHPLEPLSGRFGNSR 60
OY		61 QVVEODEEDELTLKYGAKHVIMLFVPVTLGVVVVAITIKSVSEFYTRKGQLIYPPE 120
DB		61 QVVEODEEDELTLKYGAKHVIMLFVPVTLGVVVVAITIKSVSEFYTRKGQLIYPPE 120
OY		121 DTEVGGRALHSILNAIMISVVTILLVLVLYTKRCXYIHAWLISSLLFFESFI 180
DB		121 DTEVGGRALHSILNAIMISVVTILLVLVLYTKRCXYIHAWLISSLLFFESFI 180

Db	121	DTEIVGQRALHSILNAIMISIVVXTLLVLVLYKKRYKVIHAMLLISSLLLEFFSP	180
Oy	181	YLGEVFKRYNVAADYIYVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVEIKY	240
Db	181	YLGEVFKRYNVAADYIYVALLIMNLGVGMISIHMKGPLRLQOAYLIMISALMALVEIKY	240
Oy	241	LPEWTAMLLILAVISYVDLVAVLCPKGPLRMVLVETAOERNETLEPALIYSTWMLVNMAE	300
Db	241	LPEWTAMLLILAVISYVDLVAVLCPKGPLRMVLVETAOERNETLEPALIYSTWMLVNMAE	300
Oy	301	GDPEAQRVSKNSKYNMAESTPESQDPIVAENDDGGFSEWEAQRDSHLCPHSTPESRAA	360
Db	301	GDPEAQRVSKNSKYNMAESTPESQDPIVAENDDGGFSEWEAQRDSHLCPHSTPESRAA	360
Oy	361	VOELSSSLIAEDEDEPENGKLGLEDFFYSVLVGKASATASGDMNTTACPAALLIGLCL	420
Db	361	VOELSSSLIAEDEDEPENGKLGLEDFFYSVLVGKASATASGDMNTTACPAALLIGLCL	420
Oy	421	TLLLLAIFKKALPALPISITFGVLFYFATDYLVQPFMDQLAFHQFYI	467
Db	421	TLLLLAIFKKALPALPISITFGVLFYFATDYLVQPFMDQLAFHQFYI	467
RESULT 37			
AAW05743			
ID	AAW05743 standard; Protein; 467 AA.		
XX			
AC	AAW05743;		
XX			
DT	23-JUL-1997 (first entry)		
XX			
DE	Presenilin-1-1 H163R/Y mutation.		
XX			
KW	Presenilin-1; human; hPS1-1; hps1-2; PS-2; integral membrane protein; AD		
KW	familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;		
KW	depression; antibody; gene expression modulator; therapy; muten.		
XX			
OS	Homo sapiens.		
XX			
FT	Key		
FT	Modified-site		
FT	163		
FT	/label= H163X		
FT	/note="X = Arg, Tyr"		
XX			
PN	WC9634099-A2.		
XX			
PD	31-OCT-1996.		
XX			
PF	29-APR-1996; 96WO-CA00263.		
XX			
PR	31-JUL-1995; 95US-0509359.		
PR	28-APR-1995; 95US-0431048.		
PR	28-JUN-1995; 95US-0496841.		
XX			
PA	(HSCR-) HSC RES & DEV LP.		
PA	(UTOR) UNIV TORONTO GOVERNING COUNCIL.		
XX			
PI	Fraser PE, Rommens JW, St George-Hyslop PH;		
DR	WPI; 1996-497631/49.		
XX			
PT	New presenilin genes - useful for diagnosis, therapy and drug		
PT	screening of familial Alzheimer's disease, cerebral disorders, etc.		
XX			
PS	Claim 3; Page -: 178pp; English.		
CC	AAW05736-W05760 represent mutated versions of the human presenilin-1-1		
CC	protein (see AAW05733 for wild type sequence). AAW05734 represents a		
CC	different wild type form of presenilin-1 that results from alternate		
CC	splicing of the genomic DNA sequence. The presenilins are a family of		
CC	highly conserved integral membrane proteins with a common structural		
CC	motif, common alternate splicing patterns, and common mutational hot		
CC	spot regions. Mutations in PS genes are implicated in familial		

CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 56.7% Score 265; DB 17; Length 467;

Best Local Similarity 99.6% Pred. No. 5.3e-253;

Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNHLSTNVRSONDRERQEHNDRLSLGHPPLSNGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQMSQEDNHLSTNVRSONDRERQEHNDRLSLGHPPLSNGRPGNSR 60
 QY 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFTRKDGQILYPTPE 120
 DB 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFTRKDGQILYPTPE 120
 QY 121 DRETGQRALHSLNNAIMISIVVMTLLVLYKRCYKVIHAWLIISSLLFFPSFI 180
 DB 121 DRETGQRALHSLNNAIMISIVVMTLLVLYKRCYKVIHAWLIISSLLFFPSFI 180
 QY 181 YLGEVFKTYNNAVDTYTVALLIWNIGVGMISIHMKGPLRLQOAYLIMSALMALVFIKY 240
 DB 181 YLGEVFKTYNNAVDTYTVALLIWNIGVGMISIHMKGPLRLQOAYLIMSALMALVFIKY 240
 QY 241 LPEWTAMLILAVISYDLVAVLCPKGPLRMVETAOERNETLFPALISSTWVWLVNMAE 300
 DB 241 LPEWTAMLILAVISYDLVAVLCPKGPLRMVETAOERNETLFPALISSTWVWLVNMAE 300
 QY 301 GDEPAQRVSKNSKYNAESTERESQPTVAENDGCFSEMEAROSHLPHRSTPESRAA 360
 DB 301 GDEPAQRVSKNSKYNAESTERESQPTVAENDGCFSEMEAROSHLPHRSTPESRAA 360
 QY 361 VOELSSSIAGDEPBERGVKLGIDFIIFYSVLVGKASATASGDMNTTICFVAIILGLCL 420
 DB 361 VOELSSSIAGDEPBERGVKLGIDFIIFYSVLVGKASATASGDMNTTICFVAIILGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVQPMQDLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVQPMQDLAFHQFYI 467

RESULT 38

AAW05744

ID AAW05744 standard; Protein; 467 AA.

XX AAW05744;

DT 23-JUL-1997 (first entry)

XX Presentin-1 L171P mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
 KW depression; antibody; gene expression modulator; therapy; mutuin.

OS Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 171 /label= L171P

XX W09634099-A2.

XX 31-OCT-1996.

XX

PF 29-APR-1996; 96W0-CA00263.

XX 31-JUL-1995; 95US-0509359.

PR 28-APR-1995; 95US-0431048.

PR 28-JUN-1995; 95US-0496841.

XX (HSCR-) HSC RES & DEV LP.

PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX

PI Fraser PE, Rommens JM, St George-Hyslop PH;

XX WPI; 1996-497631/49.

DR

XX New presentin genes - useful for diagnosis, therapy and drug

PT screening of familial Alzheimer's disease, cerebral disorders, etc.

XX Claim 3; Page -: 178pp; English.

XX AAW05736-W05760 represent mutated versions of the human presentin-1-1

XX protein (see AAW05733 for wild type sequence). AAW05734 represents a

XX different wild type form of presentin-1 that results from alternate

XX splicing of the genomic DNA sequence. The presentins are a family of

XX highly conserved integral membrane proteins with a common structural

XX motif, common alternate splicing patterns, and common mutational hot

XX spot regions. Mutations in PS genes are implicated in familial

XX Alzheimer's disease (AD) and possibly other diseases such as cerebral

XX haemorrhage, schizophrenia, depression etc., so detection of mutations in

XX the DNA encoding the wild type sequences can be used for diagnosis of

XX these diseases. The wild type proteins, or vectors that express them or

XX containing antisense sequences, antibodies selective for these mutant

XX forms of the proteins and modulators of PS gene expression are

XX potentially useful for treatment of AD etc. Transgenic animals are

XX useful as models for drug screening. The antibodies can also be used e.g.

XX for affinity purification and in immunoassays.

XX

XX Sequence 467 AA:

QY 1 MTELPAPLSYFQNAQMSQEDNHLSTNVRSONDRERQEHNDRLSLGHPPLSNGRPGNSR 60

DB 1 MTELPAPLSYFQNAQMSQEDNHLSTNVRSONDRERQEHNDRLSLGHPPLSNGRPGNSR 60

QY 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFTRKDGQILYPTPE 120

DB 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFTRKDGQILYPTPE 120

QY 121 DRETGQRALHSLNNAIMISIVVMTLLVLYKRCYKVIHAWLIISSLLFFPSFI 180

DB 121 DRETGQRALHSLNNAIMISIVVMTLLVLYKRCYKVIHAWLIISSLLFFPSFI 180

QY 181 YLGEVFKTYNNAVDTYTVALLIWNIGVGMISIHMKGPLRLQOAYLIMSALMALVFIKY 240

DB 181 YLGEVFKTYNNAVDTYTVALLIWNIGVGMISIHMKGPLRLQOAYLIMSALMALVFIKY 240

QY 241 LPEWTAMLILAVISYDLVAVLCPKGPLRMVETAOERNETLFPALISSTWVWLVNMAE 300

DB 241 LPEWTAMLILAVISYDLVAVLCPKGPLRMVETAOERNETLFPALISSTWVWLVNMAE 300

QY 301 GDEPAQRVSKNSKYNAESTERESQPTVAENDGCFSEMEAROSHLPHRSTPESRAA 360

DB 301 GDEPAQRVSKNSKYNAESTERESQPTVAENDGCFSEMEAROSHLPHRSTPESRAA 360

QY 361 VOELSSSIAGDEPBERGVKLGIDFIIFYSVLVGKASATASGDMNTTICFVAIILGLCL 420

DB 361 VOELSSSIAGDEPBERGVKLGIDFIIFYSVLVGKASATASGDMNTTICFVAIILGLCL 420

QY 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVQPMQDLAFHQFYI 467

DB 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVQPMQDLAFHQFYI 467

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

DB

ID	AAW05745	standard; Protein; 467 AA.
AC	AAW05745;	
DT	23-JUL-1997	(first entry)
DE	Presenilin-1-1 G209V mutation.	
KW	Presenilin-1; human; hps1-1; hps1-2; PS-2; Integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutuin.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Modified-site	209
FT		/label= G209V
PX	MO9634099-A2.	
XX		
PD	31-OCT-1996.	
PF	29-APR-1996;	96WC-CA00263.
PR	31-JUL-1995;	95US-0509359.
PR	28-APR-1995;	95US-0431048.
XX	28-JUN-1995;	95US-0496841.
PA	(HSCR-) HSC RES & DEV LP.	
XX	(UTOR) UNIV TORONTO GOVERNING COUNCIL.	
PI	Fraser PE, Rommens JM, St George-Hyslop PH;	
DR	WPI; 1996-497631/49.	
PT	New presenilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.	
PS	Claim 3; Page -: 178pp; English.	
CC	AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification and in immunoassays.	
SQ	Sequence	467 AA;
Query Match	56.7%; Score 265; DB 17; Length 467;	
Best Local Similarity	99.6%; Pred. No. 5.3e-253;	
Matches	465; Conservative 0; Mismatches 2; Indels 0; Gaps 0.	
D1	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D2	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D3	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D4	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D5	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D6	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D7	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D8	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D9	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D10	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D11	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D12	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D13	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D14	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D15	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D16	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D17	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D18	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D19	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D20	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D21	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D22	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D23	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D24	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D25	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D26	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D27	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D28	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D29	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D30	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D31	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D32	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D33	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D34	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D35	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D36	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D37	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D38	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D39	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D40	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D41	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D42	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D43	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D44	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D45	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D46	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D47	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D48	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D49	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D50	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D51	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D52	1 MTLELPALSTYFONAQMSEDNHLSTNVRSONDKREQHNDRRSLGHPPELSNGRPGNSR 60	
D53	1 MTLELPALSTY	

QY	121	DTETVGGALHSILNMAIMISVIYVMTLLVLYKXKCYVHIAWLLISSLLLPFSFI	180
Db	121	DTETVGGALHSILNMAIMISVIYVMTLLVLYKXKCYVHIAWLLISSLLLPFSFI	180
QY	181	YLGEVETKYNAVAVYITVAALLINMLGVGMISIMHGKPLRLQAVYIMISALMALVFIFY	240
Db	181	YLGEVETKYNAVAVYITVAALLINMLGVGMISIMHGKPLRLQAVYIMISALMALVFIFY	240
QY	241	LPETWAMILLAVISVYDLVAVLCKGKGLRMVETAGERNETLEPALLYSSTWMLVYNAE	300
Db	241	LPETWAMILLAVISVYDLVAVLCKGKGLRMVETAGERNETLEPALLYSSTWMLVYNAE	300
QY	301	GDPEARQVRSKNSKYNMAESTERESODIVAENDGGSFSEMEARDSHLGPHHSTPESRA	360
Db	301	GDPEARQVRSKNSKYNMAESTERESODIVAENDGGSFSEMEARDSHLGPHHSTPESRA	360
QY	361	VOELSSSTILAGEDDEBERGVKLGIDFLFYSVLVGKASATASGDWNTTACFVAILIGLCL	420
Db	361	VOELSSSTILAGEDDEBERGVKLGIDFLFYSVLVGKASATASGDWNTTACFVAILIGLCL	420
QY	421	TLULLAIFKKALPALPISTIFGVLVFRATDYLVQPMQDLAFHQFI	467
Db	421	TLULLAIFKKALPALPISTIFGVLVFRATDYLVQPMQDLAFHQFI	467
RESULT 40			
AAW05746			
ID	AAW05746	standard; Protein: 467 AA.	
AC	AAW05746;		
CC			
DT	23-JUL-1997	(first entry)	
DE	Presenilin-1-1 I211T mutation.		
XX			
KW	Presenilin-1; human; hPS1-1; hps1-2; PS-2; Integral membrane protein; AD;		
KW	familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;		
KW	depression; antibody; gene expression modulator; therapy; muteln.		
XX			
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	Modified-site	211	
FT		/label= I211T	
XX			
EN	W09634099-A2.		
XX			
PD	31-OCT-1996.		
XX			
PE	29-APR-1996;	96MO-CA00263.	
XX			
PR	31-JUL-1995;	95US-0509359.	
PR	28-APR-1995;	95US-0431048.	
XX	28-JUN-1995;	95US-0496841.	
XX			
PA	(HSCR-) HSC RES & DEV LP.		
PA	(UTOR) UNIV TORONTO GOVERNING COUNCIL.		
XX			
PI	Fraser PE, Rommens JM, St George-Hyslop PH;		
XX			
DR	WPI; 1996-497631/49.		
XX			
PT	New presenilin genes - useful for diagnosis, therapy and drug		
PT	screening of familial Alzheimer's disease, cerebral disorders, etc.		
XX			
PS	Claim 3; Page -; 178pp; English.		
XX			
CC	AAW05736-W05760 represent mutated versions of the human presenilin-1-1		
CC	protein (see AAW05733 for wild type sequence). AAW05734 represents a		
CC	different wild type form of presenilin-1 that results from alternate		
CC	splicing of the genomic DNA sequence. The presenilins are a family of		
CC	highly conserved integral membrane proteins with a common structural		

CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 56.7%; Score 265; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTELPAPLSTYFONAKMSEDNHLSNTVRSONDNREOEHNDRSLGHPPLSNGRPOGNSR 60
 DB 1 MTELPAPLSTYFONAKMSEDNHLSNTVRSONDNREOEHNDRSLGHPPLSNGRPOGNSR 60
 OY 61 QVEODEEEDDELTKYGAHVIMLFVPTVLCMVVVVATIKSVSFYTRKDQGLIYPTPE 120
 DB 61 QVEODEEEDDELTKYGAHVIMLFVPTVLCMVVVVATIKSVSFYTRKDQGLIYPTPE 120
 OY 121 DTEVVGORALHSLNMAIMSVIVMTILLVLYKRYCKYVIAHMLIISLLFFFSFI 180
 DB 121 DTEVVGORALHSLNMAIMSVIVMTILLVLYKRYCKYVIAHMLIISLLFFFSFI 180
 OY 181 YLGEVEKTNVAVDYITVALLINLGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVEKTNVAVDYITVALLINLGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 OY 241 LPMTAMLILAVISYVDLVAVLCPKGPLRLMLVETAOERNETLEPALIYSTWVLVMAE 300
 DB 241 LPMTAMLILAVISYVDLVAVLCPKGPLRLMLVETAOERNETLEPALIYSTWVLVMAE 300
 OY 301 GDEPAORRVSKSKYNAESTERESODTVAENDDGGFSEEMADRDHSLGPHRSTPESRAA 360
 DB 301 GDEPAORRVSKSKYNAESTERESODTVAENDDGGFSEEMADRDHSLGPHRSTPESRAA 360
 OY 361 VOELSSSILAGEPDEERGVALGIDFTFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
 DB 361 VOELSSSILAGEPDEERGVALGIDFTFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
 OY 421 TLLLLAIFKKALPALPISITFGLVFYPADYLVQPFMDQLAFHOQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFYPADYLVQPFMDQLAFHOQFYI 467

RESULT 41

AAW05747 ID AAW05747 standard; Protein; 467 AA.

XX AAW05747;

XX 23-JUL-1997 (first entry)

XX Presentin-1-1 I231T mutation.

XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;

KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;

KW depression; antibody; gene expression modulator; therapy; mutin.

XX Homo sapiens.

XX OS

XX FT Modified-site

XX FT /label= I231T

XX PN W09634099-A2.

PD 31-OCT-1996.
 XX
 PF 29-APR-1996; 96WO-CA00263.
 XX
 PR 31-JUL-1995; 95US-0509359.
 PR 28-APR-1995; 95US-0431048.
 PR 28-JUN-1995; 95US-0496841.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIT TORONTO GOVERNING COUNCIL.
 XX
 PI Fraser PE, Rommens JM, St George-Hyslop PH;
 XX WPI; 1996-497631/49.
 PT New presentin genes - useful for diagnosis, therapy and drug
 PT screening of familial Alzheimer's disease, cerebral disorders, etc.
 XX
 PS Claim 3; Page -; 178pp; English.

CC AAW05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

SO Sequence 467 AA:

Query Match 56.7%; Score 265; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTELPAPLSTYFONAKMSEDNHLSNTVRSONDNREOEHNDRSLGHPPLSNGRPOGNSR 60
 DB 1 MTELPAPLSTYFONAKMSEDNHLSNTVRSONDNREOEHNDRSLGHPPLSNGRPOGNSR 60
 OY 61 QVEODEEEDDELTKYGAHVIMLFVPTVLCMVVVVATIKSVSFYTRKDQGLIYPTPE 120
 DB 61 QVEODEEEDDELTKYGAHVIMLFVPTVLCMVVVVATIKSVSFYTRKDQGLIYPTPE 120
 OY 121 DTEVVGORALHSLNMAIMSVIVMTILLVLYKRYCKYVIAHMLIISLLFFFSFI 180
 DB 121 DTEVVGORALHSLNMAIMSVIVMTILLVLYKRYCKYVIAHMLIISLLFFFSFI 180
 OY 181 YLGEVEKTNVAVDYITVALLINLGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVEKTNVAVDYITVALLINLGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 OY 241 LPMTAMLILAVISYVDLVAVLCPKGPLRLMLVETAOERNETLEPALIYSTWVLVMAE 300
 DB 241 LPMTAMLILAVISYVDLVAVLCPKGPLRLMLVETAOERNETLEPALIYSTWVLVMAE 300
 OY 301 GDEPAORRVSKSKYNAESTERESODTVAENDDGGFSEEMADRDHSLGPHRSTPESRAA 360
 DB 301 GDEPAORRVSKSKYNAESTERESODTVAENDDGGFSEEMADRDHSLGPHRSTPESRAA 360
 OY 361 VOELSSSILAGEPDEERGVALGIDFTFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
 DB 361 VOELSSSILAGEPDEERGVALGIDFTFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
 OY 421 TLLLLAIFKKALPALPISITFGLVFYPADYLVQPFMDQLAFHOQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFYPADYLVQPFMDQLAFHOQFYI 467

Db 421 TLLLAIEKKALPALPISITFGLVFYFATDYLVPFMDQLAFHOFYI 467

RESULT 42
AAW05748
ID AAW05748 standard; Protein; 467 AA.
XX AAW05748;
AC AAW05748;
XX 23-JUL-1997 (first entry)
XX
DE Presenilin-1 A246E mutation.
XX
KW Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; mutlein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 246
FT /label= A246E
XX
PN W09634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX WPI; 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 3; Page -: 178pp; English.
XX
XX AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
CC different wild type form of presenilin-1 that results from alternate
CC splicing of the genomic DNA sequence. The presenilins are a family of
CC highly conserved integral membrane proteins with a common structural
CC motif, common alternate splicing patterns, and common mutational hot
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
CC the DNA encoding the wild type sequences can be used for diagnosis of
CC these diseases. The wild type proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for these mutant
CC forms of the proteins and modulators of PS gene expression are
CC potentially useful for treatment of AD etc. Transgenic animals are
CC useful as models for drug screening. The antibodies can also be used e.g.
CC for affinity purification and in immunoassays.
XX
SQ Sequence 467 AA;

Query Match 56.7%; Score 265; DB 17; Length 467;
Best Local Similarity 99.6%; Pred. No. 5.3e-253;
Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFONAMQMSDNHLSNTVRSQNDNREROHNDRLSLGHPPLSGRPOGNSR 60
DB 1 MTELPAPLSTYFONAMQMSDNHLSNTVRSQNDNREROHNDRLSLGHPPLSGRPOGNSR 60
QY 61 QVVEODEEDEBELTLTKYAKAHVIMLFVPTVLCMVVVVATIKSVSFYTRKQQLIYTPETE 120

Db 61 QVVEODEEDEBELTLTKYAKAHVIMLFVPTVLCMVVVVATIKSVSFYTRKQQLIYTPETE 120

QY 121 DPETVGORALHSTLNAINAIMSVTVVMTLLVLYKKRCYKVIHAMLISSLLFFFSFI 180
Db 121 DPETVGORALHSTLNAINAIMSVTVVMTLLVLYKKRCYKVIHAMLISSLLFFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIMWKGPLRLOQAVLIMISALMALVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIMWKGPLRLOQAVLIMISALMALVFIKY 240
QY 241 LPEWTAMLLAVISYVDLVAVLCPKGPLRMLVETAOERNEITLPALIYSTWVWLVMNAE 300
Db 241 LPEWTAMLLAVISYVDLVAVLCPKGPLRMLVETAOERNEITLPALIYSTWVWLVMNAE 300
QY 301 GPPEAORRVSKSKYNAESTERESODTVANENDGGSFEMEQROSHLGPFRSTPESRAA 360
Db 301 GPPEAORRVSKSKYNAESTERESODTVANENDGGSFEMEQROSHLGPFRSTPESRAA 360
QY 361 VOELSSILAGDPPEERGVKLGDFIFYSVLVGRASATASGDMWTTTACFVAIIIGLCL 420
Db 361 VOELSSILAGDPPEERGVKLGDFIFYSVLVGRASATASGDMWTTTACFVAIIIGLCL 420
QY 421 TLLLAIEKKALPALPISITFGLVFYFATDYLVPFMDQLAFHOFYI 467
Db 421 TLLLAIEKKALPALPISITFGLVFYFATDYLVPFMDQLAFHOFYI 467

RESULT 43
AAW05749
ID AAW05749 standard; Protein; 467 AA.
XX AAW05749;
AC AAW05749;
XX 23-JUL-1997 (first entry)
XX
DE Presenilin-1 A260V mutation.
XX
KW Presenilin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; mutlein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 260
FT /label= A260V
XX
PN W09634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX WPI; 1996-497631/49.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 3; Page -: 178pp; English.
XX
XX AAW05736-W05760 represent mutated versions of the human presenilin-1-1
CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
CC different wild type form of presenilin-1 that results from alternate

CC splicing of the genomic DNA sequence. The presenilins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot
 CC spot regions. Mutations in PS genes are implicated in familial
 CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
 CC haemorrhage, schizophrenia, depression etc., so detection of mutations in
 CC the DNA encoding the wild type sequences can be used for diagnosis of
 CC these diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are
 CC useful as models for drug screening. The antibodies can also be used e.g.
 CC for affinity purification and in immunoassays.

XX Sequence 467 AA:

Query Match 56.7%; Score 265; DB 17; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSONDRERQEHNDRLSLGHPPELSNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSONDRERQEHNDRLSLGHPPELSNGRPOGNSR 60
 OY 61 QVEODEDEDEDELTLYGAKHVIMLFVPTLCMNVVAVATIKSVSYTRKDGQLIYTPFTE 120
 DB 61 QVEODEDEDEDELTLYGAKHVIMLFVPTLCMNVVAVATIKSVSYTRKDGQLIYTPFTE 120
 OY 121 DRETVGQRALHSILNAAIMISYIVVMTLLVLYRYCKVTHAMLISSLLLEFFFSFI 180
 DB 121 DRETVGQRALHSILNAAIMISYIVVMTLLVLYRYCKVTHAMLISSLLLEFFFSFI 180
 OY 181 YLGEVFKTYNNAVVDITYVALLIMNIGVGMISIHMKGPLRLQOAVLIMSALMAVFIKY 240
 DB 181 YLGEVFKTYNNAVVDITYVALLIMNIGVGMISIHMKGPLRLQOAVLIMSALMAVFIKY 240
 OY 241 LPEWTAMLILAVISYVDLVAVLCPRGPLRLMLETAEORNETLFPALIIYSTVWMLVNAE 300
 DB 241 LPEWTAMLILAVISYVDLVAVLCPRGPLRLMLETAEORNETLFPALIIYSTVWMLVNAE 300
 OY 301 GDPEAQRVSKSKYNAESTERESODTVAENDGGFSEMEQORSHLGRHSTPESRAA 360
 DB 301 GDPEAQRVSKSKYNAESTERESODTVAENDGGFSEMEQORSHLGRHSTPESRAA 360
 OY 361 VOELSSSILAGDPBERGKVLGLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
 DB 361 VOELSSSILAGDPBERGKVLGLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
 OY 421 TLLLLAIFKKALPALPISTTGLVFFATDYLVPFMDLAFHOFYI 467
 DB 421 TLLLLAIFKKALPALPISTTGLVFFATDYLVPFMDLAFHOFYI 467

RESULT 44
 AAW27176 ID AAW27176 standard; Protein: 467 AA.

AC AAW27176:

DT 09-DEC-1997 (first entry)
 DE Human S182 gene, P51 locus, product related to Alzheimer's disease.
 KW Mutant; antisense; antibody; vaccine; Alzheimer's disease.
 OS Homo sapiens.
 XX MO9708319-A1.
 XX 06-MAR-1997.
 XX 03-SEP-1996; 96WO-US14114.
 PF
 XX

PR 30-AUG-1996; 96US-0706344.
 PR 31-AUG-1995; 95US-0003054.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Tanzi RE, Masco W;
 XX
 DR WPI; 1997-179276/16.
 DR N-PSDB; AAT85332.

PT Chromosome 14 early-onset familial Alzheimer's disease gene PS1
 PT mutants - useful for diagnosing likelihood of developing Alzheimer's
 PT disease, also anti-sense sequences, antibodies and vaccines to delay
 PT onset

PS Claim 12; Page 72-73; 99pp; English.

CC The present sequence represents the human S182 gene, PS1 locus, product.
 CC Mutant PS1 produces a gene product that increases the probability of
 CC Alzheimer's disease. A nucleic acid sequence able to hybridise to
 CC sequences coding for a mutant PS1 polypeptide can be used as probes for
 CC diagnosing an increased likelihood of contracting Alzheimer's disease.
 CC Antibodies against the mutant polypeptide can also be used for this
 CC purpose. Vectors containing or expressing a nucleic acid molecule,
 CC protein or antibody specific for mutant PS1 can be administered to a
 CC patient to reduce the likelihood, or delay the onset, of Alzheimer's
 CC disease, e.g. anti-sense RNA expression can be used to decrease
 CC expression of the PS1 peptide. Transgenic animals expressing the
 CC Alzheimer's disease protein can be used to test candidate therapeutics
 CC and to investigate the normal role of PS1. The PS1 peptide may also be
 CC included in pharmaceutical compositions (vaccines) for Alzheimer's
 CC disease therapy.

XX Sequence 467 AA:

Query Match 56.7%; Score 265; DB 18; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSONDRERQEHNDRLSLGHPPELSNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAOMSEDNHLSNTVRSONDRERQEHNDRLSLGHPPELSNGRPOGNSR 60
 OY 61 QVEODEDEDEDELTLYGAKHVIMLFVPTLCMNVVAVATIKSVSYTRKDGQLIYTPFTE 120
 DB 61 QVEODEDEDEDELTLYGAKHVIMLFVPTLCMNVVAVATIKSVSYTRKDGQLIYTPFTE 120
 OY 121 DRETVGQRALHSILNAAIMISYIVVMTLLVLYRYCKVTHAMLISSLLLEFFFSFI 180
 DB 121 DRETVGQRALHSILNAAIMISYIVVMTLLVLYRYCKVTHAMLISSLLLEFFFSFI 180
 OY 181 YLGEVFKTYNNAVVDITYVALLIMNIGVGMISIHMKGPLRLQOAVLIMSALMAVFIKY 240
 DB 181 YLGEVFKTYNNAVVDITYVALLIMNIGVGMISIHMKGPLRLQOAVLIMSALMAVFIKY 240
 OY 241 LPEWTAMLILAVISYVDLVAVLCPRGPLRLMLETAEORNETLFPALIIYSTVWMLVNAE 300
 DB 241 LPEWTAMLILAVISYVDLVAVLCPRGPLRLMLETAEORNETLFPALIIYSTVWMLVNAE 300
 OY 301 GDPEAQRVSKSKYNAESTERESODTVAENDGGFSEMEQORSHLGRHSTPESRAA 360
 DB 301 GDPEAQRVSKSKYNAESTERESODTVAENDGGFSEMEQORSHLGRHSTPESRAA 360
 OY 361 VOELSSSILAGDPBERGKVLGLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
 DB 361 VOELSSSILAGDPBERGKVLGLGDFIFYSVLVGKASATASGDMWTTTACFAAILIGLCL 420
 OY 421 TLLLLAIFKKALPALPISTTGLVFFATDYLVPFMDLAFHOFYI 467
 DB 421 TLLLLAIFKKALPALPISTTGLVFFATDYLVPFMDLAFHOFYI 467

RESULT 45

```

AAW56770
ID AAW56770 standard; Protein; 467 AA.
XX
AC AAW56770;
XX
DT 13-OCT-1998 (first entry)
XX
DE Homo sapiens PS-1.
XX
KW PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease;
KW serine protease; neurodegeneration; predisposition; diagnosis.
XX
OS Homo sapiens.
XX
PN EP828003-A2.
XX
PD 11-MAR-1998.
XX
PF 26-AUG-1997; 97EP-0306501.
XX
PR 13-DEC-1996; 96US-0032875.
PR 06-SEP-1996; 96US-0025436.
PR 25-OCT-1996; 96US-0027873.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Browne MJ, Clinkenbeard HE, Creasy CL, Karren EH;
PI Liyi GP, Southan CD;
XX
DR WPI: 1998-161101/15.
DR N-PSDB; AAV29525.
XX
PT Nucleic acids encoding human serum protease protein(s) - used for
PT diagnosing pre-disposition to Alzheimer's disease, etc.
XX
PS Example 1, Page 25-26; 65pp; English.
XX
CC The sequence is that of of presenilin PS-1 which was used
CC in the cloning and isolation of the serine protease PSPI.
XX
XX
SO Sequence 467 AA;

Query Match 56.7%; Score 265; DB 19; Length 467;
Best Local Similarity 99.6%; Pred. No. 5.3e-253;
Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYQNMQMSDNLSTNRQNDNRKQEHNDNRSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAPLSTYQNMQMSDNLSTNRQNDNRKQEHNDNRSLGHPPLSNGRPOGNSR 60
QY 61 QVEDODEEDELTKYAKHVMLEFVTCMVVVATIKSVSFYTRKDQLYTPTE 120
DB 61 QVEDODEEDELTKYAKHVMLEFVTCMVVVATIKSVSFYTRKDQLYTPTE 120
QY 121 DTEVVGQALSHSLNAAIMISIVVMTLLVLYKRYCYVIMHMLTSSLLFFESFI 180
DB 121 DTEVVGQALSHSLNAAIMISIVVMTLLVLYKRYCYVIMHMLTSSLLFFESFI 180
QY 121 DTEVVGQALSHSLNAAIMISIVVMTLLVLYKRYCYVIMHMLTSSLLFFESFI 180
DB 121 DTEVVGQALSHSLNAAIMISIVVMTLLVLYKRYCYVIMHMLTSSLLFFESFI 180
QY 181 YLGEVFKYNNAVDYITVALLIMLVGGVGMSTHMKGLRQOAYLMTSLMALVPTKY 240
DB 181 YLGEVFKYNNAVDYITVALLIMLVGGVGMSTHMKGLRQOAYLMTSLMALVPTKY 240
QY 181 YLGEVFKYNNAVDYITVALLIMLVGGVGMSTHMKGLRQOAYLMTSLMALVPTKY 240
DB 181 YLGEVFKYNNAVDYITVALLIMLVGGVGMSTHMKGLRQOAYLMTSLMALVPTKY 240
QY 241 LPEWTAMILLAVISYDVAVLCPKGPLRMVETAQERNEFLPALIYSSFMVLYNNAE 300
DB 241 LPEWTAMILLAVISYDVAVLCPKGPLRMVETAQERNEFLPALIYSSFMVLYNNAE 300
QY 241 LPEWTAMILLAVISYDVAVLCPKGPLRMVETAQERNEFLPALIYSSFMVLYNNAE 300
DB 241 LPEWTAMILLAVISYDVAVLCPKGPLRMVETAQERNEFLPALIYSSFMVLYNNAE 300
QY 301 GDPEAORRVKSKYNNASTERESQDTVAENDDGFSEEMEAQRDSDLGPRSTPESRAA 360
DB 301 GDPEAORRVKSKYNNASTERESQDTVAENDDGFSEEMEAQRDSDLGPRSTPESRAA 360
QY 301 GDPEAORRVKSKYNNASTERESQDTVAENDDGFSEEMEAQRDSDLGPRSTPESRAA 360
DB 301 GDPEAORRVKSKYNNASTERESQDTVAENDDGFSEEMEAQRDSDLGPRSTPESRAA 360
QY 361 VOELSSSLAGEDPEBGRVKGLGDFIFYSVLVKASATASGDMNTTIACFAVAILGLCL 420
DB 361 VOELSSSLAGEDPEBGRVKGLGDFIFYSVLVKASATASGDMNTTIACFAVAILGLCL 420

```

```

DB 361 VOELSSSLAGEDPEBGRVKGLGDFIFYSVLVKASATASGDMNTTIACFAVAILGLCL 420
QY 421 TLLLAIFRKALPALPISTFGLVFPADYVOPFMDLAHPHYI 467
DB 421 TLLLAIFRKALPALPISTFGLVFPADYVOPFMDLAHPHYI 467

RESULT 46
AAE05563
ID AAE05563 standard; Protein; 467 AA.
XX
AC AAE05563;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human presenilin PS1-FAD mutant M146V.
XX
KW Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
KW NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
KW peripheral neuropathy; motor neuron disorder; neurodegenerative disorder;
KW Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
KW Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
KW nerve deafness; Alzheimer's disease; epilepsy; mutant; mutain.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 146 /note="Wild type Met substituted with Val"
FT W0200151671-A2.
XX
PD 19-JUL-2001.
XX
PE 08-JAN-2001; 2001WO-US00526.
XX
PR 10-JAN-2000; 2000US-0175200.
PR 04-JAN-2001; 2001US-0754949.
XX
PA (SCIO-) SCIOS INC.
XX
PI McCarthy J, Cordell B;
PI WPI: 2001-451872/48.
XX
PT Identifying inhibitors of neuronal degeneration useful for treating
PT e.g. Alzheimer's disease, by determining the ability of a compound to
PT induce nuclear factor kappa B activation, with the involvement of
PT presenilin or Par-4
XX
PS Example 2; Page -: 66pp; English.
XX
CC The invention relates to human Par-4 protein, presenilin protein (PS1
CC and PS2) and their corresponding DNA molecules. The invention also
CC relates to a method for identifying inhibitors of neuronal degeneration,
CC comprising cotransfecting eukaryotic host cells expressing presenilin
CC (PS), with a par-4 DNA, and an NF-kappa B dependent reporter construct,
CC exposing the cotransfected cells to a candidate molecule and monitoring
CC the ability of the candidate molecule to induce NF-kappa B activation.
CC Presenilin proteins participate in nuclear factor kappa B (NF-kappa B)
CC signalling and activation. The inhibitors of neuronal degeneration
CC are useful for treating neurodegenerative disorders such as Alzheimer's
CC disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
CC chorea, Down's syndrome, nerve deafness, Meniere's disease and also for
CC treating peripheral neuropathies, motor neuron disorders such as
CC amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions
CC involving spinal muscular atrophy and paralysis. The present sequence
CC is human presenilin PS1-FAD (familial Alzheimer's disease) mutant.
CC Note: This sequence is not shown in the specification but is derived from
CC human presenilin (PS1) protein (SEQ ID NO: 4) shown in page 60-61 of the
CC specification (AAE05466).
XX

```

SQ Sequence 467 AA:

Query Match 56.7%; Score 265; DB 22; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFONAOSEDNHLSNTYVRSONDREROEHNDRLSLGHPPLSLNGRQGNR 60
 DB 1 MTELPAPLSTYFONAOSEDNHLSNTYVRSONDREROEHNDRLSLGHPPLSLNGRQGNR 60
 QY 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMNVVVAITKVSFTTRKDGOLITPPE 120
 DB 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMNVVVAITKVSFTTRKDGOLITPPE 120
 QY 121 DRETGORALHSILNAAIMISYIVVMTLLVLYKRCYKVIHAWLIISSLLLEFFSFI 180
 DB 121 DRETGORALHSILNAAIMISYIVVMTLLVLYKRCYKVIHAWLIISSLLLEFFSFI 180
 QY 181 YLGEVFKTYNNAVDTYVALLLIMNGVGMISIHMKGPLRLQOAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNNAVDTYVALLLIMNGVGMISIHMKGPLRLQOAVLIMISALMALVFIKY 240
 QY 241 LPBWTAMLILAVISYDLVAVLCPKGPLMLVETAOERNETLFPALITYSTWMLVNMME 300
 DB 241 LPBWTAMLILAVISYDLVAVLCPKGPLMLVETAOERNETLFPALITYSTWMLVNMME 300
 QY 301 GDEAQRVSKSKYNAESTERESODTVVAENDDGFSEMEAROSHLCPRSTPESRA 360
 DB 301 GDEAQRVSKSKYNAESTERESODTVVAENDDGFSEMEAROSHLCPRSTPESRA 360
 QY 361 VOELSSSILAGEDPERGVKLGDFIFYSVYVGRASATASGDMWTTTACFAAILIGLCL 420
 DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVYVGRASATASGDMWTTTACFAAILIGLCL 420
 QY 421 TLLLAIFKKALPALPISTITGTVFATDYLVOFPMQDLARHOFYI 467
 DB 421 TLLLAIFKKALPALPISTITGTVFATDYLVOFPMQDLARHOFYI 467

RESULT 47

AAE05564 ID AAE05564 standard; Protein: 467 AA.

XX AAE05564;

XX 24-SEP-2001 (first entry)

XX Human presenilin PS1-FAD mutant E280G.

XX Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;

XX NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralytic;

XX peripheral neuropathy; motorneuron disorder; neurodegenerative disorder;

XX Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;

XX Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;

XX nerve deafness; Alzheimer's disease; epilepsy; mutant; mutain.

XX Homo sapiens.

XX Synthetic.

XX OS

XX Key

XX Location/Qualifiers

XX MISC-difference 280

XX /note= "Wild type Glu substituted with Gly"

XX WO200151671-A2.

XX 19-JUL-2001.

XX 08-JAN-2001; 2001MO-US00526.

XX 10-JAN-2000; 2000US-0175200.

XX 04-JAN-2001; 2001US-0754949.

XX (SCIO-) SCIOS INC.

XX PA

XX Mccarthy J, Cordell B;
 XX WPI: 2001-451872/48.
 XX

PT Identifying inhibitors of neuronal degeneration useful for treating
 PT e.g. Alzheimer's disease, by determining the ability of a compound to
 PT induce nuclear factor kappa B activation, with the involvement of
 PT presenilin or Par-4 -
 XX
 PS Example 2; Page -: 66pp; English.

The invention relates to human Par-4 protein, presenilin protein (PS1 and PS2) and their corresponding DNA molecules. The invention also relates to a method for identifying inhibitors of neuronal degeneration, comprising cotransfecting eukaryotic host cells expressing presenilin (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct, exposing the cotransfected cells to a candidate molecule and monitoring the ability of the candidate molecule to induce NF-kappa B activation. Presenilin proteins participate in nuclear factor kappa B (NF-kappa B) signalling and activation. The inhibitors of neuronal degeneration are useful for treating neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and also for treating peripheral neuropathies, motorneuron disorders such as amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions involving spinal muscular atrophy and paralysis. The present sequence is human presenilin PS1-FAD (familial Alzheimer's disease) mutant. Note: This sequence is not shown in the specification but is derived from human presenilin (PS1) protein [SEQ ID NO: 4] shown in page 60-61 of the specification (AAE05466).

SQ Sequence 467 AA:

Query Match 56.7%; Score 265; DB 22; Length 467;
 Best Local Similarity 99.6%; Pred. No. 5.3e-253;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFONAOSEDNHLSNTYVRSONDREROEHNDRLSLGHPPLSLNGRQGNR 60
 DB 1 MTELPAPLSTYFONAOSEDNHLSNTYVRSONDREROEHNDRLSLGHPPLSLNGRQGNR 60
 QY 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMNVVVAITKVSFTTRKDGOLITPPE 120
 DB 61 QVVEDEDEDELTLKYGAKHYIMLFVPTLCMNVVVAITKVSFTTRKDGOLITPPE 120
 QY 121 DRETGORALHSILNAAIMISYIVVMTLLVLYKRCYKVIHAWLIISSLLLEFFSFI 180
 DB 121 DRETGORALHSILNAAIMISYIVVMTLLVLYKRCYKVIHAWLIISSLLLEFFSFI 180
 QY 181 YLGEVFKTYNNAVDTYVALLLIMNGVGMISIHMKGPLRLQOAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNNAVDTYVALLLIMNGVGMISIHMKGPLRLQOAVLIMISALMALVFIKY 240
 QY 241 LPBWTAMLILAVISYDLVAVLCPKGPLMLVETAOERNETLFPALITYSTWMLVNMME 300
 DB 241 LPBWTAMLILAVISYDLVAVLCPKGPLMLVETAOERNETLFPALITYSTWMLVNMME 300
 QY 301 GDEAQRVSKSKYNAESTERESODTVVAENDDGFSEMEAROSHLCPRSTPESRA 360
 DB 301 GDEAQRVSKSKYNAESTERESODTVVAENDDGFSEMEAROSHLCPRSTPESRA 360
 QY 361 VOELSSSILAGEDPERGVKLGDFIFYSVYVGRASATASGDMWTTTACFAAILIGLCL 420
 DB 361 VOELSSSILAGEDPERGVKLGDFIFYSVYVGRASATASGDMWTTTACFAAILIGLCL 420
 QY 421 TLLLAIFKKALPALPISTITGTVFATDYLVOFPMQDLARHOFYI 467
 DB 421 TLLLAIFKKALPALPISTITGTVFATDYLVOFPMQDLARHOFYI 467

RESULT 48

AAM42375

ID AAM42375 standard: Protein; 463 AA.
 XX AAM42375;
 AC
 XX
 DF 08-JUN-1998 (first entry)
 XX
 DE Human presenilin 1 gene product.
 XX
 XX Presenilin 1 gene; familial adult onset Alzheimer's disease; FAD;
 KW diagnosis; marker; VRXQ motif; human.
 XX
 OS Homo sapiens.
 XX
 PN EP814157-A2.
 XX
 PD 29-DEC-1997.
 XX
 PF 17-JUN-1997; 97EP-0304249.
 XX
 PR 18-JUN-1996; 96US-0019991.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (UYSEF-) UNIV SOUTH FLORIDA.
 PA (UNIM) UNIV WASHINGTON.
 PI Barton AJL, Goate AM, Hardy J;
 XX
 DR WPI: 1998-044335/05.
 DR N-PSDB; AAV03246.
 XX
 PT DNA encoding presenelin I - useful for diagnosis of Alzheimer's
 PT disease, drug screening, etc.
 XX
 PS
 XX
 XX Claim 4; Page 13-14; 20pp; English.

This protein comprises the 463-amino acid human presenilin I (PS-1) gene product. A novel variant of PS-1 encoded by a clone isolated from a human cerebellar cDNA library contains a 4-amino acid insertion (VRXQ) between residues 26 and 27. This variant arises from alternative use of a 5' exon donor site in the exon 3/intron 3 boundary of the PS-1 gene (see also AAV03246). The 4-amino acid motif can be used as a diagnostic marker for variants of presenilin genes associated with Alzheimer's disease and familial adult onset Alzheimer's disease (FAD). Methods are provided for detecting the presence or absence of a 4-amino acid motif (VRXQ, where x is a hydrophilic amino acid) in expressed proteins that arise from aberrant alternative splicing of pre-mRNA in genes associated with normal neurological function, which are useful for detecting neurodegenerative disease. The presence of these variants suggest that mutational events have occurred. Methods to measure the levels of gene expression of such genes to detect neurodegenerative diseases are provided. Nucleotide sequences and intron-exon junctional sequences of examples of this splicing variant and probes (see AAV03247-49) for detecting this variant which are useful as diagnostic reagents are also provided.

Sequence 463 AA;
 SQ

Query Match 54.2%; Score 253; DB 19; Length 463;
 Best Local Similarity 99.7%; Pred. No. 3.8e-241;
 Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

30 NDNREQEHNDNRSLGHEPLSNGRPOGNSQOVVEQDEDEDELTKYGAHVIMLFVPV 89
 |||||||
 26 NDNREGRQHNDRSLGHEPLSNGRPOGNSQOVVEQDEDEDELTKYGAHVIMLFVPV 85
 |||||||
 90 TLCAVVVAATKSVSEFYRKDGQILYPTFEDTETVGQALHSLINAAIMISVIYVMTIL 149
 |||||||
 86 TLCAVVVAATKSVSEFYRKDGQILYPTFEDTETVGQALHSLINAAIMISVIYVMTIL 145
 |||||||
 150 LVLIYKYRCYVHIAWMLISLLLFPSFTYLGVEFTYVAVDYITVALLINNLGYVG 209
 |||||||
 146 LVLIYKYRCYVHIAWMLISLLLFPSFTYLGVEFTYVAVDYITVALLINNLGYVG 205
 |||||||

QY 210 MISIMKGPRLRQQAAYLIMISALMALVFIRKYLEPTAWMLILAVISYDVLVAVLCRKGPLR 269
 |||||||
 Db 206 MISIMKGPRLRQQAAYLIMISALMALVFIRKYLEPTAWMLILAVISYDVLVAVLCRKGPLR 265
 |||||||
 QY 270 MLVETAQERNETLFPALLYSTTMWLVNMAEGDPEAQRVRSKSKYNAESTERESQDTVA 329
 |||||||
 Db 266 MLVETAQERNETLFPALLYSTTMWLVNMAEGDPEAQRVRSKSKYNAESTERESQDTVA 325
 |||||||
 QY 330 ENDDGGSFEEMEAQRDSHLGPHRSTPESRAAVQELSSILAGEDEERGKVLGL 383
 |||||||
 Db 326 ENDDGGSFEEMEAQRDSHLGPHRSTPESRAAVQELSSILAGEDEERGKVLGL 379
 |||||||

RESULT 49
 AAY51393
 ID AAY51393 standard: Peptide; 465 AA.
 XX
 AC AAY51393;
 XX
 DT 04-MAY-2000 (first entry)
 XX
 DE Human S182 protein.
 XX
 KW SPE-4; immunogen; diagnosis; nematode; Alzheimer's disease; brain;
 KW muscle; peripheral blood cell; neuroprotectant; nootropic; S182; human.
 XX
 OS Homo sapiens.
 XX
 PN US6019974-A.
 XX
 PD 01-FEB-2000.
 XX
 PF 24-JAN-1997; 97US-0788231.
 XX
 PR 26-JAN-1996; 96US-0010672.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI L'Hernault SW;
 XX
 DR WPI: 2000-146863/13.
 DR
 XX
 PT Immunogenic composition comprising an antigenic component, useful for
 PT diagnosing Alzheimer's disease -
 XX
 PS Example 4; Column 33-36; 23pp; English.

This invention describes a novel immunogenic composition comprising at least 1 antigenic component selected from an antigenic peptide (I) (linked to a carrier) or a multiantigenic peptide (II). The composition is useful for diagnosing or monitoring SPE-4-related protein profiles of nematodes and/or Alzheimer's disease patients, either in postmortem tissue, or from other tissue samples, where the tissue is from the brain, muscle or peripheral blood cells. The immunogenic composition can be used to diagnose Alzheimer's noninvasively and has neuroprotective and nootropic activity. This sequence represents the human S182 protein which is used in the method of the invention.

Sequence 465 AA;
 SQ

Query Match 52.2%; Score 244; DB 21; Length 465;
 Best Local Similarity 100.0%; Pred. No. 3e-232;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

224 AYLMISALMALVFIRKYLEPTAWMLILAVISYDVLVAVLCRKGPLRMLVETAQERNETLF 283
 |||||||
 Db 222 AYLMISALMALVFIRKYLEPTAWMLILAVISYDVLVAVLCRKGPLRMLVETAQERNETLF 281
 |||||||
 QY 284 PALIYSSSTMWLVNMAEGDPEAQRVRSKSKYNAESTERESQDTVAENDDGGSFEEMEAQ 343
 |||||||
 Db 282 PALIYSSSTMWLVNMAEGDPEAQRVRSKSKYNAESTERESQDTVAENDDGGSFEEMEAQ 341
 |||||||


```

OY 344 RDSHGGPHRSTPESRAAVQELSSSILAGEDPEERGCVKLGDFIFYSVLVGKASATASGD 403
    |||
DB 342 RDSHGGPHRSTPESRAAVQELSSSILAGEDPEERGCVKLGDFIFYSVLVGKASATASGD 401
OY 404 WNTTACFAVAILIGLCTLLLLAIFKKALPALPISITFGLVFFATDYLVQPFMDQLAFH 463
    |||
DB 402 WNTTACFAVAILIGLCTLLLLAIFKKALPALPISITFGLVFFATDYLVQPFMDQLAFH 461
OY 464 OFYI 467
    |||
DB 462 OFYI 465

RESULT 50
AAM12376
ID AAM12376 standard; Protein: 463 AA.
AC AAM12376;
XX 17-JUN-1997 (first entry)
DT 17-JUN-1997 (first entry)
XX Human S182 gene product.
DE Human S182 gene product.
XX S182 gene; familial Alzheimer's disease; diagnosis;
KW transgenic animal.
XX Homo sapiens.
OS Homo sapiens.
XX MO9703999-A1.
PN 06-FEB-1997.
XX 26-JUN-1996; 96WO-US11065.
PE 02-AUG-1995; 95US-0001800.
PR 18-JUL-1995; 95US-0001500.
XX (UNSF-) UNIV SOUTH FLORIDA.
PA (UNIV) UNIV WASHINGTON SCHOOL MED.
XX Goale AM, Hardy JA;
PI WPI: 1997-132571/12.
DR N-PSDB: AAT63207.
XX New mutants of the S182 gene associated with familial Alzheimer's
PT disease - and related protein and transgenic animals, useful as
PT models for screening and assessing potential drugs
XX
PS Disclosure; Fig 1A-D; 26pp; English.
XX
CC A polypeptide (AAM12376) is the product of an S182 gene cDNA clone
CC (AAT63207) isolated from a human brain library. Several mutations in
CC the S182 gene have been found in families with members affected by
CC early onset Alzheimer's disease (AD): in 2 families Met to Val at
CC position 135; in 3 families Met to Val at 142; in 1 family Pro to
CC Ser at 263; in 4 families Glu to Ala at 276; and in 1 family Glu to
CC Gly at 280. Detection of the mutations is used to diagnose AD, or
CC a predisposition to it. Transgenic animals can be produced that
CC are useful as models for screening and assessing potential drugs.
XX
SQ Sequence 463 AA:

Query Match 50.5%; Score 236; DB 18; Length 463;
Best Local Similarity 99.5%; Pred. No. 2.4e-224;
Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 30 NDNRERHNDRRSLGHPPLSNGRPGNSROVVEODEDEDELTLYGAKHVMLEFVPV 89
    |||
DB 26 NDNRERHNDRRSLGHPPLSNGRPGNSROVVEODEDEDELTLYGAKHVMLEFVPV 85
OY 90 TLCAVVVAVTIKSVSFYTRKDGQLIYPTEDTETVGRALHSILNAAIMISIVVMTIL 149
    |||

```

```

DB 86 TLCAVVVAVTIKSVSFYTRKDGQLIYPTEDTETVGRALHSILNAAIMISIVVMTIL 145
OY 150 LVVLYKYRCYKVIHAWLLISSLILFFPSFTYLGVEFPTNYNAVDTYVALLIHWLGVYG 209
    |||
DB 146 LVVLYKYRCYKVIHAWLLISSLILFFPSFTYLGVEFPTNYNAVDTYVALLIHWLGVYG 205
OY 210 MISIMKGPRLQOAYLIMISALMALVFTKYLPEWTAMLLAVISVYDLVAVLCRGPRLR 269
    |||
DB 206 MISIMKGPRLQOAYLIMISALMALVFTKYLPEWTAMLLAVISVYDLVAVLCRGPRLR 265
OY 270 MLVETAQERNETLFPALIVSSTWVLVNMAGEGPEAQRVSKNSKYNAESTERESQDTVA 329
    |||
DB 266 MLVETAQERNETLFPALIVSSTWVLVNMAGEGPEAQRVSKNSKYNAESTERESQDTVA 325
OY 330 EMDDGGFSEWEAQRDSSHGPHRSTPESRAAVQELSSSILAGEDPEERGCVKLGDFIFY 389
    |||
DB 326 EMDDGGFSEWEAQRDSSHGPHRSTPESRAAVQELSSSILAGEDPEERGCVKLGDFIFY 385
OY 390 SVLVGKASATASGDMNTTIACFVAILIGLCTLLLLAIFKKALPALPISITFGLVFFAT 449
    |||
DB 386 SVLVGKASATASGDMNTTIACFVAILIGLCTLLLLAIFKKALPALPISITFGLVFFAT 445
OY 450 DYLVQPFMDQLAFHQFYI 467
    |||
DB 446 DYLVQPFMDQLAFHQFYI 463

```

Search completed: February 6, 2003, 14:18:59
 Job time : 86.0394 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:17:07 ; Search time 51.3506 Seconds
(without alignments)
1873.862 Million cell updates/sec

Title: US-09-689-159a-2

Sequence: 1 MRELPAPLSYFQNAQMSDN.....ATDYLVQPEMDLAFHQFYI 467

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_podent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriapi:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	204	43.7	289	4	Q9UIF0	Q9UIF0 homo sapien
2	161	34.5	184	4	Q95465	Q95465 homo sapien
3	127	27.2	378	4	Q96P33	Q96P33 homo sapien
4	87	18.6	261	11	Q91WK6	Q91WK6 mus musculu
5	63	13.5	468	13	Q90X08	Q90X08 gallus gall
6	59	12.6	384	13	Q73869	Q73869 cyprinus ca
7	42	9.0	456	13	Q9W6T7	Q9W6T7 brachydanto
8	39	8.4	441	13	Q91991	Q91991 brachydanto
9	39	8.4	441	13	Q902E4	Q902E4 brachydanto
10	35	7.5	504	5	Q8WS58	Q8WS58 branchiosto
11	35	7.5	525	5	Q8WS59	Q8WS59 branchiosto
12	28	6.0	332	11	Q9D616	Q9D616 mus musculu
13	28	6.0	330	4	Q96P32	Q96P32 homo sapien
14	28	6.0	448	11	Q91VS3	Q91VS3 mus musculu
15	23	4.9	451	13	Q90X07	Q90X07 gallus gall
16	20	4.3	582	5	Q9GU38	Q9GU38 helix lucor

17	15	3.2	397	10	Q9S1K7	Q9S1K7 arabidopsis
18	15	3.2	478	10	Q9SDG2	Q9SDG2 oryza sativ
19	9	1.9	334	17	Q97UC3	Q97UC3 sulfolobus
20	8	1.7	64	13	Q9PV06	Q9PV06 pleocoglossu
21	8	1.7	67	13	Q9PV05	Q9PV05 harpador sp
22	8	1.7	83	2	Q93EP9	Q93EP9 helicobacte
23	8	1.7	104	12	Q80TD1	Q80TD1 white spot
24	8	1.7	105	12	Q8VAV0	Q8VAV0 white spot
25	8	1.7	139	11	Q63071	Q63071 rattus norv
26	8	1.7	288	2	Q8VQL7	Q8VQL7 bruceia ab
27	8	1.7	314	10	Q9SLP4	Q9SLP4 tulipa bake
28	8	1.7	317	16	Q8ZFL5	Q8ZFL5 yersinia pe
29	8	1.7	347	16	Q9RR94	Q9RR94 deinococcus
30	8	1.7	354	3	Q60121	Q60121 schizosacch
31	8	1.7	369	6	Q77794	Q77794 canis famli
32	8	1.7	379	5	Q966H2	Q966H2 caenorhabdi
33	8	1.7	392	10	Q92PX3	Q92PX3 arabidopsis
34	8	1.7	519	5	Q9V4U2	Q9V4U2 drosophila
35	8	1.7	522	2	Q52557	Q52557 amycolators
36	8	1.7	538	11	Q03982	Q03982 cricetus
37	8	1.7	563	11	Q8R569	Q8R569 mus musculu
38	8	1.7	581	16	Q97178	Q97178 clostridium
39	8	1.7	628	4	Q95052	Q95052 homo sapien
40	8	1.7	668	6	Q8WNU6	Q8WNU6 canis famli
41	8	1.7	749	11	Q8RUK1	Q8RUK1 mus musculu
42	8	1.7	1022	11	Q63828	Q63828 mus sp. big
43	8	1.7	1163	6	Q9TSU2	Q9TSU2 felis silve
44	8	1.7	1169	11	Q60502	Q60502 cricetus
45	8	1.7	1231	5	Q97140	Q97140 dictyosteli
46	8	1.7	1272	11	Q9UK64	Q9UK64 rattus norv
47	8	1.7	1272	11	Q92AL6	Q92AL6 rattus norv
48	8	1.7	1280	6	Q46605	Q46605 canis famli
49	8	1.7	1285	6	Q02793	Q02793 ovis aries
50	8	1.7	1726	5	Q02569	Q02569 plasmidium
51	8	1.7	2958	5	Q9VDY5	Q9VDY5 drosophila
52	8	1.5	19	15	Q905H6	Q905H6 human immun
53	8	1.5	29	8	Q9G355	Q9G355 trapezoid sa
54	8	1.5	45	16	Q8U5R7	Q8U5R7 agrobacteri
55	8	1.5	62	2	Q50445	Q50445 mycobacteri
56	8	1.5	62	13	Q90WP7	Q90WP7 rana pipien
57	8	1.5	70	13	Q8QFQ3	Q8QFQ3 rana pipien
58	7	1.5	71	13	Q13103	Q13103 cyprinus ca
59	7	1.5	78	16	Q9ZNM5	Q9ZNM5 helicobacte
60	7	1.5	86	13	Q91RX7	Q91RX7 petromyzon
61	7	1.5	86	16	Q84166	Q84166 chlamydia t
62	7	1.5	87	13	Q918X9	Q918X9 petromyzon
63	7	1.5	90	17	Q8UOW3	Q8UOW3 pyrococcus
64	7	1.5	91	10	Q9AS79	Q9AS79 oryza sativ
65	7	1.5	94	2	Q8VLS5	Q8VLS5 enterococu
66	7	1.5	95	4	Q8WYR9	Q8WYR9 homo sapien
67	7	1.5	95	13	Q918X8	Q918X8 petromyzon
68	7	1.5	97	11	Q9ERU0	Q9ERU0 mus musculu
69	7	1.5	99	11	Q9ERU1	Q9ERU1 rattus norv
70	7	1.5	103	16	Q8XEP2	Q8XEP2 salmonella
71	7	1.5	104	16	Q9HYV9	Q9HYV9 pseudomonas
72	7	1.5	105	2	Q9EYX3	Q9EYX3 klebsiella
73	7	1.5	107	17	Q9YAQ5	Q9YAQ5 aeropyrum p
74	7	1.5	108	17	Q9YC54	Q9YC54 aeropyrum p
75	7	1.5	109	17	Q9YG06	Q9YG06 aeropyrum p
76	7	1.5	115	12	Q65536	Q65536 baboon herp
77	7	1.5	117	3	Q96014	Q96014 neurospora
78	7	1.5	125	11	Q9D9E2	Q9D9E2 mus musculu
79	7	1.5	125	16	Q8UQJ9	Q8UQJ9 agrobacteri
80	7	1.5	131	16	Q9A6X3	Q9A6X3 caulobacter
81	7	1.5	132	16	Q8XHT7	Q8XHT7 clostridium
82	7	1.5	139	2	Q9X541	Q9X541 corynebacte
83	7	1.5	139	5	Q9V556	Q9V556 drosophila
84	7	1.5	149	11	Q35327	Q35327 mus musculu
85	7	1.5	149	16	Q8R7B1	Q8R7B1 thermotanaer
86	7	1.5	155	8	Q9MN98	Q9MN98 galacthealin
87	7	1.5	155	11	Q9DB92	Q9DB92 mus musculu
88	7	1.5	157	10	Q8RV90	Q8RV90 oryza sativ
89	7	1.5	157	12	Q8VAG6	Q8VAG6 white spot

90	7	1.5	168	12	036423	036423 alcelaphine	163	7	1.5	299	10	092VK1	092VK1 arabisopsis
91	7	1.5	169	17	09YC98	09YC98 aeropyrum p	164	7	1.5	310	10	09LRX5	09LRX5 arabisopsis
92	7	1.5	175	12	08Q587	08Q587 chimpanzee	165	7	1.5	311	12	08V719	08V719 simian herp
93	7	1.5	176	16	09KJ34	09KJ34 bacillus ha	166	7	1.5	312	8	09MFM8	09MFM8 cochlomyia
94	7	1.5	178	5	09M2H1	09M2H1 drosophila	167	7	1.5	314	8	09MM08	09MM08 anthoceros
95	7	1.5	178	17	097C37	097C37 thermoplas	168	7	1.5	315	17	08TLX3	08TLX3 methanosarc
96	7	1.5	179	5	09NAC5	09NAC5 caenorhabdi	169	7	1.5	316	11	08R2A2	08R2A2 mus musculu
97	7	1.5	180	8	08SI08	08SI08 dekenia im	170	7	1.5	317	16	08U848	08U848 agrobacteri
98	7	1.5	183	16	08XTM6	08XTM6 raistonia s	171	7	1.5	318	8	09G805	09G805 ixodes hexa
99	7	1.5	184	10	022258	022258 arabisopsis	172	7	1.5	319	8	09G8P6	09G8P6 diiryns wint
100	7	1.5	192	5	09NTN6	09NTN6 leishmania	173	7	1.5	321	8	09GFR8	09GFR8 dioscorea b
101	7	1.5	194	11	09IXB5	09IXB5 mus musculu	174	7	1.5	323	8	09B635	09B635 anguilla ja
102	7	1.5	194	17	09YFK1	09YFK1 aeropyrum p	175	7	1.5	323	8	09GFG8	09GFG8 asarum cana
103	7	1.5	195	2	09FOP4	09FOP4 listeria mo	176	7	1.5	324	16	034616	034616 bacillus su
104	7	1.5	201	4	09UM05	09UM05 homo sapien	177	7	1.5	324	8	09GFE6	09GFE6 liliidondro
105	7	1.5	210	13	091596	091596 xenopus lae	178	7	1.5	324	8	09GFE6	09GFE6 trochodendr
106	7	1.5	210	16	09KAP8	09KAP8 bacillus ha	179	7	1.5	324	8	09GFE2	09GFE2 felis silve
107	7	1.5	211	16	099R14	099R14 staphylococ	180	7	1.5	325	6	09BR43	09BR43 leopardus p
108	7	1.5	212	11	09CRJ0	09CRJ0 mus musculu	181	7	1.5	325	6	09BR41	09BR41 panthera on
109	7	1.5	213	16	08XN92	08XN92 clostridium	182	7	1.5	325	6	09BR41	09BR41 acorus cala
110	7	1.5	216	8	09TAG4	09TAG4 uma exsul.	183	7	1.5	325	8	09GFR0	09GFR0 ceratophyll
111	7	1.5	216	9	08W628	08W628 bacterioph	184	7	1.5	325	8	09GFR2	09GFR2 cercidiphyll
112	7	1.5	216	13	090228	090228 ambystoma m	185	7	1.5	325	8	09GFR0	09GFR0 cercidiphyll
113	7	1.5	217	8	09TAG5	09TAG5 uma inornat	186	7	1.5	325	8	09GFE8	09GFE8 lactoris fe
114	7	1.5	217	8	09T3Y7	09T3Y7 uma notata.	187	7	1.5	325	8	09GFE4	09GFE4 saurus ce
115	7	1.5	217	13	090WM4	090WM4 xenopus lae	188	7	1.5	325	13	09PSX3	09PSX3 xenopus lae
116	7	1.5	218	16	092BS8	092BS8 listeria in	189	7	1.5	326	6	09BR48	09BR48 sus scrofa
117	7	1.5	218	10	09KHT8	09KHT8 listeria mo	190	7	1.5	326	6	09BR48	09BR48 cabomba car
118	7	1.5	219	10	09FOZ8	09FOZ8 nicotiana t	191	7	1.5	326	8	09GFR6	09GFR6 calycanthus
119	7	1.5	221	10	08S032	08S032 oryza sativ	192	7	1.5	326	8	09GFR4	09GFR4 ginkgo billo
120	7	1.5	226	12	072839	072839 porcine epi	193	7	1.5	326	8	09GFR4	09GFR4 zania furfu
121	7	1.5	226	12	091A09	091A09 porcine epi	194	7	1.5	326	8	09MSQ7	09MSQ7 zania furfu
122	7	1.5	226	12	037351	037351 porcine epi	195	7	1.5	326	8	09MSP5	09MSP5 nymphalea t
123	7	1.5	226	12	007504	007504 porcine epi	196	7	1.5	326	8	09GCE32	09GCE32 amborella t
124	7	1.5	228	11	064057	064057 rattus sp.	197	7	1.5	326	11	09QNR4	09QNR4 hystrix dra
125	7	1.5	232	5	09SRA2	09SRA2 drosophila	198	7	1.5	326	11	09QNR4	09QNR4 ethelizon d
126	7	1.5	235	11	08VH42	08VH42 sigmodon hi	199	7	1.5	326	11	09QNR1	09QNR1 heteroceph
127	7	1.5	236	5	09GCV9	09GCV9 caenorhabdi	200	7	1.5	327	16	09A5T8	09A5T8 caluopacter
128	7	1.5	237	8	08WED7	08WED7 pamalescin	201	7	1.5	330	10	09LM19	09LM19 arabisopsis
129	7	1.5	241	2	09VPK4	09VPK4 drosophila	202	7	1.5	333	8	09BR08	09BR08 gullardia
130	7	1.5	241	2	09JN88	09JN88 streptomyc	203	7	1.5	337	13	042344	042344 cynops pyr
131	7	1.5	241	11	062076	062076 mus musculu	204	7	1.5	338	16	08Y0B2	08Y0B2 raiistonia s
132	7	1.5	243	4	09MTB3	09MTB3 homo sapien	205	7	1.5	340	5	0907C9	0907C9 dictyostell
133	7	1.5	252	6	09BFA0	09BFA0 canis famli	206	7	1.5	341	5	09GSC01	09GSC01 caenorhabdi
134	7	1.5	252	10	09SHZ4	09SHZ4 arabisopsis	207	7	1.5	342	10	P93153	P93153 gossypium h
135	7	1.5	252	10	09C811	09C811 arabisopsis	208	7	1.5	343	8	09B1J5	09B1J5 uma inornat
136	7	1.5	257	5	08SMV1	08SMV1 drosophila	209	7	1.5	343	8	09B1J4	09B1J4 uma notata.
137	7	1.5	257	11	09D1H9	09D1H9 mus musculu	210	7	1.5	343	8	09B1J3	09B1J3 uma notata
138	7	1.5	257	17	09HJTO	09HJTO thermoplasm	211	7	1.5	343	8	09B0S7	09B0S7 uma notata
139	7	1.5	259	16	08RCM5	08RCM5 thermoaer	212	7	1.5	343	8	09B4I1	09B4I1 uma inornat
140	7	1.5	259	17	09V206	09V206 pyrococcus	213	7	1.5	343	8	09B4I0	09B4I0 uma notata
141	7	1.5	262	16	09KDD1	09KDD1 bacillus ha	214	7	1.5	343	8	09B4H9	09B4H9 uma notata.
142	7	1.5	264	13	09YGE1	09YGE1 oncorhynch	215	7	1.5	343	8	09B4H7	09B4H7 uma notata.
143	7	1.5	265	5	017895	017895 caenorhabdi	216	7	1.5	343	8	09B4H5	09B4H5 uma scopari
144	7	1.5	267	13	09YGE2	09YGE2 oncorhynch	217	7	1.5	343	16	09BAV4	09BAV4 rhizobium m
145	7	1.5	269	2	09FAH1	09FAH1 pseudomonas	218	7	1.5	344	16	092VZ0	092VZ0 rhizobium l
146	7	1.5	269	16	09ACS2	09ACS2 streptomyc	219	7	1.5	344	5	09NL379	09NL379 homo sapien
147	7	1.5	274	5	022843	022843 caenorhabdi	220	7	1.5	346	5	09NL379	09NL379 asterina pe
148	7	1.5	275	5	09BPN1	09BPN1 caenorhabdi	221	7	1.5	346	5	09BSV9	09BSV9 asterina pe
149	7	1.5	276	4	09H913	09H913 homo sapien	222	7	1.5	346	8	0954E1	0954E1 pseudochelr
150	7	1.5	278	8	09NTJ8	09NTJ8 sphagnum fa	223	7	1.5	347	8	021636	021636 darevskia c
151	7	1.5	280	4	09TNJ3	09TNJ3 haplomitrin	224	7	1.5	347	8	021647	021647 darevskia c
152	7	1.5	283	4	09BOJ0	09BOJ0 homo sapien	225	7	1.5	347	8	09MNY7	09MNY7 darevskia m
153	7	1.5	285	5	09Q2H9	09Q2H9 caenorhabdi	226	7	1.5	347	8	09MNS3	09MNS3 lacerta nai
154	7	1.5	286	17	08TF83	08TF83 methanosarc	227	7	1.5	347	8	0954E0	0954E0 trichosurus
155	7	1.5	290	8	09TNL2	09TNL2 physcomitre	228	7	1.5	347	8	095255	095255 trichosurus
156	7	1.5	291	2	093TU0	093TU0 acidithioba	229	7	1.5	351	5	08R3I8	08R3I8 drosophila
157	7	1.5	294	10	094AK1	094AK1 arabisopsis	230	7	1.5	351	16	08XFA5	08XFA5 anabaena sp
158	7	1.5	295	10	09LSZ8	09LSZ8 arabisopsis	231	7	1.5	353	8	09BBT0	09BBT0 lotus japon
159	7	1.5	296	16	09LA44	09LA44 shigella dy	232	7	1.5	353	8	08W119	08W119 psilocium nu
160	7	1.5	296	16	08X7F2	08X7F2 escherichia	233	7	1.5	353	10	08S8X8	08S8X8 atropa bell
161	7	1.5	298	2	09REN4	09REN4 zymomonas m	234	7	1.5	355	17	097WJ7	097WJ7 sulfolobus
162	7	1.5	299	8	09TN18	09TN18 adiantum ca	235	7	1.5	356	13	09DE33	09DE33 xenopus lae

236	7	1.5	357	16	08YUZ5	08YUZ5 anabaena sp	309	7	1.5	479	17	027332	027332 methanobact
237	7	1.5	358	16	08YIP7	08YIP7 ralstonia s	310	7	1.5	482	10	09FPT4	09FPT4 arabisdpsis
238	7	1.5	360	16	08UBM3	08UBM3 agrobacteri	311	7	1.5	482	10	0949Y0	0949Y0 arabisdpsis
239	7	1.5	361	4	096C80	096C80 homo sapien	312	7	1.5	480	10	09C8H9	09C8H9 arabisdpsis
240	7	1.5	361	11	091Y81	091Y81 rattus norv	313	7	1.5	483	5	017554	017554 caenorhabdi
241	7	1.5	364	3	09USL0	09USL0 schizosacch	314	7	1.5	494	10	09LHF1	09LHF1 arabisdpsis
242	7	1.5	364	5	09VK91	09VK91 drosophila	315	7	1.5	494	12	09QJL1	09QJL1 cercopithec
243	7	1.5	365	16	08RBB7	08RBB7 thermomae	316	7	1.5	494	17	080246	080246 pyrococcus
244	7	1.5	366	2	08VO93	08VO93 uncultured	317	7	1.5	497	16	092X23	092X23 rhizobium m
245	7	1.5	367	16	08ZDY6	08ZDY6 yersinia pe	318	7	1.5	498	12	091ML7	091ML7 lumpy skin
246	7	1.5	368	10	09SCMR6	09SCMR6 arabisdpsis	319	7	1.5	498	16	092087	092087 rhizobium m
247	7	1.5	371	3	09HFR1	09HFR1 cryptococcu	320	7	1.5	499	12	0913H9	0913H9 pseudorabie
248	7	1.5	373	12	08U2J8	08U2J8 cercopithec	321	7	1.5	500	10	0940M4	0940M4 arabisdpsis
249	7	1.5	375	17	057876	057876 pyrococcus	322	7	1.5	502	8	09MGK6	09MGK6 chrysodidym
250	7	1.5	376	16	0926X9	0926X9 listeria in	323	7	1.5	508	4	015208	015208 homo sapien
251	7	1.5	376	16	08Y3R5	08Y3R5 listeria in	324	7	1.5	514	16	0930U7	0930U7 rhizobium m
252	7	1.5	377	5	017446	017446 caenorhabdi	325	7	1.5	515	2	P96182	P96182 wolfinella s
253	7	1.5	378	4	09BWI3	09BWI3 homo sapien	326	7	1.5	517	5	09U266	09U266 caenorhabdi
254	7	1.5	379	8	09B6F0	09B6F0 thryonomy	327	7	1.5	520	5	09GNK5	09GNK5 drosophila
255	7	1.5	379	16	0983P6	0983P6 rhizobium l	328	7	1.5	522	16	09RUT4	09RUT4 delnoccocus
256	7	1.5	379	17	09YFW4	09YFW4 aetopyrum p	329	7	1.5	527	4	014706	014706 homo sapien
257	7	1.5	381	8	063532	063532 antechinus	330	7	1.5	531	10	09FE08	09FE08 arabisdpsis
258	7	1.5	381	8	09AM96	09AM96 Isodon mac	331	7	1.5	534	13	093296	093296 gallus gall
259	7	1.5	381	8	035545	035545 planigale s	332	7	1.5	535	16	092L32	092L32 rhizobium m
260	7	1.5	385	3	09P981	09P981 robillarda	333	7	1.5	537	10	09S638	09S638 arabisdpsis
261	7	1.5	385	16	0914M7	0914M7 pseudomonas	334	7	1.5	545	5	09VMT4	09VMT4 drosophila
262	7	1.5	385	16	098F78	098F78 rhizobium l	335	7	1.5	555	16	099PTD2	099PTD2 staphylococ
263	7	1.5	387	10	0942S1	0942S1 oryza sativ	336	7	1.5	561	5	0960U5	0960U5 drosophila
264	7	1.5	388	12	065360	065360 oryza pseu	337	7	1.5	566	4	09UPE8	09UPE8 homo sapien
265	7	1.5	391	5	09N6C3	09N6C3 caenorhabdi	338	7	1.5	566	11	09ERQ3	09ERQ3 mus musculu
266	7	1.5	392	16	067276	067276 aquifex aeo	339	7	1.5	569	13	09PYL1	09PYL1 gallus gall
267	7	1.5	393	5	0967G9	0967G9 chironomus	340	7	1.5	579	4	043386	043386 homo sapien
268	7	1.5	395	5	0955S2	0955S2 drosophila	341	7	1.5	579	4	096J15	096J15 homo sapien
269	7	1.5	396	13	073669	073669 gallus gall	342	7	1.5	580	5	09VDV5	09VDV5 drosophila
270	7	1.5	397	10	09FHB1	09FHB1 arabisdpsis	343	7	1.5	581	5	022620	022620 caenorhabdi
271	7	1.5	397	16	054177	054177 streptomyc	344	7	1.5	585	5	08SX51	08SX51 drosophila
272	7	1.5	398	4	09H3Q3	09H3Q3 homo sapien	345	7	1.5	585	12	089244	089244 woodchuck h
273	7	1.5	401	10	09LXU7	09LXU7 arabisdpsis	346	7	1.5	596	10	09LSG6	09LSG6 arabisdpsis
274	7	1.5	402	4	08WVX6	08WVX6 homo sapien	347	7	1.5	605	13	09M6Q9	09M6Q9 fugu rubrip
275	7	1.5	405	11	091W19	091W19 mus musculu	348	7	1.5	610	16	09K6U0	09K6U0 bacillus ha
276	7	1.5	406	3	012161	012161 saccharomyc	349	7	1.5	611	5	09VSV9	09VSV9 drosophila
277	7	1.5	416	12	09YPA9	09YPA9 kaposi's sa	350	7	1.5	616	4	096PK3	096PK3 homo sapien
278	7	1.5	417	4	08WXX6	08WXX6 homo sapien	351	7	1.5	622	11	0923C5	0923C5 mus musculu
279	7	1.5	417	5	016377	016377 caenorhabdi	352	7	1.5	622	16	092BP2	092BP2 rhizobium m
280	7	1.5	425	3	012700	012700 debaromyce	353	7	1.5	624	5	09M2R0	09M2R0 drosophila
281	7	1.5	425	5	09WUT8	09WUT8 drosophila	354	7	1.5	641	5	08T5O6	08T5O6 heterodera
282	7	1.5	427	2	09ZSD5	09ZSD5 rhodobacter	355	7	1.5	643	4	096EAL	096EAL homo sapien
283	7	1.5	428	10	08S3Q9	08S3Q9 oryza sativ	356	7	1.5	652	17	0976X0	0976X0 sulfolobus
284	7	1.5	428	8	0950U6	0950U6 hyaloraphid	357	7	1.5	657	4	08TAM1	08TAM1 homo sapien
285	7	1.5	429	2	08RNN2	08RNN2 legionella	358	7	1.5	671	10	09FRT9	09FRT9 arabisdpsis
286	7	1.5	429	17	08RPG9	08RPG9 methanosarc	359	7	1.5	682	5	09GRT3	09GRT3 plasmodium
287	7	1.5	432	5	09TXH6	09TXH6 caenorhabdi	360	7	1.5	684	10	09LOX1	09LOX1 arabisdpsis
288	7	1.5	434	4	09BS03	09BS03 homo sapien	361	7	1.5	685	5	017378	017378 caenorhabdi
289	7	1.5	438	16	08XEV7	08XEV7 salmonella	362	7	1.5	685	5	020423	020423 caenorhabdi
290	7	1.5	440	16	09KRL9	09KRL9 vibrio chol	363	7	1.5	687	5	094960	094960 mycobacteri
291	7	1.5	444	5	09XVA2	09XVA2 caenorhabdi	364	7	1.5	687	16	007753	007753 mycobacteri
292	7	1.5	444	11	09D5R4	09D5R4 mus musculu	365	7	1.5	689	10	065312	065312 arabisdpsis
293	7	1.5	446	10	09AC58	09AC58 arabisdpsis	366	7	1.5	692	2	033448	033448 proteus mir
294	7	1.5	448	5	09NFT7	09NFT7 echinococcu	367	7	1.5	695	13	09D6J8	09D6J8 gallus gall
295	7	1.5	449	4	09H6S4	09H6S4 caulobacter	368	7	1.5	702	4	09HOK9	09HOK9 homo sapien
296	7	1.5	449	16	09ABE3	09ABE3 caulobacter	369	7	1.5	712	11	054729	054729 rattus norv
297	7	1.5	452	10	09ZQO0	09ZQO0 arabisdpsis	370	7	1.5	714	2	08RPL9	08RPL9 ehrlchia c
298	7	1.5	453	4	09NY27	09NY27 homo sapien	371	7	1.5	715	11	09Q2X1	09Q2X1 rattus norv
299	7	1.5	460	10	023014	023014 arabisdpsis	372	7	1.5	722	5	09UAB8	09UAB8 leishmania
300	7	1.5	460	10	09SH79	09SH79 arabisdpsis	373	7	1.5	731	10	09EVB8	09EVB8 ureaplasma
301	7	1.5	461	2	051524	051524 pseudomonas	374	7	1.5	731	16	09POU4	09POU4 oryza sativ
302	7	1.5	462	10	038698	038698 asarum euro	375	7	1.5	738	10	08S6U7	08S6U7 oryza sativ
303	7	1.5	462	11	0923F4	0923F4 mus musculu	376	7	1.5	738	11	09OX02	09OX02 rattus norv
304	7	1.5	465	3	08WZM0	08WZM0 yarrowia li	377	7	1.5	740	4	014747	014747 homo sapien
305	7	1.5	465	3	006525	006525 saccharomyc	378	7	1.5	740	4	09UER7	09UER7 homo sapien
306	7	1.5	470	10	09LSH7	09LSH7 arabisdpsis	379	7	1.5	740	4	015141	015141 homo sapien
307	7	1.5	474	10	08RY61	08RY61 arabisdpsis	380	7	1.5	743	5	08SX92	08SX92 drosophila
308	7	1.5	478	5	043955	043955 leishmania	381	7	1.5	746	11	063553	063553 rattus norv

382	7	1.5	748	5	Q9W091	Q9W091 drosophila	455	7	1.5	1237	16	Q8YH6	Q8YH6 anabaena sp
383	7	1.5	748	11	Q91WX6	Q91WX6 mus musculus	456	7	1.5	1245	5	Q96195	Q96195 plasmodium
384	7	1.5	748	11	Q8VDU5	Q8VDU5 mus musculus	457	7	1.5	1254	10	Q9SR21	Q9SR21 arabidopsis
385	7	1.5	748	16	Q8Z411	Q8Z411 salmoneilla	458	7	1.5	1262	5	Q61771	Q61771 caenorhabd1
386	7	1.5	748	16	Q8X6K3	Q8X6K3 escherichia	459	7	1.5	1287	4	Q92549	Q92549 homo sapien
387	7	1.5	751	3	Q9P749	Q9P749 neotropora	460	7	1.5	1288	13	Q93437	Q93437 gallus gall
388	7	1.5	751	13	Q9DGJ7	Q9DGJ7 gallus gall	461	7	1.5	1291	11	Q61812	Q61812 mus musculus
389	7	1.5	765	4	Q9NRH2	Q9NRH2 homo sapien	462	7	1.5	1317	16	Q91181	Q91181 pseudomonas
390	7	1.5	765	13	Q9W6L9	Q9W6L9 fundulus he	463	7	1.5	1342	10	Q9FKN5	Q9FKN5 arabidopsis
391	7	1.5	775	10	Q8RWV9	Q8RWV9 arabidopsis	464	7	1.5	1343	11	Q64730	Q64730 mus musculus
392	7	1.5	782	16	Q8UCO3	Q8UCO3 agrobacteri	465	7	1.5	1391	4	Q8TEU6	Q8TEU6 homo sapien
393	7	1.5	782	5	Q9GV92	Q9GV92 caenorhabd1	466	7	1.5	1407	10	Q80635	Q80635 arabidopsis
394	7	1.5	782	5	Q19633	Q19633 caenorhabd1	467	7	1.5	1432	16	Q935P0	Q935P0 salmoneilla
395	7	1.5	789	2	Q93M73	Q93M73 xanthomonas	468	7	1.5	1457	4	Q96PS7	Q96PS7 homo sapien
396	7	1.5	790	5	Q01264	Q01264 caenorhabd1	469	7	1.5	1457	11	Q920J0	Q920J0 mus musculus
397	7	1.5	796	13	Q8UW36	Q8UW36 fuqua rubrip	470	7	1.5	1457	11	Q920I8	Q920I8 rattus norv
398	7	1.5	799	4	Q94874	Q94874 homo sapien	471	7	1.5	1469	10	Q9LKR1	Q9LKR1 pismu sativ
399	7	1.5	808	16	Q9ZSS9	Q9ZSS9 rhizobium m	472	7	1.5	1480	4	Q96G04	Q96G04 homo sapien
400	7	1.5	809	16	Q8ZCB5	Q8ZCB5 yersinia pe	473	7	1.5	1484	9	Q96G0G	Q96G0G roseophaga
401	7	1.5	815	5	Q44385	Q44385 caenorhabd1	474	7	1.5	1488	11	Q9ERH3	Q9ERH3 rattus norv
402	7	1.5	817	4	Q9BRK2	Q9BRK2 homo sapien	475	7	1.5	1489	11	Q920I9	Q920I9 mus musculus
403	7	1.5	820	11	Q9Z2R5	Q9Z2R5 mus musculu	476	7	1.5	1509	4	Q96PC1	Q96PC1 homo sapien
404	7	1.5	820	16	Q9ZTA0	Q9ZTA0 rhizobium m	477	7	1.5	1508	3	Q74415	Q74415 schizosacch
405	7	1.5	822	10	Q41370	Q41370 spinactia ol	478	7	1.5	1596	5	Q23178	Q23178 caenorhabd1
406	7	1.5	851	5	Q46093	Q46093 drosophila	479	7	1.5	1601	4	Q8TEU7	Q8TEU7 homo sapien
407	7	1.5	879	10	Q41010	Q41010 pismu sativ	480	7	1.5	1621	5	Q8TEJ5	Q8TEJ5 dictyostell
408	7	1.5	882	12	Q918N6	Q918N6 woodchuck h	481	7	1.5	1664	10	Q9ZOK0	Q9ZOK0 arabidopsis
409	7	1.5	884	12	Q918N8	Q918N8 woodchuck h	482	7	1.5	1687	5	Q18259	Q18259 caenorhabd1
410	7	1.5	884	12	Q918N8	Q918N8 woodchuck h	483	7	1.5	1761	10	Q48867	Q48867 daucus caro
411	7	1.5	884	12	Q918N7	Q918N7 woodchuck h	484	7	1.5	1905	5	Q9Y4V8	Q9Y4V8 drosophila
412	7	1.5	884	12	Q918N5	Q918N5 woodchuck h	485	7	1.5	1972	4	Q9UIF8	Q9UIF8 homo sapien
413	7	1.5	884	12	Q918N4	Q918N4 woodchuck h	486	7	1.5	2047	4	Q15019	Q15019 homo sapien
414	7	1.5	884	12	Q918N3	Q918N3 woodchuck h	487	7	1.5	2078	5	Q8BPN1	Q8BPN1 oikopleura
415	7	1.5	904	16	Q9HUM7	Q9HUM7 pseudomonas	488	7	1.5	2102	5	Q8TIP7	Q8TIP7 dictyostell
416	7	1.5	910	12	Q9G915	Q9G915 avian adeno	489	7	1.5	2157	3	Q00333	Q00333 coprinus cl
417	7	1.5	914	5	Q16530	Q16530 caenorhabd1	490	7	1.5	2276	4	Q75050	Q75050 homo sapien
418	7	1.5	920	5	Q9N306	Q9N306 caenorhabd1	491	7	1.5	2380	5	Q96266	Q96266 plasmodium
419	7	1.5	938	5	Q9V3X5	Q9V3X5 drosophila	492	7	1.5	2410	5	Q8SR14	Q8SR14 encephalit
420	7	1.5	939	16	Q9PLB7	Q9PLB7 chlamydia m	493	7	1.5	2448	2	Q51338	Q51338 pseudomonas
421	7	1.5	950	4	Q9P2G0	Q9P2G0 homo sapien	494	7	1.5	2448	16	Q91182	Q91182 pseudomonas
422	7	1.5	959	16	Q9RL12	Q9RL12 streptomyc	495	7	1.5	3933	5	Q97239	Q97239 plasmodium
423	7	1.5	960	2	Q9RGV2	Q9RGV2 salmoneilla	496	7	1.5	4106	6	Q8WN21	Q8WN21 equus cabal
424	7	1.5	964	16	Q9AAH5	Q9AAH5 caulobacter	497	7	1.5	4144	6	Q8WN22	Q8WN22 canis fam11
425	7	1.5	968	13	Q9PT19	Q9PT19 oncorhynch	498	7	1.5	4146	13	Q9DEI1	Q9DEI1 xenopus lae
426	7	1.5	976	12	Q9DUM0	Q9DUM0 kaposi's sa	499	7	1.5	4498	5	Q9M2Z3	Q9M2Z3 drosophila
427	7	1.5	978	5	Q9W542	Q9W542 drosophila	500	7	1.5	5183	4	Q8TDN5	Q8TDN5 homo sapien
428	7	1.5	979	13	Q93509	Q93509 xenopus lae	501	7	1.5	20	2	Q9R5A6	Q9R5A6 thioabacillu
429	7	1.5	1003	12	Q91LX9	Q91LX9 kaposi's sa	502	7	1.5	22	4	Q9UCQ3	Q9UCQ3 drosophila
430	7	1.5	1022	5	Q9V7A9	Q9V7A9 drosophila	503	7	1.5	23	11	Q62594	Q62594 rattus leuc
431	7	1.5	1033	10	Q9XEX5	Q9XEX5 chlamydomon	504	7	1.5	24	11	Q9QVE1	Q9QVE1 rattus sp.
432	7	1.5	1036	12	Q9DUM3	Q9DUM3 kaposi's sa	505	7	1.5	29	16	Q8XU13	Q8XU13 raietonia s
433	7	1.5	1062	5	Q9VTV2	Q9VTV2 drosophila	506	7	1.5	30	8	Q34903	Q34903 lastorinus
434	7	1.5	1070	3	Q9Y7B9	Q9Y7B9 kluverowyc	507	7	1.5	31	4	Q9NYP6	Q9NYP6 homo sapien
435	7	1.5	1089	12	Q40947	Q40947 kaposi's sa	508	7	1.5	32	4	Q9UDE9	Q9UDE9 homo sapien
436	7	1.5	1112	13	Q9O381	Q9O381 caracharhinu	509	7	1.5	34	11	Q99KX7	Q99KX7 mus musculu
437	7	1.5	1114	4	Q9H0Y6	Q9H0Y6 homo sapien	510	7	1.5	34	11	Q9QV55	Q9QV55 mus sp. cyt
438	7	1.5	1129	12	Q9QR71	Q9QR71 kaposi's sa	511	7	1.5	36	12	Q9QOS6	Q9QOS6 tanapox vir
439	7	1.5	1134	4	Q9NRC3	Q9NRC3 homo sapien	512	7	1.5	37	11	Q9GLX8	Q9GLX8 mus musculu
440	7	1.5	1134	4	Q9E1P7	Q9E1P7 homo sapien	513	7	1.5	37	13	Q8UW71	Q8UW71 xenopus lae
441	7	1.5	1139	5	Q90280	Q90280 caenorhabd1	514	7	1.5	42	10	Q9LE26	Q9LE26 psilocum nu
442	7	1.5	1143	4	Q16614	Q16614 homo sapien	515	7	1.5	43	10	Q41997	Q41997 arabidopsis
443	7	1.5	1145	5	Q9VSP0	Q9VSP0 drosophila	516	7	1.5	44	12	P87665	P87665 duck adenov
444	7	1.5	1159	5	Q9VVC9	Q9VVC9 drosophila	517	7	1.5	45	10	Q49771	Q49771 arabidopsis
445	7	1.5	1160	2	Q9EUN8	Q9EUN8 corynebacte	518	7	1.5	46	16	Q8X3T3	Q8X3T3 escherichia
446	7	1.5	1162	12	Q98148	Q98148 kaposi's sa	519	7	1.5	47	16	Q942W8	Q942W8 caulobacter
447	7	1.5	1164	2	Q8VVJ4	Q8VVJ4 corynebacte	520	7	1.5	48	5	Q9VR85	Q9VR85 drosophila
448	7	1.5	1179	12	Q91L98	Q91L98 white spot	521	7	1.5	48	16	Q25451	Q25451 helicobacte
449	7	1.5	1180	12	Q8VAS9	Q8VAS9 white spot	522	7	1.5	48	16	Q92L87	Q92L87 canis fam11
450	7	1.5	1185	12	Q8OTC5	Q8OTC5 white spot	523	7	1.5	49	6	Q28871	Q28871 canis fam11
451	7	1.5	1204	4	Q9UHV4	Q9UHV4 homo sapien	524	7	1.5	49	16	Q98708	Q98708 rhizobium l
452	7	1.5	1217	11	Q9QW29	Q9QW29 rattus sp.	525	7	1.5	53	9	Q8SDM7	Q8SDM7 staphylococ
453	7	1.5	1218	11	Q9JUE6	Q9JUE6 rattus norv	526	7	1.5	53	16	Q99SQ2	Q99SQ2 staphylococ
454	7	1.5	1236	3	Q9C105	Q9C105 schizosacch	527	7	1.5	53	16	Q931J8	Q931J8 staphylococ

528	6	1.3	53	17	029381	029381 archaeoglob	601	6	1.3	80	5	Q9BP59	Q9BP59 conus ventr
529	6	1.3	54	12	099398	099398 hepatitis c	602	6	1.3	80	8	Q47577	Q47577 onchocerca
530	6	1.3	54	12	099404	099404 hepatitis c	603	6	1.3	80	10	Q08164	Q08164 secale cere
531	6	1.3	54	12	099403	099403 hepatitis c	604	6	1.3	80	12	Q70797	Q70797 tt virus. s
532	6	1.3	55	11	098547	098547 mus musculu	605	6	1.3	80	12	Q70803	Q70809 tt virus. s
533	6	1.3	55	16	08VK74	08VK74 mycobacteri	606	6	1.3	80	12	Q70809	Q70809 tt virus. s
534	6	1.3	56	2	Q9RFV2	Q9RFV2 salmonella	607	6	1.3	81	10	Q9M3G5	Q9M3G5 arabidopsis
535	6	1.3	57	16	Q8ZFW9	Q8ZFW9 yersinia pe	608	6	1.3	81	16	Q8XLM8	Q8XLM8 clostridium
536	6	1.3	57	17	Q974H3	Q974H3 sulfobobus	609	6	1.3	83	7	Q19220	Q19220 rangifer ta
537	6	1.3	58	2	Q47832	Q47832 enterococcu	610	6	1.3	83	7	Q19221	Q19221 rangifer ta
538	6	1.3	58	11	Q9CR05	Q9CR05 mus musculu	611	6	1.3	83	7	Q19222	Q19222 rangifer ta
539	6	1.3	58	11	Q9JH07	Q9JH07 mus musculu	612	6	1.3	83	7	Q19227	Q19227 rangifer ta
540	6	1.3	59	4	Q43705	Q43705 homo sapien	613	6	1.3	83	9	Q38065	Q38065 bacterioph
541	6	1.3	59	6	Q28675	Q28675 oryctolagus	614	6	1.3	83	16	Q915K6	Q915K6 pseudomonas
542	6	1.3	61	2	P94471	P94471 bacillus su	615	6	1.3	83	16	Q8RF71	Q8RF71 bruceella me
543	6	1.3	61	5	Q9NFP9	Q9NFP9 ceratitlis c	616	6	1.3	85	4	Q9U0B0	Q9U0B0 homo sapien
544	6	1.3	61	5	Q9NFP8	Q9NFP8 ceratitlis c	617	6	1.3	85	4	Q95419	Q95419 homo sapien
545	6	1.3	61	5	Q8STG3	Q8STG3 echinococcu	618	6	1.3	85	5	Q44629	Q44629 caenorhabdi
546	6	1.3	61	11	Q9ES48	Q9ES48 mus musculu	619	6	1.3	85	5	Q8T0W5	Q8T0W5 plasmia hypo
547	6	1.3	62	13	Q91801	Q91801 xenopus lae	620	6	1.3	85	10	Q8VZW8	Q8VZW8 arabidopsis
548	6	1.3	63	5	Q9VBH1	Q9VBH1 drosophila	621	6	1.3	85	12	Q98433	Q98433 parametium
549	6	1.3	65	15	Q12385	Q12385 simian t-ly	622	6	1.3	85	12	Q996X8	Q996X8 helicoverpa
550	6	1.3	66	17	Q8TW36	Q8TW36 methanopyru	623	6	1.3	86	3	Q9S4W5	Q9S4W5 escherichia
551	6	1.3	67	2	Q87442	Q87442 pseudomonas	624	6	1.3	86	3	Q9C2X8	Q9C2X8 candida alb
552	6	1.3	67	3	Q94112	Q94112 pneumocysti	625	6	1.3	86	15	Q8USX0	Q8USX0 human immun
553	6	1.3	67	5	Q02400	Q02400 teladorsagi	626	6	1.3	87	15	Q8UAX0	Q8UAX0 agrobacteri
554	6	1.3	68	8	Q9MOK8	Q9MOK8 hydra atren	627	6	1.3	87	15	Q80794	Q80794 human t-lym
555	6	1.3	68	17	Q9HM00	Q9HM00 thermoplasma	628	6	1.3	87	15	Q9PYZ8	Q9PYZ8 human t-lym
556	6	1.3	69	12	Q67840	Q67840 hepatitis b	629	6	1.3	87	15	Q9PYX6	Q9PYX6 human t-lym
557	6	1.3	69	12	Q67846	Q67846 hepatitis b	630	6	1.3	87	16	Q92PY6	Q92PY6 rhizobium m
558	6	1.3	69	12	Q67847	Q67847 hepatitis b	631	6	1.3	88	15	Q90BK4	Q90BK4 human immun
559	6	1.3	69	12	Q67848	Q67848 hepatitis b	632	6	1.3	89	2	Q9ATF6	Q9ATF6 actinobacill
560	6	1.3	69	13	Q8OR05	Q8OR05 rana pipien	633	6	1.3	89	10	Q8S6T9	Q8S6T9 oryza sativ
561	6	1.3	69	16	Q9AA82	Q9AA82 caulobacter	634	6	1.3	89	16	Q9USK2	Q9USK2 chlamydia p
562	6	1.3	69	16	Q8RD68	Q8RD68 thermotanaer	635	6	1.3	89	16	Q9CE15	Q9CE15 lactococcus
563	6	1.3	71	12	Q93PY4	Q93PY4 pseudomonas	636	6	1.3	90	16	P72713	P72713 synechocyst
564	6	1.3	71	12	Q8VAS3	Q8VAS3 white spot	637	6	1.3	90	16	Q8YBMS	Q8YBMS bruceella me
565	6	1.3	71	12	Q8ORC3	Q8ORC3 white spot	638	6	1.3	91	10	Q8SAR5	Q8SAR5 arabidopsis
566	6	1.3	71	13	Q8ORC4	Q8ORC4 rana pipien	639	6	1.3	91	16	Q9CCB9	Q9CCB9 mycobacteri
567	6	1.3	71	17	Q971H4	Q971H4 sulfobobus	640	6	1.3	91	16	Q8X7S2	Q8X7S2 escherichia
568	6	1.3	72	3	Q9C174	Q9C174 aspergillus	641	6	1.3	92	10	Q9A6S5	Q9A6S5 oryza sativ
569	6	1.3	72	15	P89228	P89228 walleye der	642	6	1.3	93	16	Q934X2	Q934X2 salmonella
570	6	1.3	72	16	Q97GV7	Q97GV7 clostridium	643	6	1.3	94	4	Q14057	Q14057 homo sapien
571	6	1.3	72	16	Q8ZJ13	Q8ZJ13 yersinia pe	644	6	1.3	94	5	Q9U705	Q9U705 plasmodium
572	6	1.3	74	5	Q25016	Q25016 helix asper	645	6	1.3	94	5	Q8U708	Q8U708 plasmodium
573	6	1.3	74	10	Q8S221	Q8S221 oryza sativ	646	6	1.3	94	5	Q9U706	Q9U706 plasmodium
574	6	1.3	74	17	Q974F5	Q974F5 sulfobobus	647	6	1.3	94	5	Q9U705	Q9U705 plasmodium
575	6	1.3	75	5	Q9BP58	Q9BP58 conus ventr	648	6	1.3	94	17	Q8TK50	Q8TK50 methanosarc
576	6	1.3	75	12	Q84587	Q84587 parametium	649	6	1.3	96	5	Q9VK38	Q9VK38 drosophila
577	6	1.3	76	2	Q9FB50	Q9FB50 corynebacte	650	6	1.3	96	11	Q8RA44	Q8RA44 phodopus su
578	6	1.3	76	5	Q8GPN6	Q8GPN6 schistosoma	651	6	1.3	96	12	Q98554	Q98554 parametium
579	6	1.3	76	5	Q9BP60	Q9BP60 conus ventr	652	6	1.3	96	17	Q8TL15	Q8TL15 methanosarc
580	6	1.3	76	10	Q9ASL0	Q9ASL0 oryza sativ	653	6	1.3	98	8	Q950L7	Q950L7 rhizophydlu
581	6	1.3	76	12	Q98541	Q98541 parametium	654	6	1.3	98	15	Q9END6	Q9END6 human immun
582	6	1.3	76	16	Q9JTT8	Q9JTT8 neisseria m	655	6	1.3	98	16	P73230	P73230 synechocyst
583	6	1.3	77	5	Q9BP68	Q9BP68 conus arena	656	6	1.3	98	16	Q92CK3	Q92CK3 listeria in
584	6	1.3	77	5	Q9BP65	Q9BP65 conus arena	657	6	1.3	98	16	Q877R6	Q877R6 listeria mo
585	6	1.3	77	16	Q816P4	Q816P4 listeria mo	658	6	1.3	99	12	Q91NV0	Q91NV0 hepatitis b
586	6	1.3	78	5	Q9BP76	Q9BP76 conus tessu	659	6	1.3	99	12	Q91NV8	Q91NV8 hepatitis b
587	6	1.3	78	5	Q9BP66	Q9BP66 conus arena	660	6	1.3	99	12	Q91NM0	Q91NM0 hepatitis b
588	6	1.3	78	5	Q9BP64	Q9BP64 conus penna	661	6	1.3	99	12	Q91NV8	Q91NV8 hepatitis b
589	6	1.3	78	7	Q8WM11	Q8WM11 rangifer ta	662	6	1.3	99	12	Q91NV6	Q91NV6 hepatitis b
590	6	1.3	78	9	Q8WM08	Q8WM08 rangifer ta	663	6	1.3	99	12	Q91NV4	Q91NV4 hepatitis b
591	6	1.3	78	9	Q9WB09	Q9WB09 staphylococ	664	6	1.3	99	12	Q73557	Q73557 lassa virus
592	6	1.3	78	10	Q9M5S9	Q9M5S9 ipomoea bat	665	6	1.3	99	16	Q9S1W3	Q9S1W3 streptomyce
593	6	1.3	79	5	Q9BP73	Q9BP73 conus tessu	666	6	1.3	100	2	Q9RPF5	Q9RPF5 rhodobacter
594	6	1.3	79	5	Q9BP72	Q9BP72 conus arena	667	6	1.3	100	2	Q93T83	Q93T83 bruceella ab
595	6	1.3	79	5	Q9BP71	Q9BP71 conus arena	668	6	1.3	100	2	Q8RPY7	Q8RPY7 rhizobium l
596	6	1.3	79	5	Q9BP70	Q9BP70 conus arena	669	6	1.3	100	5	Q96640	Q96640 ceratitlis c
597	6	1.3	79	5	Q9BP69	Q9BP69 conus arena	670	6	1.3	100	8	Q8WAN2	Q8WAN2 hemisplinus
598	6	1.3	79	5	Q9BP67	Q9BP67 conus arena	671	6	1.3	100	15	Q80322	Q80322 human immun
599	6	1.3	79	5	Q9BP63	Q9BP63 conus penna	672	6	1.3	100	16	Q98CY3	Q98CY3 rhizobium l
600	6	1.3	80	5	Q9BP62	Q9BP62 conus ventr	673	6	1.3	100	17	Q28004	Q28004 archaeoglob

674	6	1.3	101	8	020826	020826	Ierista dor	747	6	1.3	114	15	09YL60	09YL60 human immun
675	6	1.3	101	16	092GB3	092GB3	ricketsia	748	6	1.3	114	17	096ZM3	096ZM3 sulfolobus
676	6	1.3	102	10	09SBH8	09SBH8	solanum tub	749	6	1.3	115	2	08VMW7	08VMW7 listeria se
677	6	1.3	102	15	077143	077143	human immun	750	6	1.3	115	4	09PLU3	09PLU3 homo sapien
678	6	1.3	102	17	096XB9	096XB9	sulfolobus	751	6	1.3	115	4	09S325	09S325 homo sapien
679	6	1.3	103	2	093EX2	093EX2	rhodococcus	752	6	1.3	115	10	09S9A1	09S9A1 viscum albu
680	6	1.3	103	2	049853	049853	mycobacteri	753	6	1.3	115	15	09WLS9	09WLS9 human immun
681	6	1.3	103	5	09U3J9	09U3J9	caenorhabdi	754	6	1.3	115	15	09YLS38	09YLS38 human immun
682	6	1.3	103	10	09VM03	09VM03	drosophila	755	6	1.3	115	15	080318	080318 human immun
683	6	1.3	103	5	09M045	09M045	arabidopsis	756	6	1.3	115	15	070106	070106 human immun
684	6	1.3	103	16	09PH85	09PH85	xyliella fas	757	6	1.3	115	15	P88778	P88778 human immun
685	6	1.3	103	16	096257	096257	mycobacteri	758	6	1.3	115	16	09YTX8	09YTX8 anabaena sp
686	6	1.3	104	10	09FEX6	09FEX6	hordum vul	759	6	1.3	115	17	09YET6	09YET6 aetopyrum p
687	6	1.3	104	16	033291	033291	pyrococcul	760	6	1.3	116	6	097AU6	097AU6 thermoplas
688	6	1.3	104	17	08U0B2	08U0B2	pyrococcul	761	6	1.3	116	6	09BCS3	09BCS3 macaca fasc
689	6	1.3	104	17	08U0B2	08U0B2	corynebacte	762	6	1.3	116	6	037127	037127 arabcia ltx
690	6	1.3	105	5	08W0E9	08W0E9	caenorhabdi	763	6	1.3	116	17	09YHP4	09YHP4 aetopyrum p
691	6	1.3	105	12	056310	056310	egyptian su	764	6	1.3	117	8	009315	009315 eidmannella
692	6	1.3	105	12	09YXZ2	09YXZ2	egyptian su	765	6	1.3	117	10	09LH43	09LH43 arabidopsis
693	6	1.3	105	12	09YXD8	09YXD8	egyptian su	766	6	1.3	117	12	08OP43	08OP43 dengue viru
694	6	1.3	105	12	09YXD5	09YXD5	egyptian su	767	6	1.3	118	10	09LCU3	09LCU3 arabidopsis
695	6	1.3	105	12	09YXD5	09YXD5	egyptian su	768	6	1.3	119	2	093RT7	093RT7 thermotoga
696	6	1.3	105	16	09Z9D1	09Z9D1	chlamydia p	769	6	1.3	119	2	093RT5	093RT5 thermotoga
697	6	1.3	105	16	08Y2P7	08Y2P7	raistonia s	770	6	1.3	119	2	093RU4	093RU4 thermotoga
698	6	1.3	106	16	P92346	P92346	arabidopsis	771	6	1.3	119	3	09UX74	09UX74 schizosacch
699	6	1.3	106	16	P93239	P93239	arabidopsis	772	6	1.3	119	5	08T5W1	08T5W1 caenorhabdi
700	6	1.3	106	16	08ZBP5	08ZBP5	yersinia pe	773	6	1.3	119	5	08T5V5	08T5V5 caenorhabdi
701	6	1.3	106	17	08TML6	08TML6	methanosarc	774	6	1.3	119	5	08T5V4	08T5V4 caenorhabdi
702	6	1.3	107	16	08UCS6	08UCS6	methanosarc	775	6	1.3	119	12	09LH78	09LH78 cherry necr
703	6	1.3	108	3	013531	013531	saccharomyc	776	6	1.3	119	15	09U678	09U678 human immun
704	6	1.3	108	12	084259	084259	european el	777	6	1.3	120	2	032318	032318 bacillus th
705	6	1.3	108	16	091097	091097	pseudomonas	778	6	1.3	120	5	08T5W2	08T5W2 caenorhabdi
706	6	1.3	108	16	08Z7M2	08Z7M2	salmonella	779	6	1.3	120	8	099150	099150 rivulus del
707	6	1.3	108	17	09YB07	09YB07	aetopyrum p	780	6	1.3	120	8	099151	099151 rivulus sp.
708	6	1.3	109	2	P71157	P71157	desulfotibr	781	6	1.3	120	8	099157	099157 rivulus apl
709	6	1.3	109	2	043891	043891	acetobacter	782	6	1.3	120	8	099158	099158 rivulus pun
710	6	1.3	109	3	013543	013543	saccharomyc	783	6	1.3	120	8	099164	099164 neofundulus
711	6	1.3	109	12	09WAZ5	09WAZ5	tyt virus. o	784	6	1.3	120	8	035732	035732 rivulus mag
712	6	1.3	109	16	09PFR4	09PFR4	xyliella fas	785	6	1.3	120	8	035711	035711 rivulus cry
713	6	1.3	109	17	08TR36	08TR36	methanosarc	786	6	1.3	120	8	P87398	P87398 tritonectes
714	6	1.3	110	11	09D2G6	09D2G6	methanosarc	787	6	1.3	120	8	099142	099142 rivulus fire
715	6	1.3	110	16	09CDP7	09CDP7	mus musculu	788	6	1.3	120	12	067428	067428 dengue viru
716	6	1.3	110	17	09Y1P0	09Y1P0	pyrococcus	789	6	1.3	120	16	098PB3	098PB3 rhizobium l
717	6	1.3	110	17	014502	014502	homo sapien	790	6	1.3	120	16	053437	053437 mycobacteri
718	6	1.3	111	12	09WAZ3	09WAZ3	tyt virus. o	791	6	1.3	121	4	08TCU2	08TCU2 homo sapien
719	6	1.3	111	12	09WAZ7	09WAZ7	tyt virus. o	792	6	1.3	121	8	09TGS4	09TGS4 rhinolophus
720	6	1.3	111	12	08OSAO	08OSAO	felis domes	793	6	1.3	121	8	09BPD6	09BPD6 cilix glauc
721	6	1.3	111	16	005219	005219	baclillus su	794	6	1.3	121	16	08XBE4	08XBE4 escherichia
722	6	1.3	111	16	08T0B4	08T0B4	raistonia s	795	6	1.3	121	16	08R103	08R103 fusobacteri
723	6	1.3	112	8	09Z2L3	09Z2L3	uta antiqua	796	6	1.3	122	2	09P928	09P928 pseudomonas
724	6	1.3	112	9	080205	080205	methanobact	797	6	1.3	122	2	049696	049696 mycobacteri
725	6	1.3	112	10	09FWM6	09FWM6	oryza sativ	798	6	1.3	122	10	P82178	P82178 spinacia ol
726	6	1.3	112	10	08R2W6	08R2W6	oryza sativ	799	6	1.3	122	16	067205	067205 aquilex aeo
727	6	1.3	112	11	060880	060880	mus musculu	800	6	1.3	122	16	09RTW6	09RTW6 deinococcus
728	6	1.3	112	11	08R1E9	08R1E9	mus musculu	801	6	1.3	123	2	09RC10	09RC10 salmonella
729	6	1.3	112	16	08ZSA9	08ZSA9	anabaena sp	802	6	1.3	123	11	09CSU8	09CSU8 mus musculu
730	6	1.3	112	17	09YDD6	09YDD6	aetopyrum p	803	6	1.3	124	2	09RLT0	09RLT0 lacobacill
731	6	1.3	113	2	045610	045610	baclillus su	804	6	1.3	124	16	08X114	08X114 clostridium
732	6	1.3	113	13	012967	012967	fugu rubrip	805	6	1.3	124	17	057846	057846 pyrococcus
733	6	1.3	113	15	070647	070647	simian t-ly	806	6	1.3	125	5	045212	045212 brugia paha
734	6	1.3	113	16	09K9L4	09K9L4	baclillus ha	807	6	1.3	125	10	09SWM1	09SWM1 argyroxiphil
735	6	1.3	114	3	09HEN7	09HEN7	cocchiobolu	808	6	1.3	125	12	09DM60	09DM60 rat cytomeg
736	6	1.3	114	3	09HEN5	09HEN5	cocchiobolu	809	6	1.3	125	17	059155	059155 pyrococcus
737	6	1.3	114	3	09HEP2	09HEP2	bipolaris s	810	6	1.3	126	17	08TMZ0	08TMZ0 methanosarc
738	6	1.3	114	3	003502	003502	kluyveromyc	811	6	1.3	127	4	09HB18	09HB18 homo sapien
739	6	1.3	114	5	08T5V8	08T5V8	caenorhabdi	812	6	1.3	127	8	09PE60	09PE60 homo sapien
740	6	1.3	114	8	09XPZ7	09XPZ7	suaeda japo	813	6	1.3	127	8	09MP37	09MP37 ctenomys bo
741	6	1.3	114	10	09SDS3	09SDS3	capsicum an	814	6	1.3	127	16	09B390	09B390 oryza sativ
742	6	1.3	114	10	09SDS2	09SDS2	lycopersico	815	6	1.3	127	16	09ZRT8	09ZRT8 rhizobium m
743	6	1.3	114	10	024037	024037	lycopersico	816	6	1.3	127	16	09A1Z0	09A1Z0 streptomyc
744	6	1.3	114	10	024038	024038	lycopersico	817	6	1.3	128	1	033155	033155 methanosarc
745	6	1.3	114	12	08V7E6	08V7E6	tyt virus. o	818	6	1.3	128	6	09MY8	09MY8 oryctolagus
746	6	1.3	114	12	080YC2	080YC2	tyt virus. o	819	6	1.3	128	8	P92832	P92832 colastes ln

820	6	1.3	128	11	Q9D1X3	Q9d1x3 mus musculu	893	6	1.3	139	16	Q9RSF2	Q9rsf2 deinococcus
821	6	1.3	128	12	Q8V7E4	Q8v7e4 tt virus. o	894	6	1.3	139	16	Q9KIV0	Q9kiv0 vibrio chol
822	6	1.3	128	12	Q8V7C7	Q8v7c7 tt virus. o	895	6	1.3	140	10	Q9SHZ7	Q9shz7 arabidopsis
823	6	1.3	128	12	Q8UY10	Q8uy10 tt virus. o	896	6	1.3	140	11	Q9D1M5	Q9d1m5 mus musculu
824	6	1.3	128	16	Q9PMX6	Q9pmx6 campylobact	897	6	1.3	140	16	Q8XVY7	Q8xvy7 rai.stonia s
825	6	1.3	129	8	Q9B0N3	Q9b0n3 paragonimus	898	6	1.3	141	9	Q9MCJ2	Q9mcj2 streptococc
826	6	1.3	129	8	Q03367	Q03367 paragonimus	899	6	1.3	141	16	Q60148	Q60148 pseudomonas
827	6	1.3	129	8	Q9B3H5	Q9b3h5 paragonimus	900	6	1.3	141	16	Q9CF46	Q9cf46 lactococcus
828	6	1.3	129	10	Q22933	Q22933 arabidopsis	901	6	1.3	141	16	Q8XC15	Q8xc15 escherichia
829	6	1.3	129	10	Q9FWY6	Q9fwy6 arabidopsis	902	6	1.3	142	10	Q9FS06	Q9fs06 triticum ae
830	6	1.3	129	11	Q9ESG1	Q9esg1 mus musculu	903	6	1.3	142	10	Q9LF87	Q9lf87 arabidopsis
831	6	1.3	129	15	Q36916	Q36916 human immun	904	6	1.3	142	11	Q9NMK6	Q9nmk6 cricetus
832	6	1.3	129	15	Q9Q8K7	Q9q8k7 human immun	905	6	1.3	142	13	Q9PWP2	Q9pwp2 xenopus lae
833	6	1.3	129	15	Q9Q8K6	Q9q8k6 human immun	906	6	1.3	142	13	Q9PWP1	Q9pwp1 xenopus lae
834	6	1.3	129	15	Q9Q8K5	Q9q8k5 human immun	907	6	1.3	142	16	Q9Z0R0	Q9z0r0 rhizodium m
835	6	1.3	129	17	Q8U237	Q8u237 pyrococcus	908	6	1.3	142	17	Q9YEO9	Q9y eo9 aeropyrum p
836	6	1.3	130	2	Q9R918	Q9r918 bacillus su	909	6	1.3	142	17	Q9YAO0	Q9yao0 aeropyrum p
837	6	1.3	130	2	Q9L7W8	Q9l7w8 bacillus su	910	6	1.3	142	17	Q9HMA4	Q9hma4 halobacteri
838	6	1.3	130	8	Q03366	Q03366 paragonimus	911	6	1.3	143	5	Q20396	Q20396 caenorhabdi
839	6	1.3	130	8	Q03558	Q03558 paragonimus	912	6	1.3	143	5	Q20396	Q20396 caenorhabdi
840	6	1.3	130	8	Q03560	Q03560 paragonimus	913	6	1.3	143	17	Q99RQ4	Q99rq4 staphylococ
841	6	1.3	130	8	Q03573	Q03573 paragonimus	914	6	1.3	144	16	Q8TY77	Q8ty77 methanopyru
842	6	1.3	130	8	Q9T394	Q9t394 euparagonim	915	6	1.3	144	16	Q54184	Q54184 streptomyc
843	6	1.3	130	8	Q21214	Q21214 paragonimus	916	6	1.3	145	2	Q93V25	Q93v25 rhodobacter
844	6	1.3	130	8	Q21225	Q21225 paragonimus	917	6	1.3	145	2	Q56614	Q56614 vibrio chol
845	6	1.3	130	8	Q9T6X4	Q9t6x4 paragonimus	918	6	1.3	145	4	Q9BXM9	Q9bxm9 homo sapien
846	6	1.3	130	8	Q9T6X3	Q9t6x3 paragonimus	919	6	1.3	145	11	Q9UKP7	Q9ukp7 mus musculu
847	6	1.3	130	8	Q9T6X2	Q9t6x2 paragonimus	920	6	1.3	145	11	Q8RI98	Q8ri98 mus musculu
848	6	1.3	130	8	Q9T6X1	Q9t6x1 paragonimus	921	6	1.3	145	15	Q40526	Q40526 human immun
849	6	1.3	130	8	Q9T6X0	Q9t6x0 paragonimus	922	6	1.3	145	15	Q40527	Q40527 human immun
850	6	1.3	130	8	Q03368	Q03368 paragonimus	923	6	1.3	145	15	Q40545	Q40545 human immun
851	6	1.3	130	8	Q03365	Q03365 paragonimus	924	6	1.3	145	15	Q40550	Q40550 human immun
852	6	1.3	130	10	Q9M3C3	Q9m3c3 arabidopsis	925	6	1.3	145	15	Q40551	Q40551 human immun
853	6	1.3	130	16	Q34506	Q34506 bacillus su	926	6	1.3	145	15	Q40552	Q40552 human immun
854	6	1.3	130	17	Q29584	Q29584 archaeoglob	927	6	1.3	145	15	Q40553	Q40553 human immun
855	6	1.3	131	2	Q50281	Q50281 pseudomonas	928	6	1.3	145	15	Q40554	Q40554 human immun
856	6	1.3	131	2	Q93137	Q93137 streptomyc	929	6	1.3	145	15	Q42030	Q42030 human immun
857	6	1.3	131	5	Q960H9	Q960h9 drosophila	930	6	1.3	145	15	Q42057	Q42057 human immun
858	6	1.3	131	8	Q35865	Q35865 strongyloce	931	6	1.3	145	16	Q92K19	Q92k19 human immun
859	6	1.3	131	8	Q35903	Q35903 strongyloce	932	6	1.3	145	16	Q92K01	Q92k01 heliobacte
860	6	1.3	131	10	Q9FRL0	Q9frl0 arabidopsis	933	6	1.3	146	2	Q45052	Q45052 vibrio chol
861	6	1.3	131	11	Q9CZL2	Q9czl2 mus musculu	934	6	1.3	146	5	Q9N5S5	Q9n5s5 caenorhabdi
862	6	1.3	131	16	Q921W9	Q921w9 rickettsia	935	6	1.3	146	5	Q9V5U2	Q9v5u2 drosophila
863	6	1.3	131	16	Q8XFX4	Q8xfx4 salmonella	936	6	1.3	146	12	Q9QZR8	Q9qzr8 human papil
864	6	1.3	132	4	Q8TRF9	Q8trf9 homo sapien	937	6	1.3	146	16	Q51615	Q51615 borrelia bu
865	6	1.3	132	16	Q928H3	Q928h3 listeria in	938	6	1.3	146	16	Q44659	Q44659 bacillus ha
866	6	1.3	132	16	Q8Y700	Q8y700 anabaena sp	939	6	1.3	146	17	Q8Z206	Q8z2q6 pyrobaculu
867	6	1.3	133	5	Q8T668	Q8t668 echinococcu	940	6	1.3	147	4	Q991J3	Q991j3 usitlago sc
868	6	1.3	133	5	Q8T667	Q8t667 echinococcu	941	6	1.3	147	4	Q9B7J8	Q9b7j8 homo sapien
869	6	1.3	133	8	Q35820	Q35820 strongyloce	942	6	1.3	147	10	Q9PF54	Q9pf54 arabidopsis
870	6	1.3	133	15	Q9Q0R7	Q9q0r7 human immun	943	6	1.3	147	16	Q9PHJ3	Q9phj3 campylobact
871	6	1.3	133	17	Q591S0	Q591s0 pyrococcus	944	6	1.3	147	16	Q8XET7	Q8xet7 salmonella
872	6	1.3	134	2	Q9L895	Q9l895 prochloroco	945	6	1.3	147	16	Q8UBZ7	Q8ubz7 agrobacteri
873	6	1.3	134	12	Q9DUH9	Q9duh9 tt virus. o	946	6	1.3	147	17	Q9NHF6	Q9nhf6 halobacteri
874	6	1.3	134	13	Q98S16	Q98s16 brachydanio	947	6	1.3	148	8	Q9MD16	Q9md16 pseudomonas
875	6	1.3	134	16	Q9KPK2	Q9kpk2 vibrio chol	948	6	1.3	148	8	Q03143	Q03143 cryptomeria
876	6	1.3	134	16	Q98E03	Q98e03 rhizobium i	949	6	1.3	148	8	Q03155	Q03155 sphagnum pa
877	6	1.3	135	5	Q8SUW0	Q8suw0 encephalito	950	6	1.3	148	8	Q09357	Q09357 thu.jopsis d
878	6	1.3	135	16	P72881	P72881 synchocyst	951	6	1.3	148	16	Q9A4C5	Q9a4c5 caulobacter
879	6	1.3	135	16	Q9A142	Q9a142 streptococc	952	6	1.3	148	17	Q9YFI2	Q9yfi2 aeropyrum p
880	6	1.3	135	17	Q9YCX8	Q9ycx8 aeropyrum p	953	6	1.3	148	17	Q97X16	Q97x16 sulfobius
881	6	1.3	136	4	Q9Y423	Q9y423 homo sapien	954	6	1.3	149	2	Q9RA40	Q9ra40 trichodesmi
882	6	1.3	136	10	Q9FWZ6	Q9fwz6 oryza sativ	955	6	1.3	149	4	Q8WX36	Q8wx36 homo sapien
883	6	1.3	136	10	Q946W7	Q946w7 prunus pers	956	6	1.3	149	10	Q9FJU67	Q9fju67 arabidopsis
884	6	1.3	136	11	Q9CZJ4	Q9czj4 mus musculu	957	6	1.3	149	16	Q8Z0F2	Q8z0f2 anabaena sp
885	6	1.3	136	16	Q97N79	Q97n79 mus musculu	958	6	1.3	150	8	Q9B8W1	Q9b8w1 taenia cras
886	6	1.3	136	16	Q8U8L2	Q8u8l2 agrobacteri	959	6	1.3	150	10	Q80490	Q80490 arabidopsis
887	6	1.3	137	17	Q58445	Q58445 pyrococcus	960	6	1.3	150	12	Q69291	Q69291 gallit herp
888	6	1.3	138	16	Q930H6	Q930h6 rhizobium m	961	6	1.3	151	5	Q8W0N6	Q8w0n6 anophelies g
889	6	1.3	138	16	Q9AD53	Q9ad53 streptomyc	962	6	1.3	151	10	Q9FW68	Q9fw68 oryza sativ
890	6	1.3	138	17	Q9YC20	Q9yc20 aeropyrum p	963	6	1.3	151	12	Q9QF32	Q9qf32 dengue viru
891	6	1.3	138	17	Q8U224	Q8u224 pyrococcus	964	6	1.3	151	16	Q9JTQ4	Q9jltq4 neisseria m
892	6	1.3	139	5	Q9XX29	Q9xx29 caenorhabdi	965	6	1.3	151	16	Q99RR3	Q99rr3 staphylococ

```

966 6 1.3 152 4 09BXR8 09BXR8 homo sapien
967 6 1.3 152 12 09DUD0 09DUD0 tt virus. o
968 6 1.3 152 16 09KDA2 09KDA2 bacillus. o
969 6 1.3 152 16 08UJ34 08UJ34 agrobacteri
970 6 1.3 153 8 09T5G5 09T5G5 teladorsagi
971 6 1.3 153 9 09G1B4 09G1B4 parapallase
972 6 1.3 153 9 09XJ95 09XJ95 streptococ
973 6 1.3 153 10 09LGM4 09LGM4 oryza sativ
974 6 1.3 153 12 09DS06 09DS06 foot-and-mo
975 6 1.3 153 12 08V5P5 08V5P5 foot-and-mo
976 6 1.3 153 12 08V5P4 08V5P4 foot-and-mo
977 6 1.3 153 12 08V5N7 08V5N7 foot-and-mo
978 6 1.3 153 12 08V5N6 08V5N6 foot-and-mo
979 6 1.3 153 12 08V0P7 08V0P7 foot-and-mo
980 6 1.3 153 16 09X0B4 09X0B4 thermotoga
981 6 1.3 153 16 09JR28 09JR28 neisseria m
982 6 1.3 153 16 08VP90 08VP90 anabaena sp
983 6 1.3 153 17 097BF8 097BF8 thermoplas
984 6 1.3 154 4 09H4G4 09H4G4 homo sapien
985 6 1.3 154 8 09G6Z6 09G6Z6 haplopharyn
986 6 1.3 154 11 09CYL5 09CYL5 mus musculu
987 6 1.3 154 13 09DFE0 09DFE0 oncorhynch
988 6 1.3 154 16 09KO58 09KO58 vibrio chol
989 6 1.3 154 16 08ZKE6 08ZKE6 salmonella
990 6 1.3 154 16 08Z1P8 08Z1P8 salmonella
991 6 1.3 155 8 047951 047951 oryza sativ
992 6 1.3 155 12 099AR2 099AR2 tt virus. o
993 6 1.3 156 11 062571 062571 canine herp
994 6 1.3 156 12 066091 066091 mus scrofa
995 6 1.3 156 12 099AR6 099AR6 tt virus. o
996 6 1.3 157 6 08WN54 08WN54 sus scrofa
997 6 1.3 157 8 09X1H7 09X1H7 rhinolophus
998 6 1.3 157 8 09X1H9 09X1H9 rhinolophus
999 6 1.3 157 10 08S3Z1 08S3Z1 sorghum bic
1000 6 1.3 157 12 08UZK8 08UZK8 sen virus.

```

ALIGNMENTS

```

RESULT 1
09UIFO PRELIMINARY; PRT; 289 AA.
ID 09UIFO
AC 09UIFO
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Presentin 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E.; Waterston R.;
RT "Toward a complete human genome sequence."
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Kozlowicz A.; Pape K.; Biewald T.;
RT "The sequence of Homo sapiens PAC clone RP4-687K1."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004858; AAF19253.1; -
DR InterPro; IPR001108; Presentin.
DR Pfam; PFO1080; Presentin.1.
DR PRINTS; PRO1072; PRESENTIN.
FT NON_TER 289
SQ SEQUENCE 289 AA; 33067 MW; D503395A31C0ECB CRC64;

```

```

Query Match 43.7%; Score 204; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 2e-199;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPISTFONAMSESDNHLSTNVRSONDRERQEHNDRRSLGHPPLSNGRPOGNSR 60
Db 1 MTELPAPISTFONAMSESDNHLSTNVRSONDRERQEHNDRRSLGHPPLSNGRPOGNSR 60
QY 61 QVEODEDEDEFLTKYAKAHYIMLFVPVTLQMVVAVTISVSFTYRKDQLYTPFTE 120
Db 61 QVEODEDEDEFLTKYAKAHYIMLFVPVTLQMVVAVTISVSFTYRKDQLYTPFTE 120
QY 121 DTEYVQGRALSHLNAALIMISYIVMTLLVLYKRCYKVIHAWLLISSLLFFFSFI 180
Db 121 DTEYVQGRALSHLNAALIMISYIVMTLLVLYKRCYKVIHAWLLISSLLFFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIWN 204
Db 181 YLGEVFKTYNVAVDYITVALLIWN 204

```

RESULT 2

```

ID 095465 PRELIMINARY; PRT; 184 AA.
AC 095465;
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE MINILIN.
GN PSNI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Powell C.S.; Gegg M.E.; Palmer M.S.;
RT "Human presentin 1 gene encodes an alternative protein-minilin."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E.; Waterston R.;
RT "Toward a complete human genome sequence."
RL Genome Res. 8:1097-1108(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX Kozlowicz A.; Pape K.; Biewald T.;
RT "The sequence of Homo sapiens PAC clone RP4-687K1."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AU008005; CA07825.1; -
DR EMBL; AC004858; AAF19254.1; -
DR InterPro; IPR001108; Presentin.
DR Pfam; PFO1080; Presentin.1.
SQ SEQUENCE 184 AA; 21073 MW; 95C68A7EA0020874 CRC64;

```

```

Query Match 34.5%; Score 161; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-155;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTELPAPISTFONAMSESDNHLSTNVRSONDRERQEHNDRRSLGHPPLSNGRPOGNSR 60
Db 1 MTELPAPISTFONAMSESDNHLSTNVRSONDRERQEHNDRRSLGHPPLSNGRPOGNSR 60

```

QY 61 QVVEDEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDGQIYTPETE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDGQIYTPETE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 DTEVVGORALHSILMAIMISIVVMTLLVLYKKRYCKV 161
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 DTEVVGORALHSILMAIMISIVVMTLLVLYKKRYCKV 161

RESULT 3

Q96P33 PRELIMINARY: PRT: 378 AA.
 AC Q96P33;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Presentinlin 1.
 GN PSEN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kang L., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF416717; AAL16811.1; -
 DR InterPro: IPR001108; Presentinlin.
 DR Pfam: PF01080; Presentinlin.
 DR PRINTS: PRO1072; PRESENTINLIN.
 SQ SEQUENCE 378 AA; 42658 MW; A09D6D2FC6F5618D CRC64;

Query Match 27.2%; Score 127; DB 42; Length 378;
 Best Local Similarity 100.0%; Pred. No. 9, 8e-121;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQMSQEDNHLSTVRSQNDNRROEHNDRSIGHEPELSNGRPGNSR 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MTELPALSYFQNAQMSQEDNHLSTVRSQNDNRROEHNDRSIGHEPELSNGRPGNSR 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDGQIYTPETE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 QVVEDEDEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDGQIYTPETE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 DTEVVG 127
 ||||||
 DB 121 DTEVVG 127

RESULT 4

Q91WK6 PRELIMINARY: PRT: 261 AA.
 AC Q91WK6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Similar to presentinlin 1.
 GN PSEN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Straussberg R.;
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014744; AAL14744.1; -
 DR MGD: MGI:1202717; Psen1.
 DR InterPro: IPR001108; Presentinlin.
 DR Pfam: PF01080; Presentinlin.
 SQ SEQUENCE 261 AA; 29849 MW; 16FB53FBE20E4AEB CRC64;

Query Match 18.6%; Score 87; DB 11; Length 261;
 Best Local Similarity 100.0%; Pred. No. 4, 7e-80;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 NSRQVDEDEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDGQIYTP 117
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 58 NSRQVDEDEDEDELTKYGAHVIMLFVPTLCMVVVAATIKSVSYTRKDGQIYTP 117
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 118 FTEDTEVVGORALHSILMAIMISIV 144
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 118 FTEDTEVVGORALHSILMAIMISIV 144

RESULT 5

Q90X08 PRELIMINARY: PRT: 468 AA.
 AC Q90X08;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Presentinlin 1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 NC NCBL_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EL4; TISSUE-BRAIN;
 RA Korade Mirnics Z., Keryanov S., Lovelock J., Corey S.J.;
 RT "Cloning of chicken presentinlin. ";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY043492; AAK95408.1; -
 DR InterPro: IPR001108; Presentinlin.
 DR Pfam: PF01080; Presentinlin.
 DR PRINTS: PRO1072; PRESENTINLIN.
 SQ SEQUENCE 468 AA; 52812 MW; B746BEDA3BAC0BFA CRC64;

Query Match 13.5%; Score 63; DB 13; Length 468;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-55;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 IHMKGPLRLQOAVYIMISALNALVFIKYPMTAMLIYAVSYDVAVLCPPKGPLRLMLV 272
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 214 IHMKGPLRLQOAVYIMISALNALVFIKYPMTAMLIYAVSYDVAVLCPPKGPLRLMLV 273
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 273 ETA 275
 ||||
 DB 274 ETA 276

RESULT 6

Q73869 PRELIMINARY: PRT: 384 AA.
 AC Q73869;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Psi protein (Fragment).
 GN Psi.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 NC NCBL_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337349; PubMed=9674592;
 RA Archer S., Hirano J., Diss J.K.J., Fraser S.P., Djangoz M.B.A.;
 RT "Expression and localization of the fish retina of a homologue of the
 RL Neuroreport 9:2049-2056 (1998).
 DR EMBL: Y17126; CAA76641.1; -


```
RT "Characterization of the amphioxus presentin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RL Gene 279:157-164(2001).
DR EMBL: AF369891; AAL40416.1; -.
DR EMBL: AF369890; AAL40416.1; JOINED.
DR InterPro: IPR000847; HTH_LYSR.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin.1.
DR PRINTS: PR01072; PRESENTIN.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOWN.1.
SQ SEQUENCE 504 AA; 53443 MW; 9C379AD0302859B4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 5; Length 504;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 409 ACPVAALIGLCTLLLAIFKKALPALPISITFGL 443
Db 446 ACPVAALIGLCTLLLAIFKKALPALPISITFGL 480

RESULT 11
O8WS59 PRELIMINARY; PRT; 525 AA.
ID O8WS59
AC O8WS59;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Presentin.
GN PS.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma
OX NCBI_Taxid=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21590369; Pubmed-11733140;
RA Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Alpalat R.;
RT "Characterization of the amphioxus presentin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RL Gene 279:157-164(2001).
DR EMBL: AF369891; AAL40414.1; -.
DR EMBL: AF369890; AAL40414.1; JOINED.
DR InterPro: IPR000847; HTH_LYSR.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin.1.
DR PRINTS: PR01072; PRESENTIN.
DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOWN.1.
SQ SEQUENCE 525 AA; 57598 MW; 2B14CF77A80F07DE CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 5; Length 525;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 409 ACPVAALIGLCTLLLAIFKKALPALPISITFGL 443
Db 467 ACPVAALIGLCTLLLAIFKKALPALPISITFGL 501

RESULT 12
O9D616 PRELIMINARY; PRT; 332 AA.
ID O9D616
AC O9D616;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 0 day neonate head cDNA, RIKEN full-length enriched library,
DE clone:4833416A15, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK014706; BAB29514.1; -.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin.1.
DR PRINTS: PR01072; PRESENTIN.
SQ SEQUENCE 332 AA; 37588 MW; 5728A69675A7DAD CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 11; Length 332;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 253 ISYVDLAVLCPKGPLRLVETAEGRNE 280
Db 259 ISYVDLAVLCPKGPLRLVETAEGRNE 286

RESULT 13
O96P32 PRELIMINARY; PRT; 390 AA.
ID O96P32
AC O96P32;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Presentin 2 transcript variant 2 (Fragment).
GN PSEN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu Y., Hu X., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF416718; AAL16812.1; -.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin.1.
DR NON_TER 390
FT 390
SQ SEQUENCE 390 AA; 43727 MW; A62C791CED9DCFB8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 4; Length 390;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 253 ISYVDLAVLCPKGPLRLVETAEGRNE 280
Db 259 ISYVDLAVLCPKGPLRLVETAEGRNE 286

RESULT 14
```

091VS3 ID 091VS3 PRELIMINARY; PRT; 448 AA.
 AC 091VS3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Presentin 2.
 GN PSEN2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC010403; AAI10403.1; -.
 DR MGD: MGI:109284; Psen2.
 DR InterPro: IPR001108; Presentin.
 DR Pfam: PF01080; Presentin; 1.
 DR PRINTS: PRO1072; PRESENTIN.
 SQ SEQUENCE 448 AA; 49964 MW; 2ED1DE7AFC3E0581 CRC64;

Query Match 6.0%; Score 28; DB 11; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ISYDLVAVLCPCGRLMLVETAEERNE 280
 DB 259 ISYDLVAVLCPCGRLMLVETAEERNE 286

RESULT 15
 090X07 ID 090X07 PRELIMINARY; PRT; 451 AA.
 AC 090X07;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Presentin 2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Korade Mirnics Z., Kerjanov S., Lovelock J., Corey S.J.;
 RT "Cloning of chicken presentinins."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY043493; AAK95409.1; -.
 DR InterPro: IPR001108; Presentin.
 DR Pfam: PF01080; Presentin; 1.
 DR PRINTS: PRO1080; Presentin.
 SQ SEQUENCE 451 AA; 50496 MW; 534E6364C627EBB0 CRC64;

Query Match 4.9%; Score 23; DB 13; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 EELTLKGAKHVIMLPVPLCM 93
 DB 83 EELTLKGAKHVIMLPVPLCM 105

RESULT 16
 09G038 ID 09G038 PRELIMINARY; PRT; 582 AA.
 AC 09G038;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Presentin.
 GN PS.

OS Helix lucorum.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Helicacea; Helicidae; Helix.
 OX NCBI_TaxID=31229;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rogaev E.I., Riazanskaya N.N., Dvorianchikov G., Grigorenko A.P.,
 RA Tyrsin O.;
 RT "Presentin gene isolated from mollusk Helix lucorum."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF197881; AAC28518.1; -.
 DR InterPro: IPR001108; Presentin.
 DR Pfam: PF01080; Presentin; 1.
 DR PRINTS: PRO1072; PRESENTIN.
 SQ SEQUENCE 582 AA; 63782 MW; 07934E7C452199F0 CRC64;

Query Match 4.3%; Score 20; DB 5; Length 582;
 Best Local Similarity 100.0%; Pred. No. 2.3e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 257 DLVAVLCPCGRLMLVETAAQ 276
 DB 294 DLVAVLCPCGRLMLVETAAQ 313

RESULT 17
 09S1K7 ID 09S1K7 PRELIMINARY; PRT; 397 AA.
 AC 09S1K7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative presentin.
 GN ATG29900.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Coppenhaver G.P., Preuss D., Niernman W.C., White O., Eissen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007113; AAD23630.1; -.
 DR InterPro: IPR001108; Presentin.
 DR Pfam: PF01080; Presentin; 1.
 DR PRINTS: PRO1072; PRESENTIN.
 SQ SEQUENCE 397 AA; 44011 MW; DE6804D6CA186783 CRC64;

Query Match 3.2%; Score 15; DB 10; Length 397;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 380 KIGLGDFIFYSVLVG 394
 DB 313 KIGLGDFIFYSVLVG 327

RESULT 18
Q9SDG2 PRELIMINARY; PRT; 478 AA.
AC Q9SDG2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE EST A0058092(S1536) corresponds to a region of the predicted gene.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; *Oryza*.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC clone:PO038F12.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000836; BA88182.1;
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin.1.
DR PRINTS: PRO1072; PRESENTIN.
SQ SEQUENCE 478 AA; 50100 MW; BC151E1021C96D3 CRC64;

Query Match 3.28; Score 15; DB 10; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 380 KLGGLDFEYSVLVG 394
DB 394 KLGGLDFEYSVLVG 408
|||||

RESULT 19
Q97UC3 PRELIMINARY; PRT; 334 AA.
AC Q97UC3;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical protein SSO3092.
CN SSO3092.
OS *Sulfolobus solfataricus*.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE-2133296; PubMed-1142726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweyer M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erruso G., Fletcher C., Gordon P.M.K.,
RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.B., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 334 AA; 37973 MW; 97622ED88EBF26BB CRC64;

Query Match 1.9%; Score 9; DB 17; Length 334;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LLLFFFSFI 180
DB 198 LLLFFFSFI 206
|||||

RESULT 20
Q9PV06 PRELIMINARY; PRT; 64 AA.
AC Q9PV06;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RAG1 protein (Fragment).
GN RAG1.
OS Plecopterosus altivialis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecopterosus.
OX NCBI_TaxID=61084;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAG1AYU;
RX MEDLINE-99398697; PubMed-10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137198; AAD54565.1;
FT NON_TER 1 1
SQ SEQUENCE 64 AA; 7139 MW; 4A931243C256DD35 CRC64;

Query Match 1.7%; Score 8; DB 13; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 419 CLTLLLA 426
DB 11 CLTLLLA 18
|||||

RESULT 21
Q9PV05 PRELIMINARY; PRT; 67 AA.
AC Q9PV05;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RAG1 protein (Fragment).
GN RAG1.
OS Harpadon sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Aulopiformes; Synodontidae; Harpadontinae; Harpadon.
OX NCBI_TaxID=94310;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAG1BDUCK;
RX MEDLINE-99398697; PubMed-10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137199; AAD54566.1;
FT NON_TER 1 1
SQ SEQUENCE 67 AA; 7452 MW; 3FF12959F4C8D08A CRC64;

Query Match 1.7%; Score 8; DB 13; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 419 CLTLLLA 426
DB 14 CLTLLLA 21
|||||

RESULT 22
Q93EF9 PRELIMINARY; PRT; 83 AA.
ID O93EF9
AC O93EF9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative sec-independent protein translocase (Fragment).
GN PANC.
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group.
OC Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3B1;
RA Ge Z., Feng Y., Fox J.G.;
RT "Helicobacter hepaticus genome: construction of an ordered cosmid library and sequence analysis of the selected genomic regions.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF358706; AAL16696.1; -;
DR InterPro: IPR002033; Translocase.
DR Pfam: PF00902; UPF0032; 1.
FT NON_TER 1
FT 83
SQ SEQUENCE 83 AA; 9174 MW; D887FA1218BD7F3D CRC64;
Query Match 1.7%; Score 8; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 65 QDEEDEE 72
Db 66 QDEEDEE 73
RESULT 23
Q8QTD1 PRELIMINARY; PRT; 104 AA.
ID O8QTD1
AC O8QTD1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE WSSV320.
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RX MEDLINE=20517548; PubMed=11062040;
RA Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT "Identification and characterization of a shrimp white spot syndrome virus (WSSV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase.";
RL Virology 277:100-110(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RX MEDLINE=21844071; PubMed=11853398;
RA Chen L.T., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells.";
RL Virology 293:44-53(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RA Lo C.-F., Kou G.-H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF440570; AAL89188.1; -;
SQ SEQUENCE 104 AA; 12296 MW; 4F59C6883BC7941F CRC64;
Query Match 1.7%; Score 8; DB 12; Length 104;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 SLILLEFF 177
Db 28 SLILLEFF 35
RESULT 24
Q8VAM0 PRELIMINARY; PRT; 105 AA.
ID Q8VAM0
AC Q8VAM0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE WsV265.
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21548311; PubMed=11689662;
RA Yang F., He J., Lin X., Li O., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform virus.";
RL J. Virol. 75:11811-11820(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang F., He J., Lin X., Li O., Pan D., Zhang X., Xu X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF332093; AAL33268.1; -;
SQ SEQUENCE 105 AA; 12409 MW; 7812D728683BC794 CRC64;
Query Match 1.7%; Score 8; DB 12; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 SLILLEFF 177
Db 28 SLILLEFF 35
RESULT 25
Q63071 PRELIMINARY; PRT; 139 AA.
ID Q63071
AC Q63071;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
DE Brahma protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=97154526; PubMed=9001244;
RA Oestlund-Farrants A.K., Blomquist P., Kwon H., Wrange O.;
RT "Glucocorticoid receptor-glucocorticoid response element binding site stimulates nucleosome disruption by the SWI/SNF complex.";
RL Mol. Cell. Biol. 17:895-905(1997).
DR EMBL: X99723; CAA68062.1; -;
FT NON_TER 1
FT 139
SQ SEQUENCE 139 AA; 16768 MW; B1A6F6886C011560 CRC64;
Query Match 1.7%; Score 8; DB 11; Length 139;
Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 EDEDEDE 71
|||||||

Db 3 EDEDEDE 10

RESULT 26
08VOL7 PRELIMINARY; PRT: 288 AA.

AC 08VOL7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative ABC transporter permease protein B.
GN BATN1953.0RF9.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=344;
RA Bricker B.J.;
RT "In1953, a new element from Brucella abortus";
RL EMBL: AF54951: AAL5931.1: -
DR EMBL: AF54951: AAL5931.1: -
DR InterPro: IPR000515: BPD_transp.
DR Pfam: PF00528: BPD_transp. 1.
DR PROSITE: PS00402: BPD_TRANS_PNN_MEMBER; UNKNOWN_1.
SQ SEQUENCE 288 AA; 31696 MW; B5C20EA20BCFDBE CRC64;

Query Match 1.7%; Score 8; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 SLLELFF 177
|||||||

Db 27 SLLELFF 34

RESULT 27
09SLP4 PRELIMINARY; PRT: 314 AA.
AC 09SLP4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bulb chitinase-1.
GN TBCL.
OS Tulipa bakeri.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
OX NCBI_TaxID=110455;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamagami T., Tsutsumi K., Ishiguro M.;
RT "CDNA cloning, sequence, and expression of tulip bulb chitinase-1";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
HYDROLASES).
EMBL: AB035668: BAA88408.1: -
DR InterPro: IPR000677: 2S_Globulin
DR InterPro: IPR001579: Chitinase_18/2.
DR InterPro: IPR001233: Glyco_hydro_18.
DR Pfam: PF00704: Glyco_hydro_18; 1.
DR PRINTS: PR00551: 2SGLOBULIN.
DR PROSITE: PS01095: CHITINASE_18; 1.
KW Glycosidase; Hydrolase
SQ SEQUENCE 314 AA; 35090 MW; AE9F5D31522A03E7 CRC64;

Query Match 1.7%; Score 8; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 23;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 SLLLEFF 176
|||||||

Db 7 SLLLEFF 14

RESULT 28
08ZFL5 PRELIMINARY; PRT: 317 AA.

AC 08ZFL5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative exported protein.
GN YPOL66.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Hitchen P.G., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RL Nature 413:523-527(2001).
DR EMBL: AJ414149: CAC90506.1: -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 317 AA; 34974 MW; A032A0DF974481D4 CRC64;

Query Match 1.7%; Score 8; DB 16; Length 317;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 LIISLIL 173
|||||||

Db 9 LIISLIL 16

RESULT 29
09RR94 PRELIMINARY; PRT: 347 AA.
AC 09RR94;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein DR2600.
GN DR2600.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans RI";
RL Science 286:1571-1577(1999).

DR EMBL: AE002089; AAF12144.1; -.
DR TIGR: DR2600; -.
DR InterPro: IPR002965; P-rich_extensn.
DR PRINTS: PR01217; PRICHTEXTENS.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 347 AA; 34908 MW; 1C3CEBA9C1AEAE4C CRC64;

Query Match 1.7%; Score 8; DB 16; Length 347;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 RSTPESRA 359
DB 274 RSTPESRA 281

RESULT 30

ID 060121 PRELIMINARY; PRT; 354 AA.

AC 060121;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hypothetical 39.3 kDa protein Cl65.07C in chromosome II.
GN SPBC165.07C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Beck A.,
RA Reinhardt R.;
RU Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
DR EMBL: AL023554; CAI19027.1; -.
DR InterPro: IPR001107; Band_7.
DR InterPro: IPR001972; Stomatin.
DR Pfam: PF01145; Band_7; 1.
DR SMART: SM00244; PHB; 1.
DR PROSITE: PS01270; BAND_7; FALSE-NEG.
KW Hypothetical protein.
SQ SEQUENCE 354 AA; 39274 MW; 66B09E6A12BDC30 CRC64;

Query Match 1.7%; Score 8; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 395 KASATASG 402
DB 265 KASATASG 272

RESULT 31

ID 077794 PRELIMINARY; PRT; 369 AA.

AC 077794;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Multidrug resistance protein MDRL (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=9822958; PubMed=9568108;
RA Steingold S.F., Sharp N.J., McSahan M.C., Hughes C.S., Dunn S.E.,
RA Page R.L.;
*Characterization of canine MDRL mRNA: its abundance in drug resistant

RT cell lines and in vivo.;
RL Anticancer Res. 18:393-400(1998).
DR EMBL: AF092810; AAC62505.1; -.
DR InterPro: IPR001140; ABCtranspRTM.
DR Pfam: PF00664; ABC_membrane; 1.
FT NON_TER 1
SQ SEQUENCE 369 AA; 40894 MW; DA2EC6CBF3328DBE CRC64;

Query Match 1.7%; Score 8; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLLLA1 427
DB 300 LTLLLA1 307

RESULT 32

ID 0966H2 PRELIMINARY; PRT; 379 AA.

AC 0966H2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein R0569.2.
GN R0569.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA R Wilson.;
RT "The sequence of C. elegans cosmid R0569.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006678; AAK68392.1; -.
DR InterPro: IPR001622; K+channel_pore.
SQ SEQUENCE 379 AA; 43265 MW; 551B265BB97FFBD2 CRC64;

Query Match 1.7%; Score 8; DB 5; Length 379;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 413 AIIIGLCL 420
DB 270 AIIIGLCL 277

RESULT 33

ID 092PX3 PRELIMINARY; PRT; 392 AA.

AC 092PX3;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE At2g18410 protein.
GN AT2G18410.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBITaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Unam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006439; AAD15496.1; -
 SQ SEQUENCE 392 AA: 43648 MW: 57505E9A96D9DCA CRC64;
 Query Match 1.7%; Score 8; DB 10; Length 392;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 364 LSSSILAG 371
 |||||||
 Db 44 LSSSILAG 51

RESULT 34
 09V4U2 PRELIMINARY; PRT; 519 AA.
 AC 09V4U2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG8690 protein.
 GN CG8690
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBITaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Fodor C., Gabriellian A.E., Gang N.S., Galbart W.W., Glasser K.,
 RA Goddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegian C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry B., Morris J., Mostreffi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacible J.M.,
 RA Palazzolo M., Pittman K.A., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003837; AAF59083.1; -
 DR HSSP: P21332; 1UOK
 DR FlyBase: FBgn0033297; CG8690.
 DR InterPro: IPR000461; Alpha_amyase.
 DR Pfam: PF00128; alpha-amyase; 1.
 SQ SEQUENCE 519 AA: 59513 MW: 01B36FB58CF9A57 CRC64;
 Query Match 1.7%; Score 8; DB 5; Length 519;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 420 LTLILLAI 427
 |||||||
 Db 7 LTLILLAI 14

RESULT 35
 052557 PRELIMINARY; PRT; 522 AA.
 AC 052557;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Rifamycin efflux protein.
 GN RIFP
 OS Amycolatopsis mediterranei (Nocardia mediterranei).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
 NC NCBITaxID=33910;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8699;
 RX MEDLINE=98174059; PubMed=9512878;
 RA August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Yu T.W.,
 RA Taylor M., Hoffmann D., Kim C.G., Zhang X., Hutchinson C.R.,
 RA Floss H.G.;
 RT "Biosynthesis of the ansamycin antibiotic rifamycin: deductions from
 the molecular analysis of the rif biosynthetic gene cluster of
 Amycolatopsis mediterranei 8699.";
 RL Chem. Biol. 5:69-79(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8699;
 RX MEDLINE=98165773; PubMed=9497318;
 RA Kim C.G., Yu T.W., Fryhle C.B., Handa S., Floss H.G.;
 RT "3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the
 formation of the precursor of mc7N units in rifamycin and related
 antibiotics.";
 RL J. Biol. Chem. 273:6030-6040(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8699;
 RX MEDLINE=21201076; PubMed=11278540;
 RA Yu T.-W., Mueller R., Mueller M., Zhang X., Draeger G., Kim C.-G.,

RA Leistner E., Floss H.G.;
RT Mutational analysis and reconstituted expression of the biosynthetic
genes involved in the formation of 3-amino-5-hydroxybenzoic acid, the
starter unit of rifamycin biosynthesis in Amycolatopsis mediterranei
RT 5699."
RL J. Biol. Chem. 276:12546-12555(2001).
RN (14)
RP SEQUENCE FROM N.A.
RC STRAIN-S699;
RA August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Hutchinson C.R.,
Floss H.G.;
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AF040570; AAC0125.1; -
DR InterPro: IPR004638; Efflux_Emb.
DR InterPro: IPR003662; sub.transporter.
DR TIGRFAMs: TIGR00711; efflux_Emb.1.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 522 AA; 53208 MW; F09E79A9579638EF CRC64;

Query Match 1.7%; Score 8; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 WLILAVIS 254
| | | | |
DB 16 WLILAVIS 23

RESULT 36
Q03982 PRELIMINARY; PRT; 538 AA.
ID 003982;
AC 003982;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P-glycoprotein.
GN PGP-1.
OS Cricetus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE-91154265; PubMed-1671863;
RA Devine S.E., Hussain A., Davide J.P., Melera P.W.;
RT "Full length and alternatively spliced pgp-1 transcripts in multidrug
resistant Chinese hamster lung cells.";
RL J. Biol. Chem. 266:4545-4555(1991).
CC 1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: M59252; AAA37003.1; -
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCTransporter.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00664; ABC_membrane.1.
DR Pfam: PF00005; ABC_tran.1.
DR PRODOM: PD000006; ABC_transporter.1.
DR SMART: SM00382; AAA.1.
DR PROSITE: PS00211; ABC_TRANSPORTER.1.
KW ATP-binding; Transport.
SQ SEQUENCE 538 AA; 59433 MW; 09A82E1818AE09C3 CRC64;

Query Match 1.7%; Score 8; DB 11; Length 538;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLILLAI 427
| | | | |
DB 116 LTLILLAI 123

RESULT 37
Q08569 PRELIMINARY; PRT; 563 AA.
ID 08569;
AC 08569;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to SWI/SNF related, matrix associated, actin dependent
DE regulator of chromatin, subfamily a, member 4 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC023186; AAH23186.1; -
FT NON_TER 1
SQ SEQUENCE 563 AA; 65393 MW; D90F4D3A2802B70F CRC64;

Query Match 1.7%; Score 8; DB 11; Length 563;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 EODEEDE 71
| | | | |
DB 204 EODEEDE 211

RESULT 38
Q097178 PRELIMINARY; PRT; 581 AA.
ID 097178;
AC 097178;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Predicted membrane protein.
GN CAC1775.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE-21359325; PubMed-11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007686; AAK79740.1; -
DR InterPro: IPR000566; Lipocin_cytfABP.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 581 AA; 64675 MW; 34A8C602E5149EF CRC64;

Query Match 1.7%; Score 8; DB 16; Length 581;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 187 KTYNVAVD 194
| | | | |
DB 232 KTYNVAVD 239

RESULT 39
Q095052 PRELIMINARY; PRT; 628 AA.
ID 095052

```

AC 095052;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE BRG-1-Human (Fragment).
GN SMARCA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Brower A., Stillwagen S.,
RA Phen H., Velasco N., Do L., Regala W., Terry A., Carnes J.,
RA Danganan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Atlix C., Lucase S., Bruce R., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an 800 kb region in 19p13.2 between PDE4A and
RT DIS5584."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006127; AAC97986.1; -.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR000330; SNF2_N.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00176; SNF2_N; 1.
DR SMART: SM00490; HELICC; 1.
KW ATP-binding; Helicase.
FT NON_TER 1
FT TER 628
SQ SEQUENCE 628 AA; 73264 MW; 367164900E01A45B CRC64;

Query Match
Best Local Similarity 1.7%; Score 8; DB 4; Length 628;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 EDDDEDE 71
Db 442 EDDDEDE 449

RESULT 40
O8BN06 PRELIMINARY; PRT; 668 AA.
AC O8BN06;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Multidrug resistance p-glycoprotein (Fragment).
GN MDRI.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Uozumi K., Nakaichi M.;
RT "Canine MDR."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB066299; BAB83959.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001440; ABCtransporter.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 1.
DR Prodom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
FT NON_TER 1
FT TER 668
SQ SEQUENCE 668 AA; 73546 MW; F8CD80F7C934B31A CRC64;

```

```

Query Match
Best Local Similarity 1.7%; Score 8; DB 6; Length 668;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 420 LTLILLAI 427
Db 608 LTLILLAI 615

RESULT 41
O8R0K1 PRELIMINARY; PRT; 749 AA.
AC O8R0K1;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 87.3 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026672; AAH26672.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT TER 749
SQ SEQUENCE 749 AA; 87280 MW; 1FB0CB80561A55BA CRC64;

Query Match
Best Local Similarity 1.7%; Score 8; DB 11; Length 749;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 EDDDEDE 71
Db 391 EDDDEDE 398

RESULT 42
O63928 PRELIMINARY; PRT; 1022 AA.
AC O63928;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Brg1 protein (Fragment).
GN SMARCA4 OR BRG1.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94123856; PubMed=7904967;
RA Randazzo F.M., Khavari P., Crabtree G., Tankun J., Rossant J.;
RT "Brg1: a putative murine homologue of the Drosophila brama gene, a
RT homeotic gene regulator."
RL Dev. Biol. 161:229-242(1994).
DR EMBL; S68108; AAC60670.1; -.
DR MGD; MGI:88192; Smarca4.
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR000330; SNF2_N.
DR Pfam: PF00439; bromodomain; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00176; SNF2_N; 1.
DR PRINTS: PR00503; BROMODOMAIN.
DR SMART: SM00297; BROMO; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICC; 1.

```

DR PROSITE; PS00633; BROMODOMAIN_1; 1.
 DR PROSITE; PS50014; BROMODOMAIN_2; 2.
 KW ATP-binding; Helicase.
 FT NON_TER 1
 SQ SEQUENCE 1022 AA; 117518 MW; 24F9DB4CA110436 CRC64;

Query Match 1.7%; Score 8; DB 11; Length 1022;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 64 DEDEDE 71
 |||||||
 DB 663 EDEDEDE 670

RESULT 43
 ID 09TSU2 PRELIMINARY; PRT; 1163 AA.
 AC 09TSU2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Multi-drug resistance related (Fragment).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN 11
 RP SEQUENCE FROM N.A.

RA Okai Y., Nakamura N., Matsusiro H., Kato H., Setoguchi A., Yazawa M.,
 RA Okuda M., Watarai T., Hasegawa A., Tsujimoto H.;
 RT "Molecular analysis of multidrug resistance in lymphoma cells in the
 RT cat."
 RU Am. J. Vet. Res. 0:0-0(1999).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AB029153; BAA87071.1; -.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransprtTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR Prodom: PD000006; ABC_transportr; 2.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 DR ATP-binding; Transport.
 KW NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 1163 AA; 128511 MW; 1B5BA13776A93A26 CRC64;

Query Match 1.7%; Score 8; DB 6; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 420 LTLILLAI 427
 |||||||
 DB 798 LTLILLAI 805

RESULT 44
 ID 060502 PRELIMINARY; PRT; 1169 AA.
 AC 060502;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE P-glycoprotein.
 GN Pgp-1.
 OS Cricetus sp.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10031;
 RN 11

RP SEQUENCE FROM N.A.
 RC TISSUE-LONG;
 RX MEDLINE=91154265; PubMed=1671863;
 RA Devine S.E., Hussain A., Davide J.P., Melera P.W.;
 RT "Full length and alternatively spliced pgp-1 transcripts in multidrug
 RT resistant Chinese hamster lung cells."
 RL J. Biol. Chem. 266:4545-4553(1991).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; M59254; AAA37005.1; -.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransportrTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR Prodom: PD000006; ABC_transportr; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1169 AA; 128939 MW; 72E25B7CE29DC185 CRC64;

Query Match 1.7%; Score 8; DB 11; Length 1169;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 420 LTLILLAI 427
 |||||||
 DB 747 LTLILLAI 754

RESULT 45
 ID 097140 PRELIMINARY; PRT; 1231 AA.
 AC 097140;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Prespore-specific protein (Fragment).
 GN PSPC.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
 OX NCBI_TaxID=44689;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Hsu Y.-S., Chang W.-T., Newell P.C., Gross J.D.;
 RT "A repressor controlling cell-type specific expression in
 RT Dictyostelium."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104350; AAD16881.1; -.
 FT NON_TER 1231
 SQ SEQUENCE 1231 AA; 138196 MW; 074956F6094F5A58 CRC64;

Query Match 1.7%; Score 8; DB 5; Length 1231;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 66 DEDEDEEL 73
 |||||||
 DB 1043 DEDEDEEL 1050

RESULT 46
 ID 09JK64 PRELIMINARY; PRT; 1272 AA.
 AC 09JK64;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Multidrug resistance protein 1a.
 GN PGY1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WTSTAR: TISSUE-LIVER;
RA Hooiveld G.J.E.J., Wilms J.W.J., Hagenbuch B., Jansen P.L.M.,
RT Meijer D.K.F., Muller M.;
RT "Cloning and functional characterization of the rat multidrug
resistance protein Mdr1a";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: AF257746; AAF69007.1; -
DR InterPro: IPR003593; AAA_Atpase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
DR ATP-binding; Transport.
KW SEQUENCE 1272 AA; 140326 MW; B5C1DF89DFC986C5 CRC64;

Query Match 1.7%; Score 8; DB 11; Length 1272;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LLLLLLAI 427
DB 849 LLLLLLAI 856

RESULT 47
0924L6
ID 0924L6 PRELIMINARY; PRT; 1272 AA.
AC 0924L6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE P-glycoprotein.
GN MDR1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Yamazaki M., Leake B.F., Kim R.B.;
RT "Molecular Cloning of Rat Mdr1a cDNA";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF286167; AAK83023.1; -
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN; 2.
SQ SEQUENCE 1272 AA; 140343 MW; D9A17457362DA0ED CRC64;

Query Match 1.7%; Score 8; DB 11; Length 1272;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LLLLLLAI 427
DB 849 LLLLLLAI 856

RESULT 48
046605
ID 046605 PRELIMINARY; PRT; 1280 AA.
AC 046605;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Multidrug resistance p-glycoprotein.
GN MDR1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Puel O., Lepage J.F., Alvinerie M., Gallier P., Pineau T.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: AF045016; AAC02113.1; -
DR InterPro: IPR003593; AAA_Atpase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
DR ATP-binding; Transport.
KW SEQUENCE 1280 AA; 141524 MW; 762PD5AF4C73306 CRC64;

Query Match 1.7%; Score 8; DB 6; Length 1280;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LLLLLLAI 427
DB 858 LLLLLLAI 865

RESULT 49
002793
ID 002793 PRELIMINARY; PRT; 1285 AA.
AC 002793;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Multidrug resistance protein-1.
GN MDR1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Longley M., Crawford A.M.;
RT "Ovine mdr1 gene";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL: U78609; AAB58489.1; -
DR InterPro: IPR003593; AAA_Atpase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
DR ATP-binding; Transport.
KW SEQUENCE 1285 AA; 142020 MW; 90153E617C44856F CRC64;

Query Match 1.7%; Score 8; DB 6; Length 1285;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LLLLLLAI 427
DB 862 LLLLLLAI 869

RESULT 50

```

002569
ID 002569 PRELIMINARY; PRT: 1726 AA.
AC 002569;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Merozoite surface antigen 1 precursor.
GN PV200.
OS Plasmodium vivax (Strain Belem).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=31273;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BELEM:
RX MEDLINE-91219506; PubMed-2023952;
RA del Portillo H.A., Longacre S., Khouri E., David P.H.;
RT "Primary structure of the merozoite surface antigen 1 of Plasmodium
RT vivax reveals sequences conserved between different Plasmodium
RT species.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4030-4034(1991).
DR EMBL; M60807; AAA63427.1;
DR InterPro; IPR000561; EGF-like.
DR Pfam; PF00008; EGF; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 17 POTENTIAL.
FT CHAIN 18 1726 MEROZOITE SURFACE ANTIGEN 1.
SQ SEQUENCE 1726 AA; 194434 MW; BA0DCD8333C6C727 CRC64;

Query Match 1.7%; Score 8; DB 5; Length 1726;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 173 LFFFSFI 180
DB 4 LFFFSFI 11

```

Search completed: February 6, 2003, 14:20:37
 Job time : 89.3506 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:14:41 ; Search time 17.4398 seconds
(without alignments)
1110.644 Million cell updates/sec

Title: US-09-689-159A-2

Perfect score: 467
Sequence: 1 MTELPAPLSTYFQNAQWSEDN.....ATDYLVQPFMDLAFHQFYI 467

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	366	78.4	467	1 PSN1_HUMAN	P49768 homo sapien
2	107	22.9	467	1 PSN1_MICMU	P79802 microcebus
3	104	22.3	468	1 PSN1_RAT	P97887 rattus norv
4	97	20.8	467	1 PSN1_MOUSE	P49769 mus musculu
5	95	20.3	478	1 PSN1_BOVIN	O9xt97 bos taurus
6	59	12.6	433	1 PSN1_XENLA	O12976 xenopus lae
7	28	6.0	445	1 PSN2_MICMU	P79801 microcebus
8	28	6.0	448	1 PSN2_HUMAN	P49810 homo sapien
9	28	6.0	448	1 PSN2_MOUSE	O61144 mus musculu
10	28	6.0	448	1 PSN2_RAT	O88777 rattus norv
11	28	6.0	449	1 PSN2_BOVIN	O9xt96 bos taurus
12	27	5.8	449	1 PSN2_XENLA	O12977 xenopus lae
13	22	4.7	541	1 PSN1_DROME	O02194 drosophila
14	18	3.9	444	1 PSN1_CAEEL	P52166 caenorhabdi
15	15	3.2	453	1 PSN1_ARATH	O64668 arabidopsis
16	15	1.7	103	1 YGBO_ECOLI	O46894 escherichia
17	17	1.7	176	1 P22P1_RAT	P22282 rattus norv
18	18	1.7	263	1 NGN2_MOUSE	P70447 mus musculu
19	19	1.7	707	1 DCOB_LEIDO	P27116 leishmania
20	20	1.7	1276	1 MDR3_MOUSE	P21448 cricetus
21	8	1.7	1276	1 MDR3_MOUSE	P21447 mus musculu
22	8	1.7	1280	1 MDR1_HUMAN	P08183 homo sapien
23	8	1.5	58	1 TEM1_HUMAN	P79876 rana tempor
24	24	1.5	61	1 TEM1_RANTE	P79874 rana tempor
25	25	1.5	61	1 TEM1_RANTE	P79875 rana tempor
26	26	1.5	65	1 GAE3_RANTR	P80399 rana rugosa
27	27	1.5	66	1 RLXN_RANCA	P39084 rana catesb
28	28	1.5	72	1 ATP1_BACCA	P41015 bacillus ca
29	29	1.5	72	1 ATP1_BACCP3	P00845 bacillus ps
30	30	1.5	72	1 ATP1_BACST	P42011 bacillus st
31	31	1.5	106	1 YWU0_CAEEL	P34485 caenorhabdi
32	32	1.5	120	1 R22A_YEAST	P05749 saccharomyc
33	33	1.5	167	1 LSPA_CHLTR	O84413 chlamydia t

34	7	1.5	169	1 YFJ6_YEAST	P43604 saccharomyc
35	7	1.5	170	1 Y129_MERJA	O57553 methanococc
36	7	1.5	173	1 OLE1_ARATH	P29525 arabidopsis
37	7	1.5	175	1 OLE2_BRANA	P29111 brassica na
38	7	1.5	183	1 OLE3_BRANA	P29109 brassica na
39	7	1.5	208	1 US10_HSVB	P30817 simian herp
40	7	1.5	213	1 UBC_ASPF2	P25869 african swi
41	7	1.5	243	1 RAD3_SYNY2	P52601 synechocyst
42	7	1.5	271	1 ISPE_THEMA	O9x183 thermotoga
43	7	1.5	280	1 YITP_BACSU	P39803 bacillus su
44	7	1.5	286	1 MCM1_YEAST	P11746 saccharomyc
45	7	1.5	291	1 Z1PA_VIBCH	O9kt42 vibrio chol
46	7	1.5	296	1 SAPC_ECOLI	O47624 escherichia
47	7	1.5	300	1 NKX1_HISBI	O46383 bison bison
48	7	1.5	321	1 D7_AEDAE	P18153 aedes aegypt
49	7	1.5	323	1 RAD1_SCHPO	P22153 schizosacch
50	7	1.5	326	1 YE09_SYNY3	P73594 synechocyst
51	7	1.5	339	1 CRTB_RHCCA	P17056 rhodobacter
52	7	1.5	340	1 Y100_ARCFU	O28474 archaeoglob
53	7	1.5	347	1 NU2M_DIDMA	P41305 didelphis m
54	7	1.5	348	1 NU2M_MACRO	P92660 macropus ro
55	7	1.5	350	1 GANA_ASPAC	P48842 aspergillus
56	7	1.5	351	1 PSBD_GALSI	P28253 galderia s
57	7	1.5	351	1 PSBD_ODOSI	P49478 odontella s
58	7	1.5	351	1 PSBD_PORPU	P51357 porphyra pu
59	7	1.5	352	1 PSBD_CHLYU	P56319 chlorella v
60	7	1.5	352	1 PSBD_CYAPA	P48079 cyanophora
61	7	1.5	352	1 PSBD_NEPOL	O9t100 nephrolepiml
62	7	1.5	352	1 PSBD_PEA	P06006 pisum sativ
63	7	1.5	352	1 PSBD_SPIOL	P06005 spinacia ol
64	7	1.5	352	1 PSBD_SYNP2	P20898 synechococc
65	7	1.5	352	1 PSBD_SYNP7	P11005 synechococc
66	7	1.5	352	1 PSBD_STNY3	P09182 synechocyst
67	7	1.5	353	1 PSBD_ARATH	P56761 arabidopsis
68	7	1.5	353	1 PSBD_HORVU	P1849 hordeum vul
69	7	1.5	353	1 PSBD_MAIZE	P48184 zeamays (m
70	7	1.5	353	1 PSBD_MARPO	P06404 marchantia
71	7	1.5	353	1 PSBD_ORNSA	O9mt11 cenothera h
72	7	1.5	353	1 PSBD_ORNSA	P12095 oryza sativ
73	7	1.5	353	1 PSBD_PINTH	P41644 pinus thunb
74	7	1.5	353	1 PSBD_POPE	O9xq88 populus del
75	7	1.5	353	1 PSBD_SECC	P10803 secale cere
76	7	1.5	353	1 PSBD_TOBAC	P06403 nicotiana t
77	7	1.5	353	1 PSBD_WHEAT	O36814 triticum ae
78	7	1.5	353	1 YD53_ARCFU	O28918 archaeoglob
79	7	1.5	354	1 PSBD_MESV	O2mu22 mesotigma
80	7	1.5	361	1 SEPI_DROME	P42207 drosophila
81	7	1.5	361	1 SEPI_HUMAN	O15019 homo sapien
82	7	1.5	361	1 SEPI_MOUSE	P42208 mus musculu
83	7	1.5	370	1 RECF_BACSU	P05651 bacillus su
84	7	1.5	375	1 GUN_ROBSP	P23044 robillarda
85	7	1.5	377	1 FDN_EMENT	O03114 emeticella
86	7	1.5	379	1 VPP_BPMU	P08858 bacterioph
87	7	1.5	380	1 NTG2_YEAST	O08214 saccharomyc
88	7	1.5	381	1 CYB_ANTMI	O63534 antechinus
89	7	1.5	381	1 CYB_ANTSM	O33865 antechinus
90	7	1.5	381	1 CYB_DASYI	O34399 dasynus vl
91	7	1.5	381	1 CYB_MURLO	O35070 murxelia lon
92	7	1.5	381	1 CYB_PLANE	O35675 planigale t
93	7	1.5	396	1 SX11_CHICK	P48445 gallus galli
94	7	1.5	397	1 PACA_BPPI	P28813 bacterioph
95	7	1.5	404	1 YVBF_BACSU	P74748 bacillus su
96	7	1.5	405	1 SPI2_HUMAN	O75880 homo sapien
97	7	1.5	409	1 NU4M_ASCSU	P24880 ascaris suu
98	7	1.5	409	1 PROA_MYCLE	O9cbe5 mycobacteri
99	7	1.5	411	1 YAL2_SCHPO	O09665 schizosacch
100	7	1.5	415	1 PROA_BACSU	P39821 bacillus su
101	7	1.5	415	1 PROA_MYCTU	P71921 bacillus b
102	7	1.5	419	1 RNBP_MOUSE	P82313 mus musculu
103	7	1.5	421	1 NXP2_CAEEL	O9xv68 caenorhabdi
104	7	1.5	434	1 T147_HUMAN	O60664 homo sapien
105	7	1.5	440	1 Y284_AOUAE	O66658 aquifex aeo
106	7	1.5	440	1 YGR4_YEAST	P53107 saccharomyc

107	7	1.5	454	1	MYC2_MARMO	P20389	marmota mon	180	6	1.3	78	1	VNS7_CVPEFS	P05992	porcine tra
108	7	1.5	454	1	MYC2_SPEBE	Q64210	spermophilu	181	6	1.3	87	1	DEFA_RAT	Q62713	rattus norv
109	7	1.5	460	1	MYC2_MARMO	Q61976	marmota mon	182	6	1.3	87	1	DEFA_RAT	Q92113	rattus norv
110	7	1.5	462	1	MYC2_MOUSE	P03966	mus musculus	183	6	1.3	88	1	SABP_SARPE	P31529	sarcophaga
111	7	1.5	462	1	MYC2_RAT	P03379	rattus norv	184	6	1.3	88	1	YMS0_ARCFU	O28053	archaeoglob
112	7	1.5	464	1	MYC2_HUMAN	P04198	homo sapien	185	6	1.3	89	1	EF1B_METTH	O22734	methanobact
113	7	1.5	477	1	EX02_DROPS	Q24617	drosophila	186	6	1.3	93	1	DEFA_RAT	Q62714	rattus norv
114	7	1.5	482	1	MTA1_ANASP	P70602	anaeabena sp	187	6	1.3	93	1	RL23_HELPY	P56048	helicobacte
115	7	1.5	498	1	VGLX_PVRI	P07562	pseudorobie	188	6	1.3	100	1	URE3_RHIME	P42887	rhizobium m
116	7	1.5	507	1	IRX3_MOUSE	P81067	mus musculus	189	6	1.3	100	1	THRP_HUMAN	P20962	homo sapien
117	7	1.5	509	1	MTB1_BACST	P70886	bacillus st	190	6	1.3	101	1	VE4_HPVA1	P27953	human papil
118	7	1.5	512	1	SYM_MCPN	P37501	mycoplasma	191	6	1.3	101	1	YG09_YEAST	P53116	saccharomyc
119	7	1.5	532	1	YABM_BACSU	P37555	bacillus su	192	6	1.3	102	1	AP42_RAT	P04638	rattus norv
120	7	1.5	535	1	HTRI_HALN1	P33741	halobacteri	193	6	1.3	102	1	HSP3_MOUSE	Q62100	mus musculus
121	7	1.5	535	1	HTRI_HALSA	P33955	halobacteri	194	6	1.3	104	1	HSP3_RAT	Q64256	rattus norv
122	7	1.5	555	1	GPI_CHIRE	Q9f066	chlamydomon	195	6	1.3	106	1	YF81_ARCFU	O28691	archaeoglob
123	7	1.5	556	1	DPOL_MHV6	P11292	woodchuck h	196	6	1.3	108	1	CSGC_SALTY	P55527	salmoneila
124	7	1.5	566	1	CC45_HUMAN	O75419	homo sapien	197	6	1.3	109	1	Y819_METUA	Q58229	methanococc
125	7	1.5	591	1	YN48_YEAST	P42846	saccharomyc	198	6	1.3	110	1	CSGC_ECOLI	P52107	escherichia
126	7	1.5	599	1	CENB_MOUSE	P27790	mus musculus	199	6	1.3	110	1	YB5A_METUA	P81316	methanococc
127	7	1.5	606	1	CENB_CRIGR	P48988	cricetus	200	6	1.3	111	1	PRO2_BOVIN	Q09430	bos taurus
128	7	1.5	630	1	YCF2_ORNVI	P31569	oenothera v	201	6	1.3	114	1	HMG4_CHITE	P40622	chironomus
129	7	1.5	632	1	YK65_CABEL	P46555	caenorhabdi	202	6	1.3	114	1	NLR2_LYCES	P27056	lycopersico
130	7	1.5	665	1	PTH2_STY3	P73179	synchocyst	203	6	1.3	114	1	NLR2_TOBAC	Q03461	nicotiana t
131	7	1.5	687	1	WHIT_STY3	P10090	drosophila	204	6	1.3	116	1	VAMS_HUMAN	O95183	homo sapien
132	7	1.5	694	1	NUCL_CHICK	P15771	gallus gall	205	6	1.3	119	1	TBCA_SCHPO	O97703	schizosacch
133	7	1.5	713	1	NUCL_MESAU	P08199	mesocricetu	206	6	1.3	120	1	NU3C_LUPLU	P52765	lupinus lut
134	7	1.5	721	1	YCF2_OENPI	P31568	oenothera p	207	6	1.3	126	1	PAND_XYTRA	O90977	xytella fas
135	7	1.5	726	1	FAT4_VIBAN	P11461	vibrio angu	208	6	1.3	126	1	VEBC_RAT	Q35357	rattus norv
136	7	1.5	742	1	NEB1_HUMAN	Q9u1j8	homo sapien	209	6	1.3	127	1	NRPF_ECO57	O8X555	escherichia
137	7	1.5	748	1	PT1P_ECOLI	P37177	escherichia	210	6	1.3	127	1	NRPF_ECOLI	P32711	escherichia
138	7	1.5	766	1	SMZ7_BRARE	P37178	salmonella	211	6	1.3	127	1	TRX3_YEAST	P23712	saccharomyc
139	7	1.5	830	1	JTP2_MOUSE	O9Y9X4	brachydanio	212	6	1.3	129	1	RS8_ECOLI	P02361	escherichia
140	7	1.5	879	1	DPOL_MHV1	O909e9	mus musculus	213	6	1.3	131	1	YECN_ECOLI	P76829	escherichia
141	7	1.5	883	1	DPOL_MHV8	P03160	woodchuck h	214	6	1.3	132	1	TFW2_HUMAN	O01629	homo sapien
142	7	1.5	883	1	DPOL_MHV59	P06275	woodchuck h	215	6	1.3	134	1	LY6F_MOUSE	P35460	mus musculus
143	7	1.5	884	1	DPOL_MHV7	P12899	woodchuck h	216	6	1.3	135	1	Y549_RICPR	Q92401	ricketsia
144	7	1.5	884	1	DPOL_MHV81	P12899	woodchuck h	217	6	1.3	138	1	YCX1_CHILVU	O20118	chlorella v
145	7	1.5	906	1	FOX2_CANTR	P22414	candida tro	218	6	1.3	139	1	IGF_MYXGL	P22618	myxine glut
146	7	1.5	932	1	SYL_ARCFU	O30250	archaeoglob	219	6	1.3	139	1	PRO2_HUMAN	P35080	homo sapien
147	7	1.5	1085	1	YAFR_SCHPO	O09663	schizosacch	220	6	1.3	139	1	PRO2_MOUSE	O9J1V2	mus musculus
148	7	1.5	1152	1	CD45_MOUSE	P06600	mus musculus	221	6	1.3	139	1	PRO2_RAT	O9epc6	rattus norv
149	7	1.5	1160	1	WDR7_HUMAN	O9Y4e6	homo sapien	222	6	1.3	141	1	LYSA_BPP2	P151769	bacterioph
150	7	1.5	1166	1	CY46_RAT	Q03343	rattus norv	223	6	1.3	144	1	PAZA_HUMAN	P45455	homo sapien
151	7	1.5	1234	1	PIP3_HUMAN	O01970	homo sapien	224	6	1.3	145	1	CY2_RHOSH	P00095	rhodobacter
152	7	1.5	1234	1	PIP3_MOUSE	P51432	mus musculus	225	6	1.3	145	1	EXSC_PSEAE	P26995	pseudomonas
153	7	1.5	1255	1	CD45_RAT	P04157	rattus norv	226	6	1.3	146	1	CYTC_HUMAN	P01034	homo sapien
154	7	1.5	1259	1	MDR3_HUMAN	P21439	homo sapien	227	6	1.3	146	1	CYTC_MACMU	O19092	macaca mula
155	7	1.5	1302	1	MDR4_DROME	Q00449	drosophila	228	6	1.3	146	1	CYTC_SAISC	O19093	saimiri sci
156	7	1.5	1304	1	CD45_HUMAN	P08575	homo sapien	229	6	1.3	146	1	Y0E1_MOUSE	P58283	mus musculus
157	7	1.5	1444	1	ADP1_MYCGE	P20796	mycoplasma	230	6	1.3	148	1	YOEY_BACSU	P54464	bacillus su
158	7	1.5	2004	1	MOZ_HUMAN	O92794	homo sapien	231	6	1.3	151	1	HSPH_BRAJA	O86110	bradyrhizob
159	7	1.5	2175	1	HMCU_DROME	P10180	drosophila	232	6	1.3	151	1	YG27_METUA	O59021	methanococc
160	7	1.5	2349	1	FLNA_HUMAN	P12270	homo sapien	233	6	1.3	152	1	Y38A_MYCPN	P75213	mycoplasma
161	7	1.5	2647	1	MY15_HUMAN	P21333	homo sapien	234	6	1.3	152	1	YLYS_BPPHY	P13004	lactococcus
162	7	1.5	3530	1	PRKD_MOUSE	O9ukn7	homo sapien	235	6	1.3	154	1	RNM6_BOVIN	P08904	bos taurus
163	7	1.5	4128	1	FIBB_TARTE	P14539	tapirus ter	236	6	1.3	156	1	YMS6_CAEEL	P44253	haemophilus
164	6	1.3	19	1	CERB_CERCA	P36191	ceratilis c	237	6	1.3	156	1	YMBE_SALTY	P34502	caenorhabdi
165	6	1.3	23	1	PSBN_PORPU	O9p9f8	ureaplasma	238	6	1.3	157	1	Y0Y5_MYCTU	P27347	zea mays (m
166	6	1.3	56	1	RL32_UREPA	O8YVY6	anaeabena sp	239	6	1.3	157	1	U195_HUMAN	O95574	salmonella
167	6	1.3	58	1	SCR2_MESMA	O9n1i5	mesobuthus	240	6	1.3	158	1	U195_MYCTU	O95571	mycobacteri
168	6	1.3	61	1	OMP_LOCOMI	P80045	locusta mig	241	6	1.3	160	1	U195_MOUSE	O96c12	mus musculus
169	6	1.3	65	1	RPN_PPYRAB	O9v194	pyrococcus	242	6	1.3	161	1	HMGL_WHEAT	P40621	trititum ae
170	6	1.3	65	1	RPN_PYRHO	O59298	pyrococcus	243	6	1.3	166	1	CCAC_CAVPO	P38653	entamoeba h
171	6	1.3	74	1	BRTA_RANTE	P82268	rana tempor	244	6	1.3	169	1	MIR3_MOUSE	O35505	cavia porce
172	6	1.3	74	1	AKH3_LOCOMI	P19672	locusta mig	245	6	1.3	170	1	UBCG_HUMAN	O9m3j7	spinaecia ol
173	6	1.3	77	1	FEB7_METUA	Q58132	methanococc	246	6	1.3	170	1	Y019_BORBU	O94462	homo sapien
174	6	1.3	77	1	MCP1_LYCES	P01076	lycopersico	247	6	1.3	173	1	LMIP_BOVIN	P20274	bos taurus
175	6	1.3	77	1				248	6	1.3					
176	6	1.3	77	1				249	6	1.3					
177	6	1.3	77	1				250	6	1.3					
178	6	1.3	77	1				251	6	1.3					
179	6	1.3	77	1				252	6	1.3					

399	6	1.3	292	1	RS0A_SCHPO	Q9y718	schizosacch	472	6	1.3	347	1	ELO2_YEAST	P23538	saccharomyc
400	6	1.3	292	1	Y1H7_ECOLI	P32141	eschlerichia	473	6	1.3	347	1	GBA5_DICDI	P34043	dictyosteli
401	6	1.3	294	1	RL5_STYCL	Q26481	stelya clay	474	6	1.3	347	1	OXDA_RABIT	P22942	oryctolagus
402	6	1.3	294	1	VU51_HSV7J	P52383	human herpe	475	6	1.3	348	1	HMT1_YEAST	P38074	saccharomyc
403	6	1.3	296	1	COPE_YEAST	P40509	saccharomyc	476	6	1.3	348	1	OPSD_CRIGR	P28681	cricetulus
404	6	1.3	296	1	PPNK_NEIMA	Q9j919	neisseria m	477	6	1.3	348	1	OPSD_MOUSE	P15409	mus musculus
405	6	1.3	298	1	STX4_MOUSE	P70452	mus musculus	478	6	1.3	348	1	OPSD_MOUSE	P49912	oryctolagus
406	6	1.3	298	1	STX4_MOUSE	Q08850	rattus norv	479	6	1.3	348	1	OPSD_MOUSE	P51489	rattus norv
407	6	1.3	298	1	Y1H7_ECOLI	P32142	eschlerichia	480	6	1.3	349	1	VP7_BRV10	P07860	bluetongue
408	6	1.3	298	1	Y1H7_ECOLI	Q91750	salmonella	481	6	1.3	349	1	VP7_BRV10	P26560	bluetongue
409	6	1.3	299	1	NU1M_ALBEO	P48897	albimaria c	482	6	1.3	349	1	VP7_BRV10	P18259	bluetongue
410	6	1.3	300	1	SYGA_PASMO	P57904	pasteurella	483	6	1.3	349	1	VP7_BRV10	P26561	bluetongue
411	6	1.3	301	1	SCRK_ZYMO	Q03417	zymomonas m	484	6	1.3	350	1	ITP2_MOUSE	Q91000	mus musculus
412	6	1.3	302	1	CHIA_ARATH	P19172	arabidopsis	485	6	1.3	350	1	KITH_HSVTU	P25987	turkey herp
413	6	1.3	302	1	SYGA_HAEIN	P43821	haemophilus	486	6	1.3	350	1	LEGG_PEA	P05693	pisum sativ
414	6	1.3	303	1	SYGA_ECOLI	P00960	eschlerichia	487	6	1.3	351	1	VGL1_PVRI	P07446	pseudorabie
415	6	1.3	304	1	MBL2_HUMAN	Q9nuk0	homo sapien	488	6	1.3	351	1	AROB_CAMUE	P07446	pseudorabie
416	6	1.3	305	1	GSPC_VIBCH	P45777	vibriolo chol	489	6	1.3	351	1	PSBD_CVACA	Q9tm47	cyanididum c
417	6	1.3	305	1	SYGA_VIBCH	Q9k7w7	vibriolo chol	490	6	1.3	351	1	PSBD_PROHO	P51766	prochlooth
418	6	1.3	306	1	MK16_YEAST	P10962	saccharomyc	491	6	1.3	352	1	KITH_HSVTU	P17653	marek's dis
419	6	1.3	306	1	YOPD_YEREN	P37132	yersinia en	492	6	1.3	353	1	COA2_POVBO	P24849	bovine poly
420	6	1.3	310	1	CB5R_SULAC	Q54089	sulfolobus	493	6	1.3	353	1	KERA_CHICK	Q42235	gallus gall
421	6	1.3	310	1	KITH_HSVTF	P13157	turkey herp	494	6	1.3	353	1	KERA_COTJA	Q9d666	colurnix co
422	6	1.3	310	1	PUR0_MVCTU	Q50453	mycobacteri	495	6	1.3	354	1	VF11_VACCC	P21052	vaccinia vi
423	6	1.3	311	1	CHLY_HEVBR	P23472	hevea bras	496	6	1.3	355	1	NDF1_MESAU	Q60430	mesocricetu
424	6	1.3	311	1	KHSE_SULSO	Q97470	sulfolobus	497	6	1.3	355	1	UBPC_HUMAN	Q75317	homo sapien
425	6	1.3	312	1	SNAG_HUMAN	Q99747	homo sapien	498	6	1.3	356	1	COX2_BACSU	P24011	bacillus su
426	6	1.3	313	1	ARAP_BACSU	P94529	bacillus su	499	6	1.3	357	1	CHVE_AZOB	P54083	azospirillu
427	6	1.3	313	1	NUZM_RHISA	Q99817	rhicicephal	500	6	1.3	357	1	NDF1_CHICK	P79765	gallus gall
428	6	1.3	313	1	ZS11_HUMAN	Q9y619	homo sapien	501	6	1.3	357	1	Y180_ARATH	Q80543	arabidopsis
429	6	1.3	314	1	AA3R_CANFA	Q28309	canis famli	502	6	1.3	358	1	HOP1_CANEL	Q02100	caenorhabd
430	6	1.3	314	1	O5F1_HUMAN	Q95221	homo sapien	503	6	1.3	358	1	UXDA_LACLA	Q95050	lactococcus
431	6	1.3	316	1	O2G1_HUMAN	Q9h205	homo sapien	504	6	1.3	359	1	LACH_DROME	Q24372	drosophila
432	6	1.3	316	1	SRG8_CAEEL	P45655	caenorhabd	505	6	1.3	359	1	WNSB_HUMAN	Q9h177	homo sapien
433	6	1.3	317	1	AA3R_SHEEP	P35342	ovis aries	506	6	1.3	363	1	PAC1_SCHPO	P22192	schizosacch
434	6	1.3	317	1	MURB_STNY3	P74529	synecocyst	507	6	1.3	363	1	UL16_VZVD	P09293	varicella-z
435	6	1.3	318	1	SYGA_MORCA	P77992	moraxella c	508	6	1.3	363	1	U162_METJA	Q58049	methanococc
436	6	1.3	319	1	L1P1_MORSP	P19833	moraxella s	509	6	1.3	364	1	IE68_PVKA	P24827	pseudorabie
437	6	1.3	321	1	FCCE2_HUMAN	P06734	homo sapien	510	6	1.3	364	1	RECE_XYLEFA	Q9p818	xyella fas
438	6	1.3	321	1	MRAY_ENTFA	Q07107	enterococcu	511	6	1.3	365	1	RAPG_BACSU	Q32924	bacillus su
439	6	1.3	321	1	SAPB_HAEIN	P45286	haemophilus	512	6	1.3	366	1	CHNA_ECOLI	P31801	eschlerichia
440	6	1.3	322	1	ACSD_MOOTH	Q07741	moorella th	513	6	1.3	366	1	ILVC_XYLEFA	Q9p819	xyella fas
441	6	1.3	322	1	YMO2_MARPO	P38451	marichantia	514	6	1.3	367	1	DIAC_RAT	Q01460	rattus norv
442	6	1.3	324	1	FXB1_HUMAN	Q99853	homo sapien	515	6	1.3	368	1	CHBE_PVRAB	Q9uyf3	pyrococcus
443	6	1.3	325	1	FXB1_MOUSE	Q64732	mus musculu	516	6	1.3	368	1	CHBE_PVRHO	P54957	pyrococcus
444	6	1.3	327	1	OPT_CANFA	P83286	canis famli	517	6	1.3	370	1	YXER_BACSU	P54957	pyrococcus
445	6	1.3	327	1	RL5_ANOGA	Q44348	anopheles g	518	6	1.3	371	1	CYB_CASDU	Q48827	casarea dus
446	6	1.3	327	1	YDAM_ECOLI	P76054	eschlerichia	519	6	1.3	371	1	YMI8_PSEAE	Q01809	pseudomonas
447	6	1.3	328	1	THIL_HAEIN	Q57190	haemophilus	520	6	1.3	372	1	FLHB_BORBU	Q44760	borrella bu
448	6	1.3	329	1	YKBB_YEAST	P36104	saccharomyc	521	6	1.3	372	1	YBYR_ECOLI	P75788	eschlerichia
449	6	1.3	330	1	YP64_MYCTU	Q50734	mycobacteri	522	6	1.3	373	1	HISZ_RHIL0	Q98789	rhizobium l
450	6	1.3	332	1	TWFI_YEAST	P53250	saccharomyc	523	6	1.3	374	1	E13B_HEVBR	P52407	hevea bras
451	6	1.3	333	1	GPBB_HUMAN	P48146	homo sapien	524	6	1.3	374	1	VENV_FOWPY	P36316	fowlpox vir
452	6	1.3	333	1	OLR3_RAT	P23265	rattus norv	525	6	1.3	378	1	FLAB_VIBPA	Q56702	vibrio para
453	6	1.3	333	1	PTHB_ERWAM	Q32522	erwinia amy	526	6	1.3	378	1	FLAD_VIBPA	Q56713	vibrio para
454	6	1.3	334	1	SRB7_CAEEL	P54142	caenorhabd	527	6	1.3	378	1	HISZ_BRUME	Q8746	bruceella me
455	6	1.3	335	1	EBAA2_FLAME	P36912	flavobacter	528	6	1.3	379	1	CYB_LAMGU	Q34891	lama glama
456	6	1.3	337	1	AMBP_PIG	P04366	sus scrofa	529	6	1.3	379	1	CYB_LAMGU	Q34891	lama glama
457	6	1.3	337	1	FSA_SHEEP	P31514	ovis aries	530	6	1.3	379	1	HISZ_RHIME	Q92416	rhizobium m
458	6	1.3	337	1	VF11_VACCP	P29688	vaccinia vi	531	6	1.3	379	1	METX_MYCTU	Q53391	mycobacteri
459	6	1.3	337	1	YJUN_ECOLI	P39400	eschlerichia	532	6	1.3	380	1	CYB_HYDPE	Q79206	hydrobates
460	6	1.3	338	1	YD49_THEMEA	Q9x170	thermocoga	533	6	1.3	380	1	DSVB_DESVH	P45575	desulfovibr
461	6	1.3	339	1	RSPB_ECOLI	P38105	eschlerichia	534	6	1.3	380	1	Y699_METJA	Q58110	methanococc
462	6	1.3	339	1	SRG7_CAEEL	P54129	caenorhabd	535	6	1.3	381	1	CYB_TRIVU	Q03503	trichosurus
463	6	1.3	340	1	PLDB_ECOLI	P07000	eschlerichia	536	6	1.3	381	1	HUPN_BRATA	Q45247	bradyrhizob
464	6	1.3	340	1	TF2B_SCHPO	Q13749	schizosacch	537	6	1.3	382	1	METX_MYCLE	Q32874	mycobacteri
465	6	1.3	342	1	GGH_SOYBN	P93164	glycine max	538	6	1.3	382	1	OPS3_DROPS	P28680	drosophila
466	6	1.3	342	1	YOC6_CAEEL	Q09975	caenorhabd	539	6	1.3	383	1	INSI_ECOLI	P37246	eschlerichia
467	6	1.3	344	1	FSA_BOVIN	P50291	bos taurus	540	6	1.3	385	1	DH48_HUMAN	P48448	homo sapien
468	6	1.3	345	1	YAT2_SCHPO	Q10149	schizosacch	541	6	1.3	385	1	ITPA5_BOVIN	Q27977	bos taurus
469	6	1.3	346	1	IC28_PANTR	P16215	pan troglod	542	6	1.3	385	1	LPXB_XYLEFA	Q9p816	xyella fas
470	6	1.3	346	1	DHAS_HELPJ	Q92828	helicobacte	543	6	1.3	385	1	MTLD_BUCAL	P57634	buchnera ap
471	6	1.3	346	1	DHAS_HELPJ	Q25801	helicobacte	544	6	1.3	385	1	TEBB_OXYNO	P16458	oxytricha n

545	6	1.3	386	1	CVCB_PEA	P13919	pisum sativ	618	6	1.3	428	1	ENO_CHLPN	O927a6	chlamydia p
546	6	1.3	386	1	NUCM_TRYBB	P21301	trypanosoma	619	6	1.3	428	1	HDA3_CHICK	P65520	gallus gall
547	6	1.3	386	1	RNAL_SCHPO	P41391	schizosacch	620	6	1.3	428	1	MTT8_THETH	P29749	thermus the
548	6	1.3	387	1	ASPP_AEPAE	Q03168	aedes aegypt	621	6	1.3	428	1	SSR3_MOUSE	P30935	mus musculus
549	6	1.3	387	1	QIN_AVIS3	P56260	avian sarco	622	6	1.3	428	1	SSR3_MOUSE	P20936	rattus norv
550	6	1.3	388	1	YM67_MYCTU	Q50695	mycobacteri	623	6	1.3	429	1	THRC_BUCAI	P57289	buchnera ap
551	6	1.3	389	1	YND5_YEAST	P53962	saccharomyc	624	6	1.3	431	1	CST1_HUMAN	O05048	homo sapien
552	6	1.3	390	1	UGAT_MOUSE	Q910m8	mus musculu	625	6	1.3	432	1	VTS4_YEAST	O05054	saccharomyc
553	6	1.3	392	1	TEBB_STMYX	P29548	stylonychia	626	6	1.3	434	1	PRSA_YEAST	P33257	saccharomyc
554	6	1.3	392	1	YU1J_ECOLI	P39381	escherichia	627	6	1.3	434	1	RP54_YEAST	Q01194	rhodobacter
555	6	1.3	393	1	HEMX_ECOLI	P09127	escherichia	628	6	1.3	435	1	ARRB_CABEL	P114b5	caenorhabdi
556	6	1.3	393	1	TYRH_MOUSE	P21761	mus musculu	629	6	1.3	436	1	IF4B_YEAST	P5080	gallus gall
557	6	1.3	393	1	XFLH_ECOLI	P37389	escherichia	630	6	1.3	436	1	NOSD_PSBST	P194167	saccharomyc
558	6	1.3	394	1	URTG_DESRO	P49150	desmodus ro	631	6	1.3	438	1	ALG3_HUMAN	O92655	homo sapien
559	6	1.3	394	1	YD2C_SCHPO	Q10260	schizosacch	632	6	1.3	439	1	TEA3_MOUSE	P70210	mus musculu
560	6	1.3	395	1	SDC_DROME	P49419	drosophila	633	6	1.3	440	1	PUR8_HELPJ	Q92k42	helicobacte
561	6	1.3	396	1	TRT_DROME	P19351	drosophila	634	6	1.3	440	1	PUR8_HELPJ	P56468	helicobacte
562	6	1.3	396	1	UGAT_HUMAN	P78381	homo sapien	635	6	1.3	442	1	MEAL_CHICK	P55080	gallus gall
563	6	1.3	397	1	DP3B_MYCSM	P52851	mycobacteri	636	6	1.3	443	1	ARGA_ECOLI	O08205	escherichia
564	6	1.3	397	1	EFTU_PSEAE	P09591	pseudomonas	637	6	1.3	444	1	FLIT_CANCR	O05528	caulobacter
565	6	1.3	398	1	VAIP_ECOLI	Q47536	escherichia	638	6	1.3	444	1	YCXD_BACSU	Q08792	bacillus su
566	6	1.3	398	1	YUGN_ECOLI	P39338	escherichia	639	6	1.3	445	1	GNT1_HUMAN	P26572	homo sapien
567	6	1.3	400	1	ENPL_MESAU	P08712	mesocricetu	640	6	1.3	445	1	YGCS_ECOLI	Q46909	escherichia
568	6	1.3	400	1	YD01_METJA	Q58697	methanococc	641	6	1.3	446	1	GNTU_ECOLI	P46856	escherichia
569	6	1.3	402	1	LAG2_CAEEL	P45442	caenorhabdi	642	6	1.3	446	1	GRMD_HUMAN	Q9bq67	homo sapien
570	6	1.3	402	1	RNBP_PIG	P17560	sus scrofa	643	6	1.3	447	1	CASR_HUMAN	P32238	homo sapien
571	6	1.3	404	1	GITS_HAEIN	P45240	haemophilus	644	6	1.3	447	1	GNT1_MOUSE	P27808	mus musculu
572	6	1.3	405	1	YUHB_ECOLI	P39352	escherichia	645	6	1.3	447	1	GNT1_RABIT	P27115	oryctolagus
573	6	1.3	405	1	YLF2_YEAST	P38746	saccharomyc	646	6	1.3	447	1	GNT1_RABIT	O09325	rattus norv
574	6	1.3	406	1	MYC_BRARE	P52160	brachydanio	647	6	1.3	447	1	TBB3_ORYSA	P46265	oryza sativ
575	6	1.3	406	1	SNX6_HUMAN	Q20240	drosophila	648	6	1.3	448	1	TRME_NEITB	O91x14	neisseria m
576	6	1.3	406	1	ISDF_RHTLO	Q9unb7	homo sapien	649	6	1.3	448	1	TRME_NEITB	O91x14	neisseria m
577	6	1.3	407	1	EFTU_CHACO	P50371	chakra commi	650	6	1.3	449	1	LAT_MYCTU	P36895	mycobacteri
578	6	1.3	408	1	GPT_CRIGR	P24140	cricetulus	651	6	1.3	450	1	ECFE_SALTY	Q82944	salmonella
579	6	1.3	408	1	GPT_CRIGR	P23338	cricetulus	652	6	1.3	450	1	ECFE_SALTY	Q82944	salmonella
580	6	1.3	408	1	GPT_CRIGR	P23338	cricetulus	653	6	1.3	450	1	GSHR_ECOLI	P06715	escherichia
581	6	1.3	408	1	GPT_HUMAN	Q9h3b5	homo sapien	654	6	1.3	451	1	FXGB_CHICK	O90964	gallus gall
582	6	1.3	409	1	R52B_HUMAN	P54727	homo sapien	655	6	1.3	452	1	CASR_RABIT	P46657	oryctolagus
583	6	1.3	409	1	Y055_CAEEL	Q09251	caenorhabdi	656	6	1.3	452	1	CASR_RAT	P30553	rattus norv
584	6	1.3	410	1	CH60_EHRCA	O34194	erlichia c	657	6	1.3	452	1	PH4H_DROME	P17276	drosophila
585	6	1.3	410	1	EFTU_MESVI	Q4mup0	mesostigma	658	6	1.3	453	1	GASR_CANFA	P30552	canis fami
586	6	1.3	410	1	GPT_MOUSE	P42867	mus musculu	659	6	1.3	453	1	SR24_YEAST	P7124	saccharomyc
587	6	1.3	410	1	Y457_METJA	Q57899	methanococc	660	6	1.3	454	1	GASR_BOVIN	P79266	bos taurus
588	6	1.3	411	1	MP62_LYPTJ	P91753	lytechinus	661	6	1.3	454	1	YGDH_ECOLI	P37356	escherichia
589	6	1.3	411	1	PALL_HUMAN	Q9um63	homo sapien	662	6	1.3	457	1	ARLY_ECOS7	Q6x730	escherichia
590	6	1.3	411	1	RAPS_FORCA	P09106	torpedo cal	663	6	1.3	457	1	ARLY_ECOLI	P11447	escherichia
591	6	1.3	412	1	TRFR_RAT	Q01717	rattus norv	664	6	1.3	458	1	ARLY_SALTY	Q82311	salmonella
592	6	1.3	413	1	LCAT_CHICK	P53760	gallus galli	665	6	1.3	458	1	ARLY_SALTY	Q82311	salmonella
593	6	1.3	414	1	NSR1_YEAST	P27476	saccharomyc	666	6	1.3	458	1	ME31_DROME	P33128	drosophila
594	6	1.3	414	1	UT1L_HUMAN	Q9hwf9	homo sapien	667	6	1.3	459	1	NU4M_BALMU	P41298	balaeopter
595	6	1.3	415	1	VEGC_MOUSE	P97953	mus musculu	668	6	1.3	459	1	NU4M_BALMU	P41298	balaeopter
596	6	1.3	415	1	PICI_MOUSE	Q62083	mus musculu	669	6	1.3	460	1	ACM1_MACMU	P56489	macaca mula
597	6	1.3	416	1	RAGE_BOVIN	Q28173	bos taurus-	670	6	1.3	460	1	NU4M_SCYCA	O79410	scyllorhinu
598	6	1.3	416	1	WZXE_ECOLI	P27834	escherichia	671	6	1.3	460	1	NU4M_SCYCA	O79410	scyllorhinu
599	6	1.3	418	1	SSR3_HUMAN	P32742	homo sapien	672	6	1.3	461	1	MTSL_SALIN	Q92z45	squalus aca
600	6	1.3	419	1	P47B_CANBO	Q00319	candida boi	673	6	1.3	462	1	SYG_TREPA	O83678	treponema p
601	6	1.3	420	1	ODO2_BUCAI	P57389	buchnera ap	674	6	1.3	463	1	ARLY_SACDO	P41906	saccharomyc
602	6	1.3	420	1	YO20_BACHD	Q9k4r1	baecillus ha	675	6	1.3	463	1	ARLY_YEAST	P40706	saccharomyc
603	6	1.3	421	1	CHDE_MUCRO	P50325	mucor rouxi	676	6	1.3	463	1	LTV1_YEAST	P34078	saccharomyc
604	6	1.3	421	1	MTTA_THEAO	P14385	thermus aqu	677	6	1.3	465	1	VP19_HVEB	P28935	equine herp
605	6	1.3	421	1	TES_HUMAN	Q9ug48	homo sapien	678	6	1.3	467	1	TRF6_MOUSE	P74931	mus musculu
606	6	1.3	422	1	PGL1_ARATH	P49062	arabidopsis	679	6	1.3	467	1	V51K_BMYVF	P09514	beet weester
607	6	1.3	422	1	YIUC_BACSU	O31754	bacillus su	680	6	1.3	468	1	F121_BOVIN	P50448	bos taurus
608	6	1.3	423	1	EAT5_CAEEL	Q27295	caenorhabdi	681	6	1.3	468	1	KSGT_BRANA	O04160	brassica na
609	6	1.3	423	1	HNP_PLABE	Q08168	plasmodium	682	6	1.3	468	1	PMB_BACHD	P36606	schizosacch
610	6	1.3	423	1	P47A_CANBO	P21245	candida boi	683	6	1.3	468	1	PMB_BACHD	Q9K678	bacillus ha
611	6	1.3	423	1	SAT_ENTHI	O76156	entamoeba h	684	6	1.3	469	1	YUM5_CAEEL	P322717	caenorhabdi
612	6	1.3	424	1	PUR2_AOUAE	O66949	aquifex aeo	685	6	1.3	471	1	RNT1_YEAST	O02555	saccharomyc
613	6	1.3	425	1	CABL_CAEEL	Q93249	caenorhabdi	686	6	1.3	472	1	CIST_DAUCA	O80433	daucus caro
614	6	1.3	426	1	BRNQ_CONGL	O06754	corynebacte	687	6	1.3	474	1	Y068_MYGE	P47314	mycoplasma
615	6	1.3	426	1	TEAI_HUMAN	P28347	homo sapien	688	6	1.3	475	1	NCAP_SYNV	P10550	sonchus yel
616	6	1.3	426	1	TEAI_MOUSE	P30051	mus musculu	689	6	1.3	475	1	SIM1_YEAST	P40472	saccharomyc
617	6	1.3	427	1	MYCN_SERCA	P26014	serinus can	690	6	1.3	476	1	RFAE_HAEIN	O05074	haemophilus

691	6	1.3	477	1	INGR_MOUSE	P15261	mus musculus	764	6	1.3	533	1	MVIN_RHTR	O05467	rhizobium t
692	6	1.3	477	1	SYG_RHILO	Q984x8	rhizobium 1	765	6	1.3	534	1	PSD3_HUMAN	O43342	homo sapien
693	6	1.3	481	1	DDX6_XENLA	P54824	xenopus lae	766	6	1.3	535	1	C7D1_MAIZE	O43250	zea mays (m
694	6	1.3	481	1	PGKH_TOBAC	O42961	nicotiana t	767	6	1.3	535	1	UDJ1_RAT	O64550	rattus norv
695	6	1.3	481	1	TRME_RALSO	O8y3h5	ralstonia s	768	6	1.3	541	1	CATN_ASCSU	P90682	ascaris suu
696	6	1.3	482	1	NUSA_BOBBU	O51740	borrelia bu	769	6	1.3	541	1	CATG_RHOSH	P95647	rhodobacter
697	6	1.3	482	1	T2EA_YEAST	P36100	saccharomyc	770	6	1.3	542	1	EAAL_BOVIN	P46411	bos taurus
698	6	1.3	483	1	BCA_STRYL	P33569	streptomyce	771	6	1.3	542	1	EAAL_HUMAN	P43003	homo sapien
699	6	1.3	483	1	DDX6_HUMAN	P26196	homo sapien	772	6	1.3	542	1	NCAP_P12HT	P21737	human parat
700	6	1.3	483	1	DDX6_MOUSE	P54823	mus musculus	773	6	1.3	542	1	TCPE_CAEEL	P47709	caenorhabdi
701	6	1.3	483	1	IDH_RICCN	O921r7	rickettsia	774	6	1.3	542	1	TUUL_HUMAN	O00294	homo sapien
702	6	1.3	483	1	IDH_RICCR	O92d40	rickettsia	775	6	1.3	543	1	EAAL_MOUSE	P56564	mus musculus
703	6	1.3	484	1	MORE_CLOPE	O8xjy9	clostridium	776	6	1.3	543	1	EAAL_RAT	P24942	rattus norv
704	6	1.3	487	1	CATA_STRCO	O92598	streptomyce	777	6	1.3	543	1	SGEL_YEAST	P33375	saccharomyc
705	6	1.3	487	1	CIT7_ECOLI	P77405	escherichia	778	6	1.3	544	1	CH60_AGR5	P30779	agrobacteri
706	6	1.3	488	1	NU2M_OENBE	P93401	oenothera b	779	6	1.3	544	1	ESRP_DROME	P18167	drosophila
707	6	1.3	490	1	CHEL_HUMAN	O00409	homo sapien	780	6	1.3	544	1	PAK3_HUMAN	O75914	homo sapien
708	6	1.3	490	1	YNC2_YEAST	P53972	saccharomyc	781	6	1.3	544	1	PAK3_MOUSE	O61036	mus musculus
709	6	1.3	491	1	YIU0_YEAST	P40439	saccharomyc	782	6	1.3	544	1	PAK3_RAT	O62829	rattus norv
710	6	1.3	492	1	CPAC_MOUSE	P56593	mus musculus	783	6	1.3	545	1	CH60_PARDE	O92462	paracoccus
711	6	1.3	493	1	CPGL_MOUSE	O05421	mus musculus	784	6	1.3	545	1	CH60_RHOCA	P95678	rhodobacter
712	6	1.3	493	1	CPGL_RABIT	P08682	oryctolagus	785	6	1.3	545	1	CH64_RHIME	P35469	rhizobium m
713	6	1.3	493	1	HSFA_HUMAN	O9ulv5	homo sapien	786	6	1.3	545	1	CH64_RHIME	O922q4	rhizobium m
714	6	1.3	494	1	ACHE_RAT	P09660	rattus norv	787	6	1.3	546	1	CH60_RHILV	P34939	rhizobium l
715	6	1.3	495	1	CPGL_BOVIN	O18963	bos taurus	788	6	1.3	546	1	CH61_RHOSH	P20110	rhodobacter
716	6	1.3	495	1	CPGL_PIG	P79383	sus scrofa	789	6	1.3	547	1	CITR_KLEPN	P52687	klebsiella
717	6	1.3	496	1	ERGL_CANAL	O92206	candida alb	790	6	1.3	548	1	CH60_ZYMO	P48280	zymomonas m
718	6	1.3	496	1	PAL2_HUMAN	O9up88	homo sapien	791	6	1.3	548	1	ERF_HUMAN	P50548	homo sapien
719	6	1.3	496	1	PR4H_HUMAN	O13523	homo sapien	792	6	1.3	548	1	LACT_PLURA	O01579	phlebia rad
720	6	1.3	496	1	PR4H_MOUSE	O61136	mus musculus	793	6	1.3	550	1	CH60_EHRCH	O42382	ehrllichia c
721	6	1.3	496	1	PSD3_ANGA	O61470	anopheles g	794	6	1.3	551	1	CBX4_MOUSE	O55187	mus musculus
722	6	1.3	497	1	C711_ARATH	O9sab6	arabidopsis	795	6	1.3	551	1	CH60_COMRU	P48213	cowdria rum
723	6	1.3	497	1	LMP2_EBV	P13285	epstein-bar	796	6	1.3	551	1	ERF_MOUSE	P70459	mus musculus
724	6	1.3	498	1	CCS_CAPAN	O42435	capstein an	797	6	1.3	552	1	NCAP_TPMV	O9w440	tupaia para
725	6	1.3	500	1	CPGB_RAT	P08683	rattus norv	798	6	1.3	553	1	YQIK_ECOLI	P77306	escherichia
726	6	1.3	500	1	ICL1_HUMAN	P05155	homo sapien	799	6	1.3	555	1	PERF_HUMAN	P14722	homo sapien
727	6	1.3	500	1	LCYB_TOBAC	O43578	nicotiana t	800	6	1.3	556	1	CD19_HUMAN	P15941	homo sapien
728	6	1.3	500	1	PSD3_ANOST	O9u5t6	anopheles s	801	6	1.3	557	1	ATRA_CLOAB	O32327	clostridium
729	6	1.3	501	1	CSD2_DROME	O9vmt6	drosophila	802	6	1.3	558	1	CBX4_HUMAN	O00257	homo sapien
730	6	1.3	501	1	NU2C_MARPO	P06257	maranthia	803	6	1.3	558	1	CX1B_PARDE	P98062	paracoccus
731	6	1.3	501	1	PYCA_METJA	O58626	methanococc	804	6	1.3	558	1	YJ83_MYCTU	O10873	mycobacteri
732	6	1.3	503	1	CCS_CITSI	O9se80	citrus sine	805	6	1.3	560	1	YJ60_HORVU	O00531	hordeum vul
733	6	1.3	503	1	LEB3_PEA	P05692	pisum sativ	806	6	1.3	561	1	CEAC_ECOLI	P00645	escherichia
734	6	1.3	504	1	SH2B_MOUSE	O02152	mus musculu	807	6	1.3	562	1	CH60_TRYBB	O37683	trypanosoma
735	6	1.3	504	1	ICL1_MOUSE	P97290	mus musculus	808	6	1.3	562	1	CH60_TRYCR	O95046	trypanosoma
736	6	1.3	505	1	TUB_RAT	O88808	rattus norv	809	6	1.3	563	1	ENV_BAEVM	P10269	baabon endo
737	6	1.3	506	1	DHBI_YEAST	P39517	saccharomyc	810	6	1.3	565	1	COX1_RHOSH	P33817	rhodobacter
738	6	1.3	507	1	CATA_PICAN	P30263	pichia angu	811	6	1.3	565	1	NPH1_CANFA	O9t019	canis famli
739	6	1.3	507	1	GIR6_HUMAN	O9u9q3	homo sapien	812	6	1.3	571	1	CVCA_PEA	P13915	pisum sativ
740	6	1.3	508	1	EPOR_HUMAN	P19235	homo sapien	813	6	1.3	572	1	EAAL_MOUSE	P43006	mus musculus
741	6	1.3	509	1	C4A3_DROME	O9vms7	drosophila	814	6	1.3	573	1	EAAL_RAT	P31596	rattus norv
742	6	1.3	509	1	NUOM_ECOLI	P19178	escherichia	815	6	1.3	574	1	BEAL_YEAST	P47113	saccharomyc
743	6	1.3	512	1	ATPA_RICPR	O50288	rickettsia	816	6	1.3	574	1	EAAL_HUMAN	P43004	homo sapien
744	6	1.3	512	1	EMRY_ECOLI	P52600	escherichia	817	6	1.3	575	1	YWA2_BACSU	P45661	baecillus su
745	6	1.3	515	1	YAHF_ECOLI	F77187	escherichia	818	6	1.3	577	1	YGX8_YEAST	P53075	saccharomyc
746	6	1.3	516	1	SMF3_YEAST	O04174	saccharomyc	819	6	1.3	583	1	CH12_CANAL	P40953	candida alb
747	6	1.3	517	1	Y652_HUMAN	O75143	homo sapien	820	6	1.3	583	1	SCP3_SCHPO	P41000	schizosacch
748	6	1.3	518	1	ANPD_AZOVI	P16266	azotobacter	821	6	1.3	585	1	BLAR_STRAU	P18357	staphylococ
749	6	1.3	520	1	CL1A_HORSE	O46515	equus cabal	822	6	1.3	585	1	MECR_STRAAM	P26597	staphylococ
750	6	1.3	520	1	YD99_LISMO	O91738	listeria mo	823	6	1.3	586	1	SYD_BUCAT	P57401	buchnera ap
751	6	1.3	521	1	TYRR_ERWHE	O921b7	erwinia her	824	6	1.3	586	1	YCAO_ECOLI	P75638	escherichia
752	6	1.3	523	1	ASSY_ARATH	O9sxx3	arabidopsis	825	6	1.3	587	1	RGPL_HUMAN	P46600	homo sapien
753	6	1.3	524	1	HUNB_TRICA	O01791	tribolium c	826	6	1.3	587	1	TALA_BBDV	P13894	budgerigar
754	6	1.3	524	1	NAB2_HUMAN	O15742	homo sapien	827	6	1.3	589	1	RGPL_MOUSE	P46061	homo sapien
755	6	1.3	526	1	ANPD_RHOCA	O07933	rhodobacter	828	6	1.3	593	1	DR1L_HUMAN	O99956	homo sapien
756	6	1.3	526	1	CL1A_MOUSE	O9q282	mus musculus	829	6	1.3	593	1	SOWT_YEAST	P36150	saccharomyc
757	6	1.3	528	1	YEPO_YEAST	P40039	saccharomyc	830	6	1.3	593	1	US22_HCMVA	P09722	human cytom
758	6	1.3	529	1	Y632_CHLTR	O84637	schlamydia t	831	6	1.3	598	1	ABBI_RAT	P46933	rattus norv
759	6	1.3	530	1	YABD_SCHPO	O09812	schizosacch	832	6	1.3	598	1	CYLL_HUMAN	P37563	homo sapien
760	6	1.3	530	1	PR09_YEAST	P19736	saccharomyc	833	6	1.3	599	1	CENB_HUMAN	O00157	icalurid h
761	6	1.3	530	1	PSD3_MOUSE	P14685	mus musculus	834	6	1.3	599	1	YG58_HSV1L	O10110	schizosacch
762	6	1.3	530	1	UD12_HUMAN	P36509	homo sapien	835	6	1.3	599	1	YAOB_SCHPO	O00157	icalurid h
763	6	1.3	533	1	FCY2_YEAST	P17064	saccharomyc	836	6	1.3	599	1	YV06_CAEEL	O93655	caenorhabdi

837	6	1.3	600	1	SF08_YEAST	P41833 saccharomyc	910	6	1.3	687	1	CSTA_HELPJ	O92447 helicobacte
838	6	1.3	602	1	VE1_CRPVK	P03112 cottonitall	911	6	1.3	687	1	CSTA_HELPY	P56190 helicobacte
839	6	1.3	603	1	LCB2_SCHPO	O09925 schizosacch	912	6	1.3	691	1	HSF_DROME	P22813 drosophila
840	6	1.3	604	1	VE1_HPV38	O80909 human papil	913	6	1.3	692	1	ANR6_HUMAN	O94294 homo sapien
841	6	1.3	604	1	VFIC_BACSU	P54719 bacillus su	914	6	1.3	695	1	APP2_MOUSE	O06335 mus musculu
842	6	1.3	606	1	ABD4_HUMAN	O14678 homo sapien	915	6	1.3	697	1	NANB_STRPN	O044727 streptococc
843	6	1.3	606	1	ACEA_MYCLE	P46831 mycobacteri	916	6	1.3	699	1	SRCH_CHICK	P23327 homo sapien
844	6	1.3	607	1	ALBU_BOVIN	P02769 bos taurus	917	6	1.3	700	1	MR11_CHICK	O91427 homo sapien
845	6	1.3	607	1	ALBU_SHEEP	P14639 ovis aries	918	6	1.3	702	1	VCB1_ECOLI	P75864 escherichia
846	6	1.3	608	1	ALBU_FELCA	P49064 felis silve	919	6	1.3	706	1	NUCL_MOUSE	P09405 mus musculu
847	6	1.3	614	1	AL11_ARAHY	P43237 arachis hyp	920	6	1.3	711	1	MLLA_STRCO	O53902 streptomyc
848	6	1.3	614	1	VAA1_DROME	P48602 drosophila	921	6	1.3	712	1	CN4C_HUMAN	O08493 homo sapien
849	6	1.3	614	1	VAA2_DROME	O27331 drosophila	922	6	1.3	712	1	NUCL_RAT	P13383 rattus norv
850	6	1.3	614	1	VAS1_HAEIN	O57180 haemophilus	923	6	1.3	712	1	SM1A_CAEEL	O17330 caenorhabdi
851	6	1.3	615	1	HIC2_HUMAN	O961b3 homo sapien	924	6	1.3	714	1	CADD_MOUSE	O94715 mus musculu
852	6	1.3	615	1	VAA2_HUMAN	P38607 homo sapien	925	6	1.3	715	1	IGAA_YERE	O81722 yeastinia pe
853	6	1.3	615	1	VATA_AEDAE	O16109 aedes aegypt	926	6	1.3	715	1	NU5M_NEOCR	P05510 neurospora
854	6	1.3	617	1	ASMA_ECOLI	P28249 escherichia	927	6	1.3	716	1	ENPL_RABIT	O18750 oryctolagus
855	6	1.3	617	1	VAA1_BOVIN	P14404 bos taurus	928	6	1.3	725	1	VY76_YEAST	P47144 saccharomyc
856	6	1.3	617	1	VAA1_HUMAN	P34606 homo sapien	929	6	1.3	726	1	TRE_BIADI	O02942 diaberus di
857	6	1.3	617	1	VAA1_MOUSE	P50516 mus musculu	930	6	1.3	730	1	FER1_DROME	O07407 drosophila
858	6	1.3	617	1	VAA1_PIG	O29048 sus scrofa	931	6	1.3	732	1	AT2N_ECOLI	P7617 escherichia
859	6	1.3	617	1	VATA_MANSE	P13400 manduca sex	932	6	1.3	732	1	POK_DROME	O01842 drosophila
860	6	1.3	619	1	RECO_HAEIN	P71359 haemophilus	933	6	1.3	743	1	PLAK_HUMAN	P14923 homo sapien
861	6	1.3	620	1	GG95_HUMAN	O08379 homo sapien	934	6	1.3	743	1	YCR6_YEAST	P25353 saccharomyc
862	6	1.3	620	1	UL32_HSYEB	P28952 equine herp	935	6	1.3	746	1	APP_RAT	P36633 rattus norv
863	6	1.3	621	1	PLAK_MOUSE	O02257 mus musculu	936	6	1.3	747	1	DLI2_HUMAN	O914W0 homo sapien
864	6	1.3	622	1	YXDM_MOUSE	P42424 bacillus su	937	6	1.3	747	1	FHUA_ECOLI	P06971 escherichia
865	6	1.3	624	1	MTN4_MOUSE	O89029 mus musculu	938	6	1.3	757	1	IGR7_HUMAN	O94b3x homo sapien
866	6	1.3	624	1	NKX3_RAT	O9ep90 rattus norv	939	6	1.3	763	1	AC03_HUMAN	O16853 homo sapien
867	6	1.3	625	1	RPOC_ANASP	P22704 anabaena sp	940	6	1.3	763	1	APP2_HUMAN	P06481 homo sapien
868	6	1.3	630	1	M1A3_HUMAN	O9nr34 homo sapien	941	6	1.3	764	1	PGR8_HUMAN	P04831 homo sapien
869	6	1.3	631	1	YBFS_BACSU	P38816 bacillus su	942	6	1.3	765	1	APP2_RAT	P15943 rattus norv
870	6	1.3	632	1	RECO_PASMU	O9c121 pasteurella	943	6	1.3	765	1	S23A_HUMAN	O15436 homo sapien
871	6	1.3	633	1	SOHR_RHIME	P15715 rhizobium m	944	6	1.3	767	1	S23B_HUMAN	O15437 homo sapien
872	6	1.3	635	1	PTMA_KLEPN	O9xbm7 klebsiella	945	6	1.3	767	1	S23B_MOUSE	O94662 mus musculu
873	6	1.3	635	1	RPSD_RICPR	P33451 rickettsia	946	6	1.3	768	1	PURL_SYNZ3	P72644 synechocyst
874	6	1.3	636	1	GYRB_THEMA	P77993 thermotoga	947	6	1.3	769	1	UR06_VZVD	P093002 varicella-z
875	6	1.3	637	1	NU5M_STRPU	P15552 strongyloce	948	6	1.3	776	1	SM4F_RAT	O92143 rattus norv
876	6	1.3	637	1	PTMA_ECOLI	P00550 escherichia	949	6	1.3	777	1	SM4F_MOUSE	O92123 mus musculu
877	6	1.3	639	1	P2B1_CAEEL	O42773 cryptococcu	950	6	1.3	777	1	VASB_SCHPO	O10146 schizosacch
878	6	1.3	641	1	HM38_CAEEL	O19720 caenorhabdi	951	6	1.3	778	1	EXP7_STRPN	P33597 streptococc
879	6	1.3	643	1	PD4A_RAT	P38659 rattus norv	952	6	1.3	778	1	RG12_MOUSE	O61193 mus musculu
880	6	1.3	652	1	NU5M_PODAN	P20679 rodospora a	953	6	1.3	779	1	GFEL_YEAST	P37120 saccharomyc
881	6	1.3	653	1	CIK4_HUMAN	P22459 homo sapien	954	6	1.3	780	1	STRN_MOUSE	O55106 mus musculu
882	6	1.3	653	1	GP11_SCHPO	O14357 schizosacch	955	6	1.3	780	1	STRN_RAT	P70482 rattus norv
883	6	1.3	654	1	CIK4_MOUSE	O61423 mus musculu	956	6	1.3	781	1	CYNB_HUMAN	P35222 homo sapien
884	6	1.3	654	1	CIK4_MUSBF	O28527 mustela put	957	6	1.3	781	1	CYNB_MOUSE	O02248 mus musculu
885	6	1.3	655	1	CIK4_RAT	P15385 rattus norv	958	6	1.3	781	1	CYNB_RAT	O94u82 rattus norv
886	6	1.3	656	1	Y691_RICPR	O9zcm2 rickettsia	959	6	1.3	781	1	CYNB_XENLA	P26233 xenopus lae
887	6	1.3	657	1	Y023_NPYOP	O10282 ortygia pseu	960	6	1.3	783	1	K6PF_ASERG	P78985 aspergillus
888	6	1.3	660	1	CI01_SQDAC	O73925 squalus aca	961	6	1.3	784	1	TKR2_CRIGR	O9r1f8 cricetulus
889	6	1.3	660	1	FH0B_ECOLI	P06972 escherichia	962	6	1.3	785	1	SYEB_THEMA	O94wz9 thermotoga
890	6	1.3	661	1	CI80_HUMAN	O99467 homo sapien	963	6	1.3	788	1	CD8A_HUMAN	O955e5 homo sapien
891	6	1.3	661	1	Y182_SYNZ3	O55774 synechocyst	964	6	1.3	795	1	ENPL_CHICK	P08110 gallus galli
892	6	1.3	666	1	MUR2_ENTHR	P39045 enterococcu	965	6	1.3	795	1	TRKA_HUMAN	P04662 homo sapien
893	6	1.3	666	1	NU5M_CHOCR	P48920 chondrus cr	966	6	1.3	797	1	CD89_HUMAN	O955e1 homo sapien
894	6	1.3	666	1	RCD1_YEAST	P38339 saccharomyc	967	6	1.3	797	1	VG48_HSVYA	O01033 herpesviru
895	6	1.3	667	1	SUT1_STYHA	P53391 stylosanthec	968	6	1.3	801	1	BRD2_HUMAN	P23454 homo sapien
896	6	1.3	668	1	UL52_HCMVA	P16793 human cytom	969	6	1.3	805	1	CI0H_TORMA	P21564 torpedo mar
897	6	1.3	674	1	CA1A_CHICK	P08125 gallus galli	970	6	1.3	806	1	SECA_MYCCE	P47318 mycoplasma
898	6	1.3	675	1	COP1_ARATJ	P43254 arabidopsis	971	6	1.3	809	1	AK2H_ECOLI	P00562 escherichia
899	6	1.3	675	1	OR1_COTJA	P23499 coturnix co	972	6	1.3	809	1	CI0H_TORCA	P35522 torpedo cal
900	6	1.3	679	1	GR75_CRIGR	O35501 cricetulus	973	6	1.3	812	1	FAED_ECOLI	P06970 escherichia
901	6	1.3	679	1	GR75_HUMAN	P38646 homo sapien	974	6	1.3	817	1	ARM_MUSDO	O02453 musca domes
902	6	1.3	679	1	GR75_MOUSE	P38647 mus musculu	975	6	1.3	813	1	RRPO_CRY	P14595 cybidium r
903	6	1.3	679	1	GR75_RAT	P48721 rattus norv	976	6	1.3	817	1	RRPO_TBSCC	P15962 tomato bush
904	6	1.3	680	1	GFAL_HUMAN	O06210 homo sapien	977	6	1.3	820	1	MDL2_YEAST	P13311 saccharomyc
905	6	1.3	680	1	VH2X_SCHPO	O74343 schizosacch	978	6	1.3	823	1	CN8A_MOUSE	O88502 mus musculu
906	6	1.3	681	1	VE1_HPV10	P36720 human papil	979	6	1.3	824	1	UTP2_HUMAN	O13187 homo sapien
907	6	1.3	683	1	ERGL_THEMA	O9x1y4 thermotoga	980	6	1.3	826	1	RSG5_HUMAN	O43374 homo sapien
908	6	1.3	683	1	SC31_RAT	O64319 rattus norv	981	6	1.3	827	1	ATC2_RHIME	P58342 rhizobium m
909	6	1.3	685	1	FH0B_SALTY	O87656 salmonella	982	6	1.3	830	1	BGLS_BUFETI	P16084 butyribdri

PSNL_HUMAN	STANDARD	PRT	467 AA.
983	6	1.3	833
984	6	1.3	834
985	6	1.3	837
986	6	1.3	841
987	6	1.3	843
988	6	1.3	843
989	6	1.3	843
990	6	1.3	847
991	6	1.3	847
992	6	1.3	848
993	6	1.3	852
994	6	1.3	856
995	6	1.3	858
996	6	1.3	859
997	6	1.3	860
998	6	1.3	864
999	6	1.3	865
1000	6	1.3	865

1000 6 1.3 865 1 VGLR_HSYMD

ALIGNMENTS

RESULT 1

PSNL_HUMAN STANDARD; PRT; 467 AA.

AC P49768; Q14762; Q15719; Q15720;

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Presentin 1 (PS-1) (S182 protein).

GN PSEN1 OR PSNL1 OR AD3 OR PSI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_Taxid=9606;

111

SEQUENCE FROM N.A. AND VARIANTS AD (ISOFORMS I-467 AND I-463).

RC TISSUE-Brain;

RX MEDLINE=95319502; Pubmed=7596406;

RA Sherrington R., Rogae E.I., Liang Y., Rogae E.A., Levesque G., Ikeda M., Chl H., Lin C., Li G., Holman K., Tsuda T., Mar L., Pines J., F., Bunt A.C., Montesi M.P., Sorbi S., Rainero I., Sansone P., Polinsky R.J., Masco W., da Silva H.A.R., Haines J.L., Perlick-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;

RT "Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease."

RL Nature 375:754-760(1995)

112

SEQUENCE FROM N.A. (ISOFORMS I-463 AND I-374).

RC TISSUE-Blood, and Brain;

RX MEDLINE=96193901; Pubmed=8641442;

RA Sahara N., Yahagi Y.-I., Takagi H., Kondo T., Okochi M., Usami M., Shirasawa T., Mori H.;

RT "Identification and characterization of presentin I-467, I-463 and I-374."

RL FEBS Lett. 381:7-11(1996).

113

SEQUENCE FROM N.A.

RA Rowen L., Mikan A., Qin S., Abbasi N., Dors M., Ratcliffe A., Madan A., Dickhoff R., Shaffer T., James R., Lasky S., Hood L.;

RT "Complete sequence of the gene for presentin 1."

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

114

SEQUENCE OF 1-113 FROM N.A.

RA Tsujimura A., Hashimoto-Gotoh T.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

115

SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RX MEDLINE=96160372; Pubmed=8574969;

RA Kovacs D.M., Fausett H.J., Page K.J., Kim T.-W., Molr R.D.,

RA Meriam D.E., Hollister R.D., Hallmark O.G., Mancini R., Felsenstein K.M., Hyman B.T., Tanzi R.E., Masco W.;

RT "Alzheimer-associated presentin 1 and 2: neuronal expression in brain and localization to intracellular membranes in mammalian cells."

RL Nat. Med. 2:224-229(1996).

116

PROCESSING.

RX MEDLINE=97317150; Pubmed=9173929;

RA Podlany M.B., Citron M., Amarante P., Sherrington R., Xia W., Zhang J., Diehl T., Levesque G., Fraser P., Haass C., Koo E.H., Seubert P., St George-Hyslop P., Teplow D.B., Selkoe D.J.;

RT "Presentin protease undergoes heterogeneous endoproteolysis between Thr291 and Ala299 and occurs as stable N- and C-terminal fragments in normal and Alzheimer brain tissue."

RL Neurobiol. Dis. 3:325-337(1997).

117

FUNCTION, AND MUTAGENESIS OF MET-292.

RX MEDLINE=20014554; Pubmed=10545183;

RA Steiner H., Romig H., Pesold B., Philipp U., Baader M., Citron M., Loeischer H., Jacobsen H., Haass C.;

RT "Amyloidogenic function of the Alzheimer's disease-associated presentin 1 in the absence of endoproteolysis."

RL Biochemistry 38:14600-14605(1999).

118

FUNCTION.

RX MEDLINE=20062913; Pubmed=10593990;

RA Ray W.J., Yao M., Mumm J., Schroeter E.H., Safitg P., Wolfe M., Selkoe D.J., Kopan R., Goate A.M.;

RT "Cell surface presentin-1 particulates in the gamma-secretase-like proteolysis of Notch."

RL J. Biol. Chem. 274:36801-36807(1999).

119

FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.

RX MEDLINE=99221485; Pubmed=10206644;

RA Wolfe M.S., Xia W., Ostaszewski B.L., Diehl T.S., Kimberly W.T., Selkoe D.J.;

RT "Two transmembrane aspartates in presentin-1 required for presentin endoproteolysis and gamma-secretase activity."

RL Nature 398:513-517(1999).

120

FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.

RX MEDLINE=20359495; Pubmed=10899933;

RA Berzovska O., Jack C., McLean P., Aster J.C., Hicks C., Xia W., Wolfe M.S., Kimberly W.T., Weinmaster G., Selkoe D.J., Hyman B.T.;

RT "Aspartate mutations in presentin and gamma-secretase inhibitors both impair notch proteolysis and nuclear translocation with relative preservation of notch signaling."

RL J. Neurochem. 75:583-593(2000).

121

FUNCTION, AND MUTAGENESIS OF LEU-286.

RX MEDLINE=20283925; Pubmed=10811883;

RA Kulic L., Walter J., Multhaup G., Teplow D.B., Baumeister R., Romig H., Capell A., Steiner H., Haass C.;

RT "Separation of presentin function in amyloid beta-peptide generation and endoproteolysis of Notch."

RL Proc. Natl. Acad. Sci. U.S.A. 97:5913-5918(2000).

122

FUNCTION.

RX Pubmed=11226248;

RA Baki L., Marambaud P., Efthimiopoulos S., Georgakopoulos A., Wen P., Cui W., Shioi Y., Koo E., Ozawa M., Friedrich V.L., Robakis N.K.;

RT "Presentin-1 binds cytoplasmic epithelial cadherin, inhibits cadherin/p120 association, and regulates stability and function of the cadherin/catenin adhesion complex."

RL Proc. Natl. Acad. Sci. U.S.A. 98:2381-2386(2001).

123

INTERACTION WITH DELTA-2 CATEININ.

RX MEDLINE=99155075; Pubmed=10037471;

RA Levesque G., Yu G., Nishimura M., Zhang D.M., Levesque L., Yu H., Xu D., Liang Y., Rogae E., Ikeda M., Duthie M., Murgolo N., Wang L., Vanderveere P., Bayne M.L., Strader C.D., Rommens J.M., Fraser P.E., St George-Hyslop P.;

RT "Presenilins interact with armadillo proteins including
RT neural-specific plakophilin-related protein and beta-catenin."
RL J. Neurochem. 72:999-1008(1999).
RN [14]
RP REVIEW ON VARIANTS.
RX MEDLINE-97029239; PubMed-8875251.
RA Cruts M., Hendriks L., Van Broeckhoven C.;
RT "The presenilin genes: a new gene family involved in Alzheimer disease
pathology."
RL Hum. Mol. Genet. 5:1449-1455(1996).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE-98180715; PubMed-9521418;
RA Cruts M., van Broeckhoven C.;
RT "Presenilin mutations in Alzheimer's disease."
RL Hum. Mutat. 11:183-190(1998).
RN [16]
RP VARIANTS AD THR-143 AND ALA-384.
RX MEDLINE-96177673; PubMed-8634711;
RA Cruts M., Backhovens H., Wang S.-Y., van Gassen G., Theuns J.,
RA de Jonghe C., Wehnert A., de Voecht J., de Winter G., Cras P.,
RA Bryland M., Datsen N., Weissenbach J., den Dunnen J.T., Martin J.-J.,
RA Hendriks L., Van Broeckhoven C.;
RT "Molecular genetic analysis of familial early-onset Alzheimer's
disease linked to chromosome 14q24.3."
RL Hum. Mol. Genet. 4:2363-2372(1995).
RN [17]
RP VARIANTS AD L-82; H-115; T-139; R-163; T-231; L-264; V-392 AND Y-410.
RX MEDLINE-96177674; PubMed-8634712;
RA Camplon D., Flaman J.-M., Brice A., Hannequin D., Dubois B.,
RA Martin C., Moreau V., Charbonnier F., Didierjean O., Tardieu S.,
RA Peret C., Puel M., Pasquier F., Le Doze F., Bellis G., Calenda A.,
RA Agid Y., Martinez M., Mallet J., Bellis M., Clerget-Darpoux F.,
RT "Mutations of the presenilin 1 gene in families with early-onset
Alzheimer's disease."
RL Hum. Mol. Genet. 4:2373-2377(1995).
RN [18]
RP VARIANTS AD VAL-260; VAL-285 AND VAL-392.
RX MEDLINE-95379971; PubMed-7651536;
RA Rogae E.I., Sherrington R., Rogaeva E.A., Levesque G., Ikeda M.,
RA Liang Y., Chh H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
RA Nacmias B., Placentini S., Amaducci L., Chumakov I., Cohen D.,
RA Lannfelt L., Fraser P.E., Romenes J.M., St George-Hyslop P.H.;
RT "Familial Alzheimer's disease in kindreds with missense mutations in
a gene on chromosome 1 related to the Alzheimer's disease type 3
gene."
RL Nature 376:775-778(1995).
RN [19]
RP VARIANTS AD V-139; V-146; Y-163; T-267; A-280 AND G-280.
RX MEDLINE-96024664; PubMed-7550356;
RA Clark R.F., Hutton M., Fuldner R.A., Froelich S., Karran E.,
RA Talbot C., Crook R., Lendon C.L., Prihar G., He C., Korenblatt K.,
RA Martinez A., Wragg M., Busfield F., Behrens M.I., Myers A., Norton J.,
RA Morris J., Mehta N., Pearson C., Lincoln S., Baker M., Duff K.,
RA Zehr C., Perez-Tur J., Houlden H., Ruiz A., Ossa J., Lopez A.F.,
RA Arcos M., Madrigal L., Collinge J., Humphreys C., Asworth T.,
RA Sarter S., Fox N.C., Harvey R., Kennedy A., Roques P.K., Cline R.T.,
RA Phillips C.A., Venter J.C., Forsel L., Axelman K., Lilius L.,
RA Johnston J., Cowburn R., Vitanen M., Winblad B., Kosik K.S.,
RA Haltia M., Poyhonen M., Dickson D., Mann D., Neary D., Snowden J.,
RA Lantos P., Lannfelt L., Rossor M.N., Roberts G.W., Adams M.D.,
RA Hardy J., Goate A.M.;
RT "The structure of the presenilin 1 (S182) gene and identification of
six novel mutations in early onset AD families."
RL Nat. Genet. 11:219-222(1995).
RN [20]
RP VARIANTS AD PHE-96; ARG-163 AND THR-213.
RX MEDLINE-96310408; PubMed-8733303;
RA Kanino K., Sato S., Sasaki Y., Yoshiwara A., Nishiwaki Y., Takeda H.,
RA Tanabe H., Nishimura T., Li K., St George-Hyslop P.H., Miki T.,
RA Oghara T.;
RT "Three different mutations of presenilin 1 gene in early-onset

RT Alzheimer's disease families."
RL Neurosci. Lett. 208:195-198(1996).
RN [21]
RP VARIANT AD ASP-135.
RX MEDLINE-97369208; PubMed-9225696;
RA Crook R., Ellis R., Shanks M., Thal L.J., Perez-Tur J., Baker M.,
Query Match 78.4%; Score 366; DB 1; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDNREOEHNDRSLGHPPLSGNRPQNSR 60
DB 1 MTELPAPLSTYFQNAQMSQDNHLSNTVRSQNDNREOEHNDRSLGHPPLSGNRPQNSR 60
QY 61 QVEDDE 120
DB 61 QVEDDE 120
QY 121 DTEYGGORALSHLNAALIMISIVYVMTLLVLYKRYKYHAWLLISSLLFFSFTI 180
DB 121 DTEYGGORALSHLNAALIMISIVYVMTLLVLYKRYKYHAWLLISSLLFFSFTI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRQOAYLIMISALMALVFTKY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNLGVGMISIHMKGPLRQOAYLIMISALMALVFTKY 240
QY 241 LPENTAWLILAVISYVDVLAIVCPKGPLMLVETAEQERNETLFPALIVSSTWVWLVNNAE 300
DB 241 LPENTAWLILAVISYVDVLAIVCPKGPLMLVETAEQERNETLFPALIVSSTWVWLVNNAE 300
QY 301 GDPENQRVSNKSKYNAESTERESQDTVAENDGGFSEMEQORSHGPHRSTPESRAA 360
DB 301 GDPENQRVSNKSKYNAESTERESQDTVAENDGGFSEMEQORSHGPHRSTPESRAA 360
QY 361 VOELSSSTILAGEDPERGVKLGIDFIFYSVLYGKASATASGDMWTITACFAVAILIGLCL 420
DB 361 VOELSSSTILAGEDPERGVKLGIDFIFYSVLYGKASATASGDMWTITACFAVAILIGLCL 420
QY 421 TLLLIATFKKALPALPISITFGLVFYFATDYLVOPFMDQAFHOFYI 467
DB 421 TLLLIATFKKALPALPISITFGLVFYFATDYLVOPFMDQAFHOFYI 467
RESULT 2
PSNL_MICMU STANDARD: PRT: 467 AA.
ID PSNL_MICMU
AC P79802;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presenilin 1 (PS-1).
GN PSN1 OR PSNL1 OR PSL.
OS Microcebus murinus (Lesser mouse lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-97079199; PubMed-8920931;
RA Calenda A., Weste-Frances N., Czech C., Pradier L., Bons N.,
RA Bellis M.;
RT "Molecular cloning, sequencing, and brain expression of the
presenilin 1 gene in Microcebus murinus."
RL Biochem. Biophys. Res. Commun. 228:430-439(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND

```

CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: I-467 (SHOWN HERE) AND I-
CC 463; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN NEURONS OF THE
CC DIFFERENT CORTICAL LAYERS AND HIPPOCAMPUS BUT ALSO IN SUBCORTICAL
CC STRUCTURES.
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z71333; CAA95930.1; -.
DR MEROPS: A22.001; -.
DR InterPro: IPR001108; Presentilin.
DR Pfam: PF01080; Presentilin.1.
DR PRINTS: PR01072; PRESENILIN.
KM Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack;
KM Alternative splicing.
FT CHAIN 1 298 PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT CHAIN 299 467 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 81 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 82 102 POTENTIAL.
FT DOMAIN 103 132 LUMENAL (POTENTIAL).
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 160 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 161 181 POTENTIAL.
FT DOMAIN 182 190 LUMENAL (POTENTIAL).
FT TRANSSEM 191 211 POTENTIAL.
FT DOMAIN 212 220 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 221 241 POTENTIAL.
FT DOMAIN 242 243 LUMENAL (POTENTIAL).
FT TRANSSEM 244 264 POTENTIAL.
FT DOMAIN 265 407 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 408 428 POTENTIAL.
FT TRANSSEM 433 453 POTENTIAL.
FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SITE 292 293 SIMILARITY).
FT SITE 293 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SITE 293 293 SIMILARITY).
FT VARSPIC 26 29 MISSING (IN ISOFORM I-463).
FT FT MISSING (IN ISOFORM I-463).
SO SEQUENCE 467 AA: 52384 MM: D986FF2CA7F2975C CRC64;

Query Match 22.9%: Score 107; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 GYGMISIHKKGPRLQOAVLIMISALMAVFTKYLEPENTAWLLAVISYDVAVCPK 265
DB 206 GYGMISIHKKGPRLQOAVLIMISALMAVFTKYLEPENTAWLLAVISYDVAVCPK 265
QY 266 GPLMLVETAOERNETLFPALITYSSITWMLVYNAEGDEPEQORRYSKN 312
DB 266 GPLMLVETAOERNETLFPALITYSSITWMLVYNAEGDEPEQORRYSKN 312

RESULT 3
PSNL_RAT PSNL_RAT STANDARD: PRT: 468 AA.
AC P97887; P97529;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentilin 1 (PS-1) (S182 protein).
DE PSNL OR PSNL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OE

```

```

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=97199371; PubMed=9047347;
RA Taniguchi T., Hashimoto T., Taniguchi R., Shimada K., Kawamata T.,
RA Yasuda M., Nakai M., Terashima A., Koizumi T., Maeda K., Tanaka C.;
RT "Cloning of the cDNA encoding rat presentilin-1."
RL Gene 186:73-75(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=96255262; PubMed=8710164;
RA Takahashi H., Murayama M., Takashima A., Mercken M., Nakazato Y.,
RA Noguchi K., Imahori K.;
RT "Molecular cloning and expression of the rat homologue of
RT presentilin-1."
RL Neurosci. Lett. 206:113-116(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPEPTIDOLYTIC FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D82578; BAA11575.1; -.
DR EMBL: D82363; BAA11564.1; -.
DR MEROPS: A22.001; -.
DR InterPro: IPR001108; Presentilin.
DR Pfam: PF01080; Presentilin.1.
KM Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack;
KM Alternative splicing.
FT CHAIN 1 298 PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT CHAIN 299 468 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 83 103 POTENTIAL.
FT DOMAIN 104 132 LUMENAL (POTENTIAL).
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 160 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 161 181 POTENTIAL.
FT DOMAIN 182 194 LUMENAL (POTENTIAL).
FT TRANSSEM 195 215 POTENTIAL.
FT DOMAIN 216 220 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 221 241 POTENTIAL.
FT DOMAIN 242 243 LUMENAL (POTENTIAL).
FT TRANSSEM 244 264 POTENTIAL.
FT DOMAIN 265 407 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 408 428 POTENTIAL.
FT TRANSSEM 433 453 POTENTIAL.
FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SITE 292 293 SIMILARITY).
FT SITE 293 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT SITE 293 293 SIMILARITY).
FT CONFLICT 234 234 A -> S (IN REF. 2).
FT CONFLICT 381 381 K -> R (IN REF. 2).
SO SEQUENCE 468 AA: 52790 MM: 17CB791EB8A16FC0 CRC64;

Query Match 22.3%: Score 104; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 EODEDEDELTLKYGAKHVMLEVPVTLCAWVVAVATIKSVSYTRKDGQLIYPTPTDTE 123

```

```

DB 64 EGDDEDEDELTKGAKVHMLFVPTLCMVVVATIKSVSYTRKDDQLITPTEDTE 123
OY 124 TVGQALSHLNAIMISVIYVMTLLVLYKRCYKVIHAWLI 167
DB 124 TVGQALSHLNAIMISVIYVMTLLVLYKRCYKVIHAWLI 167

RESULT 4
PSNL_MOUSE STANDARD: PRT: 467 AA.
AC PA9769; Q9JLP9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presenilin 1 (PS-1) (S182 protein).
GN PSN1 OR PSNL1 OR AD3H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95319502; PubMed=7596406;
RA Sherrington R., Rogeev E.I., Liang Y., Rogeeva E.A., Levesque G.,
RA Ikeda M., Chl H., Lin C., Li G., Holman K., Tsuda T., Mar L.,
RA Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Ralnero I.,
RA Pinesasi L., Nee L., Chumakov I., Pollen D., Brooks A.,
RA Samsen P., Polinsky R.J., Masco W., da Silva H.A.R., Haines J.L.,
RA Perlick-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA Rommens J.M., St George-Hyslop P.H.;
RT "Cloning of a gene bearing missense mutations in early-onset familial
RT Alzheimer's disease."
RL Nature 375:754-760(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=97442406; PubMed=9295283;
RA Mitsuda N., Roses A.D., Vitek M.P.;
RT "Transcriptional regulation of the mouse presenilin-1 gene."
RL J. Biol. Chem. 272:23489-23497(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SAM P8; TISSUE=Hippocampus;
RA Kumar V.B., Vyas K.C., Choudhary V., Franko M., Flood J.F.,
RA Morley J.E.;
RT "Molecular cloning and tissue distribution of presenilin-1 in
RT senescence accelerated mice (SAM P8) mice."
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.
CC MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTIC FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; LA2177; AAC42094.1; -
CC EMBL; AF007560; AAB72049.1; -
CC EMBL; AF149111; AAF73153.1; -
CC MEROPS; A22.001; -
CC MCD; MGI:1202717; Psen1.

```

```

DR InterPro: IPR001108; Presenilin.
DR Pfam: PF01080; Presenilin.1.
DR PRINTS: PR01072; PRESENILIN.
KW Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 298 PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
FT CHAIN 2 467 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 2 83 103 POTENTIAL.
FT DOMAIN 3 104 132 LUMENAL (POTENTIAL).
FT DOMAIN 4 133 153 POTENTIAL.
FT DOMAIN 5 154 160 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 6 161 181 POTENTIAL.
FT DOMAIN 7 182 194 LUMENAL (POTENTIAL).
FT DOMAIN 8 195 215 POTENTIAL.
FT DOMAIN 9 216 220 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 10 221 241 POTENTIAL.
FT DOMAIN 11 242 243 LUMENAL (POTENTIAL).
FT DOMAIN 12 244 264 POTENTIAL.
FT DOMAIN 13 265 407 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 14 408 428 POTENTIAL.
FT TRANSMEM 433 453 POTENTIAL.
FT TRANSMEM 433 453 POTENTIAL.
FT SITE 291 292
FT SITE 292 293
FT SITE 292 293
FT VARIAT 9 9 S -> T (IN STRAIN SAM P8).
FT VARIAT 40 40 D -> E (IN STRAIN SAM P8).
FT VARIAT 67 67 E -> CM (IN STRAIN SAM P8).
FT VARIAT 196 196 V -> L (IN STRAIN SAM P8).
FT VARIAT 321 322 R -> RD (IN STRAIN SAM P8).
SQ SEQUENCE 467 AA; 52639 MW; D07215B4BD2549 CRC64;

Query Match 20.8%; Score 97; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.8e-86;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 213 IHMKGPLRLOQAYLYMISALMALVFPKYLPENTAMVILAVSYVDLVNVCCKGPKRLMY 272
DB 213 IHMKGPLRLOQAYLYMISALMALVFPKYLPENTAMVILAVSYVDLVNVCCKGPKRLMY 272
OY 273 EYAOERNETLFPALYYSTWVLVYMAEGDPEAQRV 309
DB 273 EYAOERNETLFPALYYSTWVLVYMAEGDPEAQRV 309

RESULT 5
PSNL_BOVIN STANDARD: PRT: 478 AA.
AC 09XU97;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presenilin 1 (PS-1).
GN PSN1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Sahara N., Shirasawa T., Mori H.;
RT "Molecular cloning of bovine presenilin 1 gene."
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC SIMILARITY).
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTIC FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).

```



```

RT proteins."
RL Neurobio1. Dis. 5:323-333(1998).
CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC SIMILARITY).
CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y10140; CAA71228.1; -.
DR MEROPS: A22.002; -.
DR InterPro: IPR001108; Presenilin.
DR Pfam: PF01080; Presenilin.1.
DR PRINTS: PR01072; PRESENILIN.
KM Transmembrane: Phosphorylation: Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 297 PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
FT CHAIN 2 298 445 PRESENILIN 2 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 88 108 LUMENAL (POTENTIAL).
FT DOMAIN 109 138 POTENTIAL.
FT TRANSSEM 139 159 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 160 166 POTENTIAL.
FT TRANSSEM 167 187 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 188 200 LUMENAL (POTENTIAL).
FT TRANSSEM 201 221 POTENTIAL.
FT DOMAIN 222 223 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 224 244 POTENTIAL.
FT DOMAIN 245 249 LUMENAL (POTENTIAL).
FT TRANSSEM 250 271 POTENTIAL.
FT DOMAIN 272 388 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 389 409 POTENTIAL.
FT TRANSSEM 414 434 POTENTIAL.
FT NON_TER 445 445
SQ SEQUENCE 445 AA; 49475 MW; 0A01A764659E052 CRC64;

```

Query Match 6.0%; Score 28; DB 1; Length 445;
 Best local similarity 100.0%; Pred. No. 4.1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 ISVYDLVAVLCPRKGPLMLVETAEERNE 280
 DB 259 ISVYDLVAVLCPRKGPLMLVETAEERNE 286

RESULT 8
 PSN2_HUMAN
 ID PSN2_HUMAN STANDARD: PRT: 448 AA.
 AC P49810;
 DT 01-OCR-1996 (Rel. 34, Created)
 DT 01-OCR-1996 (Rel. 34, Last sequence update)
 DT 16-OCR-2001 (Rel. 40, Last annotation update)
 DE Presenilin 2 (PS-2) (STM-2) (ES-1) (ADSLP) (AD5).
 GN PSN2 OR PSN2 OR AD4 OR PS2 OR STM2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCB1_Taxid=9606;
 RX [1]
 RP SEQUENCE FROM N.A., AND VARIANT PAD ILE-141.
 RX MEDLINE=95365816; PubMed=763622;
 RA Levy-Lahad E., Masco W., Poorkaj P., Romano D.M., Oshima J.,

RA Pettingell W.H., Yu C.-E., Jondro P.D., Schmidt S.D., Wang K.,
 RA Crowley A.C., Fu Y.-H., Guenette S.Y., Galas D., Nemens E.,
 RA Wajsbom E.M., Bird T.D., Schellenberg G.D., Tanzi R.E.,
 RT "Candidate gene for the chromosome 1 familial Alzheimer's disease
 RT locus.";
 RL Science 269:973-977(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS PAD ILE-141 AND VAL-239.
 RC TISSUE=Brain, and Colon;
 RX MEDLINE=95379971; PubMed=7651536;
 RA Rogaeve E.I., Sherrington R., Rogaeve E.A., Levesque G., Ikeda M.,
 RA Liang Y., Chi H., Lin C., Holman K., Tsuda T., Mar L., Sorbi S.,
 RA Nemes B., Piacentini S., Amaducci L., Chumakov I., Cohen D.,
 RA Lannfelt L., Fraser P.E., Romenes J.M., St George-Hyslop P.H.;
 RT "familial Alzheimer's disease in kindreds with missense mutations in
 RT a gene on chromosome 1 related to the Alzheimer's disease type 3
 RT gene.";
 RL Nature 376:775-778(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96109229; PubMed=8618867;
 RA Li J., Ma J., Potter H.;
 RT "Identification and expression analysis of a potential familial
 RT Alzheimer disease gene on chromosome 1 related to AD3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:12180-12184(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Levy-Lahad E., Poorkaj P., Wang K., Fu Y.H., Oshima J.,
 RA Mulligan J., Schellenberg G.D.;
 RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=96160372; PubMed=8574969;
 RA Kovacs D.M., Fausett H.J., Page K.J., Kim T.-N., Molr R.D.,
 RA Merriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
 RA Felsenstein K.M., Hyman B.T., Tanzi R.E., Masco W.;
 RT "Alzheimer-associated presenilin 1 and 2: neuronal expression in
 RT brain and localization to intracellular membranes in mammalian
 RT cells.";
 RL Nat. Med. 2:224-229(1996).
 RN [6]
 RP MUTAGENESIS OF ASP-366.
 RX MEDLINE=99428546; PubMed=10497236;
 RA Steiner H., Duff K., Capell A., Romig H., Grim M.G., Lincoln S.,
 RA Hardy J., Yu X., Picciano M., Fechter K., Clifton M., Kopan R.,
 RA Pesold B., Keck S., Baader M., Tomita T., Baumeister R.,
 RA Haass C.;
 RT "A loss of function mutation of presenilin-2 interferes with amyloid
 RT beta-peptide production and notch signaling.";
 RL J. Biol. Chem. 274:28669-28673(1999).
 RN [7]
 RP MUTAGENESIS OF ASP-263 AND ASP-366.
 RX MEDLINE=20119269; PubMed=10652302;
 RA Kimberly W.T., Xia W., Rahmati T., Wolfe M.S., Selkoe D.J.;
 RT "The transmembrane aspartates in presenilin 1 and 2 are obligatory for
 RT gamma-secretase activity and amyloid beta-protein generation.";
 RL J. Biol. Chem. 275:3173-3178(2000).
 RN [8]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=98180715; PubMed=9521418;
 RA Cruts M., van Broeckhoven C.;
 RT "Presenilin mutations in Alzheimer's disease.";
 RL Hum. Mutat. 11:183-190(1998).
 RN [9]
 RP VARIANT AD HIS-62.
 RX MEDLINE=98046005; PubMed=9384602;
 RA Cruts M., van Duijn C.M., Backhovens H., van den Broeck M.,
 RA Wehnert A., Serneels S., Sherrington R., Hutton M., Hardy J.,
 RA St George-Hyslop P.H., Hofman A., van Broeckhoven C.;
 RT "Mutation of the genetic contribution of presenilin-1 and -2
 RT mutations in a population-based study of presenile Alzheimer
 RT disease.";
 RL Hum. Mol. Genet. 7:43-51(1998).

FT	DOMAIN	109	138	LUMINAL (POTENTIAL).
FT	TRANSMEM	139	159	POTENTIAL.
FT	DOMAIN	160	166	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	167	187	POTENTIAL.
FT	DOMAIN	188	200	LUMINAL (POTENTIAL).
FT	TRANSMEM	201	221	POTENTIAL.
FT	DOMAIN	222	223	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	224	244	POTENTIAL.
FT	DOMAIN	245	249	LUMINAL (POTENTIAL).
FT	TRANSMEM	250	270	POTENTIAL.
FT	DOMAIN	271	388	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	389	409	POTENTIAL.
FT	TRANSMEM	414	434	POTENTIAL.
FT	VARSPLC	263	296	MISSING (IN SHORT ISOFORM).
FT	VARIANT	62	62	R -> H (IN FAD).
FT	VARIANT	122	122	T -> P (IN EOAD).
FT	VARIANT	141	141	/FtId-VAR_009214.
FT	VARIANT	141	141	N -> I (IN FAD); VOLGA GERMAN PATIENTS).
FT	VARIANT	148	148	/FtId-VAR_006462.
FT	VARIANT	148	148	V -> I (IN FAD); LOAD; SPANISH PATIENTS).
FT	VARIANT	239	239	/FtId-VAR_007958.
FT	VARIANT	239	239	M -> I (IN EOAD).
FT	VARIANT	239	239	/FtId-VAR_009215.
FT	MUTAGEN	263	263	M -> V (IN FAD; ITALIAN PATIENTS).
FT	MUTAGEN	366	366	/FtId-VAR_006463.
FT	CONFLICT	123	123	D->R: REDUCES PRODUCTION OF AMYLOID BETA
FT	CONFLICT	325	325	IN APP PROCESSING.
FT	CONFLICT	358	358	D->I: REDUCES PRODUCTION OF AMYLOID BETA
FT	CONFLICT	432	448	IN APP PROCESSING AND OF NICD IN NOTCH1
SO	SEQUENCE	448 AA;	50140 MW;	PROCESSING.
	Query Match	6.0%;	Score 28;	P -> T (IN REF. 1).
	Best Local Similarity	100.0%;	Pred. No. 4.1e-19;	MISSING (IN REF. 3).
	Matches 28;	Conservative 0;	Mismatches 0;	R -> SGG (IN REF. 3).
			Indels 0;	MLVPEPMTLASHQLYI -> RKHSRFIQNM (IN
			Gaps 0;	REF. 3)
Qy	253	ISYVDLAVVLCPKGPLRLMLVETAEERNE	280	
Db	259	ISYVDLAVVLCPKGPLRLMLVETAEERNE	286	
RESULT 9				
PSN2_MOUSE				
ID	PSN2_MOUSE	STANDARD;	PRT;	448 AA.
AC	Q61144; P97935; P97934; O54977;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Presenilin 2 (PS-2) (AUG-3) (Alzheimer disease 4 homolog).			
GN	PSEN2 OR PSN2L OR ALG3 OR AD4H OR PS-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=97094860; PubMed=8940094;			
RA	Vito P., Wolozin B., Ganjel J.K., Iwasaki K., Lacena E., D'Adamo L.,			
RT	"Requirement of the familial Alzheimer's disease gene PS2 for			
RL	J. Biol. Chem. 271:31025-31028(1996)."			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NIH Swiss;			
RA	Sahara N., Mori H., Shiraawa T.;			
RT	"Molecular cloning of mouse presenilin 2 gene."			

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 340-448 FROM N.A.
 RC TISSUE-liver:
 RX MEDLINE=96152375; PubMed=8560270;
 RA Vito P., Lacana E., D'Adamo L.;
 RT "interfering with apoptosis: Ca(2+)-binding protein ALG-2 and
 RT Alzheimer's disease gene ALG-3.";
 RL Science 271:521-525(1996).
 CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
 CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
 CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
 CC C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
 CC ENDOPASMIC RETICULUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: UNIDIRECTIONALLY EXPRESSED, MOSTLY IN THE LIVER.
 CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U57324; AAC52937.1; -
 DR EMBL: U57325; AAC53311.1; -
 DR EMBL: AF038935; AAB92660.1; -
 DR EMBL: U49111; AAC52935.1; -
 DR MEROPS: A22.002; -
 DR MGD: MGI:109284; Psen2.
 DR InterPro: IPR001108; Presenilin.
 DR Pfam: PF01080; Presenilin.1.
 DR PRINTS: PR01072; PRESENILIN.
 KM Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
 FT CHAIN 1 297 PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
 FT CHAIN 298 448 PRESENILIN 2 CTF SUBUNIT.
 FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 88 108 LUMENAL (POTENTIAL).
 FT DOMAIN 109 138 LUMENAL (POTENTIAL).
 FT TRANSSEM 139 159 POTENTIAL.
 FT DOMAIN 160 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 167 187 POTENTIAL.
 FT DOMAIN 188 200 LUMENAL (POTENTIAL).
 FT TRANSSEM 201 221 POTENTIAL.
 FT DOMAIN 222 223 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 224 244 POTENTIAL.
 FT DOMAIN 245 249 LUMENAL (POTENTIAL).
 FT TRANSSEM 250 270 POTENTIAL.
 FT DOMAIN 271 388 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 389 409 POTENTIAL.
 FT TRANSSEM 414 434 POTENTIAL.
 FT CONFLICT 87 87 R -> V (IN REF. 2).
 FT CONFLICT 226 226 A -> H (IN REF. 2).
 FT CONFLICT 324 324 MISSING (IN REF. 2).
 SQ SEQUENCE 448 AA; 49955 MW; D6ECA9EF6360D411 CRC64;

Query Match 6.0%; Score 28; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4; 1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC 088777; 035546; 008947;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Presenilin 2 (PS-2).
 GN PSEN2 OR PSNL2 OR PS2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheta; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RA Frenzel S., Abdel A.S., Luebert H.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=97473536; PubMed=9332390;
 RA Takahashi H., Mercken M., Nakazato Y., Noguchi K., Mureyama M.,
 RA Tanahori K., Takashima A.;
 RT "Cloning of cDNA and expression of the gene encoding rat
 RT presenilin-2.";
 RL Gene 197:383-387(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=98207716; PubMed=9545577;
 RA Tanahashi H., Tabira T.;
 RT "Cloning of the cDNA encoding rat presenilin-2.";
 RL Biochem. Biophys. Acta 1396:259-262(1998).
 CC -1- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
 CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
 CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A
 CC C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
 CC ENDOPASMIC RETICULUM (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X99267; CAA67663.1; -
 DR EMBL: D83700; BAA22832.1; -
 DR EMBL: AB004454; BAA20406.1; -
 DR MEROPS: A22.002; -
 DR InterPro: IPR001108; Presenilin.
 DR Pfam: PF01080; Presenilin.1.
 DR PRINTS: PR01072; PRESENILIN.
 KM Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
 FT CHAIN 1 297 PRESENILIN 2 NTF SUBUNIT (BY SIMILARITY).
 FT CHAIN 298 448 PRESENILIN 2 CTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 88 106 LUMENAL (POTENTIAL).
 FT DOMAIN 107 141 LUMENAL (POTENTIAL).
 FT TRANSSEM 142 159 POTENTIAL.
 FT DOMAIN 160 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 167 188 POTENTIAL.
 FT DOMAIN 189 202 LUMENAL (POTENTIAL).
 FT TRANSSEM 203 219 POTENTIAL.
 FT DOMAIN 220 229 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 230 246 POTENTIAL.
 FT DOMAIN 247 252 LUMENAL (POTENTIAL).
 FT TRANSSEM 253 269 POTENTIAL.
 FT DOMAIN 270 386 CYTOPLASMIC (POTENTIAL).

```

FT TRANSMEM 387 406 POTENTIAL.
FT TRANSMEM 414 434 POTENTIAL.
FT TRANSMEM 7 7 S -> T (IN REF. 1).
FT CONFLICT 86 87 KH -> ND (IN REF. 3).
SQ SEQUENCE 448 AA; 50051 MW; 299a7c416405046c CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 1; Length 448;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISYVDLAVLCPEKPLMLVETAEERNE 280
DB 259 ISYVDLAVLCPEKPLMLVETAEERNE 286

RESULT 11
PSN2_BOVIN
ID PSN2_BOVIN STANDARD: PRT; 449 AA.
AC 09XT96;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presentin 2 (PS-2).
GN PSN2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Sahara N., Shirasawa T., Mori H.;
RT "Molecular cloning of bovine presentin 2 gene.";
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
CC EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY
CC FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS (BY
CC SIMILARITY).
CC -I- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NPF) AND A
CC C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -I- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL: AF038937; AAD39024.1; -.
DR MEROPS: A22.002; -.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin; 1.
DR PRINTS: PRO1072; PRESENTIN.
DR TRANSMEMbrane; Phosphorylation; Endoplasmic reticulum; Golgi stack.
FT CHAIN 1 298 PRESENTIN 2 NPF SUBUNIT (BY SIMILARITY).
FT CHAIN 299 449 PRESENTIN 2 CTF SUBUNIT (BY SIMILARITY).
FT DOMAIN 1 88 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 89 109 POTENTIAL.
FT TRANSMEM 110 139 LUMENAL (POTENTIAL).
FT TRANSMEM 140 160 POTENTIAL.
FT TRANSMEM 161 167 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 189 201 LUMENAL (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 223 224 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 246 250 LUMENAL (POTENTIAL).

```

```

FT TRANSMEM 251 271 POTENTIAL.
FT TRANSMEM 272 389 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 390 410 POTENTIAL.
FT TRANSMEM 415 435 POTENTIAL.
SQ SEQUENCE 449 AA; 50301 MW; 51350D05A02B2A7D CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 1; Length 449;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISYVDLAVLCPEKPLMLVETAEERNE 280
DB 260 ISYVDLAVLCPEKPLMLVETAEERNE 287

RESULT 12
PSN2_XENLA
ID PSN2_XENLA STANDARD: PRT; 449 AA.
AC 012977;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Presentin beta.
GN PS-BETA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE-97223465; PubMed-9070286;
RA Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;
RT "Cloning of Xenopus presentin-alpha and -beta cDNAs and their
RT differential expression in oogenesis and embryogenesis.";
RT Biochem. Biophys. Res. Commun. 231:392-396(1997).
CC -I- FUNCTION: MAY PLAY A ROLE IN NEGATIVE REGULATION OF APOPTOTIC
CC CASCADES DURING OOGENESIS AND EMBRYOGENESIS. AND IN
CC DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -I- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN OVARIES AND TO A LESSER
CC EXTENT IN KIDNEY, BRAIN, EYE AND LUNG. WEAK EXPRESSION IN TESTIS,
CC INTESTINE, LIVER AND HEART. PRESENT IN TRACE AMOUNTS IN SKELETAL
CC MUSCLE.
CC -I- DEVELOPMENTAL STAGE: ABUNDANT IN EARLY STAGES OF OOGENESIS AFTER
CC WHICH IT IS NEARLY CONSTANT.
CC -I- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL: D84428; BAA19571.1; -.
DR MEROPS: A22.002; -.
DR InterPro: IPR001108; Presentin.
DR Pfam: PF01080; Presentin; 1.
DR PRINTS: PRO1072; PRESENTIN.
DR TRANSMEMbrane; Glycoprotein.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 142 162 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
FT TRANSMEM 227 247 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT TRANSMEM 363 383 POTENTIAL.
FT TRANSMEM 390 410 POTENTIAL.
FT TRANSMEM 415 435 POTENTIAL.

```


FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 449 AA; 50274 MM; 2C2C105F5C723F2B CRC64;
 Query Match 5 88; Score 27; DB 1; Length 449;
 Best Local Similarity 100.08; Pred. No. 3,9e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 81 HVIMLEPVTLCMVVATIKSVFYT 107
 ||||||||||||||||||
 Db 90 HVIMLEPVTLCMVVATIKSVFYT 116
 RESULT 13
 PSN_DROME STANDARD: PRT: 541 AA
 ID 002199; 002395; 076802; Q9V3L9; Q9Y780; Q9Y3S1; 096340;
 AC 002199 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Presentin homolog (DPS) (DMPs).
 GN PSN OR PS OR CG18803/CG5868.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND DEVELOPMENTAL STAGE.
 RC TISSUE=Embryo; PubMed-9141085;
 RX MEDLINE=97285868; PubMed-9141085;
 RA Boulianne G.L., Lyvine-Bar I., Humphreys J.M., Liang Y., Lin C.,
 RA Rojaev E., St George-Hyslop P.H.;
 RT "Cloning and characterization of the Drosophila presentin
 RT homologue.";
 RL Neuroreport 8:1025-1029(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE (SHORT ISOFORM).
 RC STRAIN=Cañton-S; TISSUE=Embryo, and Head;
 RX MEDLINE=97260623; PubMed-9106743;
 RA Hong C.-S., Koo E.H.;
 RT "Isolation and characterization of Drosophila presentin homolog.";
 RL Neuroreport 8:665-668(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), TISSUE SPECIFICITY,
 RP DEVELOPMENTAL STAGE, SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=99279250; PubMed-10349633;
 RA Ye Y., Fortini M.E.;
 RT "Characterization of Drosophila presentin and its colocalization with
 RT Notch during development.";
 RL Mech. Dev. 79:199-211(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RX MEDLINE=99221486; PubMed-10206647;
 RA Ye Y., Lukinova N., Fortini M.E.;
 RT "Neurogenic phenotypes and altered Notch processing in Drosophila
 RT presentin mutants.";
 RL Nature 398:525-529(1999).
 RN [5]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND DEVELOPMENTAL STAGE.
 RC STRAIN=Cañton-S;
 RX MEDLINE=98331525; PubMed-9666900;
 RA Matfany G., Del-Favero J., Valero R., De Jonghe C., Woodrow S.,
 RA Hendriks L., Van Broeckhoven C., Gonzalez-Duarte R.;
 RT "Identification of a Drosophila presentin homologue: evidence of
 RT alternatively spliced forms.";
 RL J. Neurogenet. 12:41-54(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99423881; PubMed-10493744;
 RA Guo Y., Lyvine-Bar I., Zhou L., Boulianne G.L.;
 RT "Drosophila presentin is required for neuronal differentiation and
 RT affects notch subcellular localization and signaling.";
 RL J. Neurosci. 19:8435-8442(1999).

RN [7]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise J.R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriil J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclele J.M.,
 RA Palazuelo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE PATTERNING OF THE
 CC OPTIC LOBES. PROTEIN MAY ACT, TOGETHER WITH NOTCH, TO SPECIFY
 CC CELL FATES THROUGHOUT DEVELOPMENT.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
 CC ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM/PS-D; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- TISSUE SPECIFICITY: MATERNALLY EXPRESSED IN NURSE CELLS AND POLICLE
 CC CELLS. IN EARLY EMBRYOS, EXPRESSED IN ALL OR MOST CELLS AND LATER
 CC INCREASES IN CNS AND EPIDERMAL TISSUES. IN LARVAE, EXPRESSION IS
 CC SEEN IN ALL IMAGINAL DISKS, BRAIN AND OPTIC LOBES. IN PUPAE,
 CC EXPRESSION IS SEEN IN EYE DISK AND BRAIN.
 CC -I- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
 CC THROUGHOUT DEVELOPMENT.
 CC -I- SIMILARITY: BELONGS TO THE PRESENTIN FAMILY.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U77934; AAB61139.1; -
 CC EMBL: U78084; AAB53369.1; -
 CC EMBL: AF084184; AAC33129.1; -
 CC EMBL: AF084184; AAC33128.1; -
 CC EMBL: AF017024; AAD01610.1; -
 CC EMBL: AF017025; AAD01611.1; -
 CC EMBL: AF017026; AAD01612.1; -

```

DR EMBL: AF093402; AAD52707.1; -.
DR EMBL: AF093402; AAD52708.1; -.
DR EMBL: AE003591; NOT ANNOTATED_CDS.
DR EMBL: AE003591; AAF51598.1; -.
DR MEROPS: A22.0PW; -.
DR FlyBase: FBgn0019947; Psn.
DR InterPro: IPR001108; Presenilin.
DR Pfam: PF01080; Presenilin; 1.
DR PRINTS: PR01072; PRESENILIN.
KW Transmembrane; Glycoprotein; Alternative splicing.
FT TRANSMEM 107 127
FT TRANSMEM 155 175
FT TRANSMEM 183 203
FT TRANSMEM 217 237
FT TRANSMEM 243 263
FT TRANSMEM 266 286
FT TRANSMEM 304 324
FT TRANSMEM 482 502
FT TRANSMEM 507 527
FT CARBOHYD 129 129
FT CARBOHYD 339 339
FT CARBOHYD 410 410
FT VARSPIC 384 397
FT CONFLICT 80 81
SQ SEQUENCE 541 AA; 59304 MW; A3B3D54348A2C03F CRC64;

Query Match 4.7%; Score 22; DB 1; Length 541;
Best Local Similarity 100.0%; Pred. No. 3; le-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 TTACFAVAILIGLCTLLAI 427
Db 480 TTACFAVAILIGLCTLLAI 501

RESULT 14
PSN CAEEL STANDARD; PRT; 444 AA.
AC P52166; Q20076; Q9U9C7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Presenilin sel-12.
GN SEL-12 OR F35H12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditia; Rhabditoidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI-TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANT SER-60.
RC STRAIN-Bristol N2;
RX MEDLINE=96032531; PubMed=7566091;
RA Levitan D., Greenwald I.;
RT "Facilitation of lin-12-mediated signalling by sel-12, a
RL Caenorhabditis elegans S182 Alzheimer's disease gene.";
RN Nature 377:351-354(1995).
RN [2]
RP REVISIONS TO 84-85.
RA Levitan D.;
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RX STRAIN-Bristol N2;
RX MEDLINE=20372200; PubMed=10917532;
RA Wittenburg N., Eimer S., Lakowski B., Roehrig S., Rudolph C.,
RA Baumeister R.;
RT "Presenilin is required for proper morphology and function of neurons
in C. elegans.";
RN Nature 406:306-309(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Nelson J., Galtung S.;

```

```

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP REVISIONS.
RA Materston R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY FACILITATE LIN-12 MEDIATED RECEPTION OF
CC INTERCELLULAR SIGNALS. IT MIGHT BE DIRECTLY INVOLVED IN LIN-12
CC MEDIATED RECEPTION, FUNCTIONING AS A CO-RECEPTOR OR AS A
CC DOWNSTREAM EFFECTOR THAT IS ACTIVATED UPON LIN-12 ACTIVATION.
CC ALTERNATIVELY IT MAY BE INVOLVED IN A MORE GENERAL CELLULAR
CC PROCESS SUCH AS RECEPTOR LOCALIZATION OR RECYCLING AND HENCE
CC INFLUENCE LIN-12 ACTIVITY INDIRECTLY. Required cell-autonomously
CC for correct neurite connectivity of the AIX cholinergic
CC interneurons and their correct functioning in thermotaxis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in most neurons.
CC -!- SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U35660; AAA85511.1; -.
DR EMBL: AF171064; AAD50991.1; -.
DR EMBL: U41540; AAK39230.1; -.
DR MEROPS: A22.0PW; -.
DR WormPep: F35H12.3; CE24946.
DR InterPro: IPR001686; Nema-presenilin.
DR InterPro: IPR001108; Presenilin.
DR Pfam: PF01080; Presenilin; 1.
DR PRINTS: PR01072; PRESENILIN.
DR PRINTS: PR01075; PRESENILINSEL.
KW Transmembrane.
FT TRANSMEM 46 66
FT TRANSMEM 102 122
FT TRANSMEM 131 151
FT TRANSMEM 164 184
FT TRANSMEM 190 210
FT TRANSMEM 213 233
FT TRANSMEM 251 271
FT TRANSMEM 385 405
FT VARIANT 60 60
FT CONFLICT 413 444
SQ SEQUENCE 444 AA; 50034 MW; 37ADB124E16429C CRC64;

Query Match 3.9%; Score 18; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 EERGKVLGLGDFIFYSVL 392
Db 354 EERGKVLGLGDFIFYSVL 371

RESULT 15
PSNH ARATH STANDARD; PRT; 453 AA.
ID PSNH ARATH
AC 064668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Presenilin homolog.
GN AT1G08700 OR F22013.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

```

OX NCBI_TaxID=3702:
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia:
RA MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Brehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huitzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
RA Miltischar J., Miranda M., Nguyen M., Nierman W.C., Osborne B.T.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PRESENTILIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AC003981; AAF9776.1; -.
DR MEROPS: A22.0PW; -.
DR InterPro: IPR001108; Presentilin.
DR Pfam: PF01080; Presentilin.1.
DR PRINTS: PRO1072; PRESENTILIN.
KW Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT TRANSMEM 181 201 POTENTIAL.
FT TRANSMEM 370 390 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 418 438 POTENTIAL.
SQ SEQUENCE 453 AA; 49308 MW; 7FBDD9B86D97955E CRC64;

Query Match 3.28; Score 15; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 KLGSGDFRFSYLVG 394
DB 369 KLGSGDFRFSYLVG 383

RESULT 16
YGBQ_ECOLI STANDARD: PRT: 103 AA.
AC Q46894;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ygbQ.
GN YGBQ OR B2748 OR Z4056 OR ECS3602.
OS Escherichia coli, and
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

```

```

OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G., III, Blythe C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U29579; AAA69258.1; -.
DR EMBL: AE000358; AAC75790.1; -.
DR EMBL: AE000502; AAC57855.1; -.
DR EMBL: AP002562; BAB37025.1; -.
DR EcoGene: EG13111; ygbQ.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 11622 MW; 9B50A7EF637809D7 CRC64;

Query Match 1.7%; Score 8; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTLALLAI 427
DB 4 LTLALLAI 11

RESULT 17
22P1_RAT STANDARD: PRT: 176 AA.
AC P22282; G63674;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cystatin related protein 1 precursor (CRP-1) (Prostatic 22 kDa
DE glycoprotein P22K16/P22K20) (Androgen regulated 20 kDa protein).
GN CRP1.
OS Rattus norvegicus (Rat).
OC

```



```

CC -----
DR EMBL: U76207: AAC53028.1: -.
DR EMBL: Y07621: CAA68900.1: -.
DR EMBL: AF303001: AAC40769.1: -.
DR MGI: 109619; Neurog2.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH; 1.
DR SMART: SMO0353; HLH; 1.
DR Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
DR PROSITE: PS00038; HLH_1; FALSE_NEG.
DR PROSITE: PS50886; HLH_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation; Activator;
DR Neurogenesis; Developmental protein; Differentiation.
FT DNA_BIND 113 124 BASIC DOMAIN.
FT DOMAIN 125 165
FT CONFLICT 60 60 E -> G (IN REF. 2).
SQ SEQUENCE 263 AA; 28215 MW; 817EF8246BDCABE CRC64;

Query Match 1.7%; Score 8; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DEEDEEL 73
   |||||||
Db 38 DEEDEEL 45

RESULT 19
DCOR_LEIDO STANDARD; PRT; 707 AA.
ID DCOR_LEIDO
AC P27116;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Ornithine decarboxylase (EC 4.1.1.17) (ODC).
OS Leishmania donovani.
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92129311; PubMed=1339439;
RA Hanson S.S., Adelman J., Ollman B.;
RT "Amplification and molecular cloning of the ornithine decarboxylase
   gene of Leishmania donovani."
RL J. Biol. Chem. 267:2350-2359(1992).
CC -1- CATALYTIC ACTIVITY: L-ornithine - putrescine + CO(2).
CC -1- Cofactor: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY
   OF POLYAMINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine
   DECARBOXYLASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M81192: AAA29259.1: -.
DR PIR: A42322; A42322.
DR PIR: S27821; S27821.
DR HSP: P00860; 70DC.
DR InterPro: IPR000183; Decarboxylase2.
DR Pfam: PF00278; Orn_DAP_Arg_dec; 1.
DR Pfam: PF02784; Orn_Arg_dec_N; 1.
DR PRINTS: PR01179; ODACRBLASE.
DR PROSITE: PS00878; ODC DC 2.1; 1.
DR PROSITE: PS00879; ODC DC 2.2; 1.
DR Lysine decarboxylase; Pyridoxal phosphate; Polyamine biosynthesis.
FT BINDING 288 288 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT ACT_SITE 634 634 BY SIMILARITY.
SQ SEQUENCE 707 AA; 77396 MW; EBDFF14F791EC572D CRC64;

```

```

Query Match 1.7%; Score 8; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 EVFKTYNV 191
   |||||||
Db 168 EVFKTYNV 175

RESULT 20
MDRL_CRIGR STANDARD; PRT; 1276 AA.
ID MDRL_CRIGR
AC P21448;
DT 01-MAR-1991 (Rel. 18, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance protein 1 (P-glycoprotein 1).
GN ABCB1 OR PGY1 OR PGP1.
OS ABCB1 OR gistsens (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92135896; PubMed=1685679;
RA Endicott J.A., Sarangi F., Ling V.;
RT "Complete cDNA sequences encoding the Chinese hamster P-glycoprotein
   gene family."
RL DNA Seq. 2:89-104(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91154265; PubMed=1671863;
RA Devine S.E., Hussain A., Davide J.P., Melera P.W.;
RT "Full length and alternatively spliced pgp1 transcripts in multidrug-
   resistant Chinese hamster lung cells."
RL J. Biol. Chem. 266:4545-4555(1991).
RN [3]
RP SEQUENCE OF 706-1276 FROM N.A.
RX MEDLINE=88122132; PubMed=2893255;
RA Endicott J.A., Juranka P.F., Sarangi F., Gerlach J.H., Deuchars K.L.,
   Ling V.;
RT "Simultaneous expression of two P-glycoprotein genes in
   drug-sensitive Chinese hamster ovary cells."
RL Mol. Cell. Biol. 7:4075-4081(1987).
CC -1- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED
   DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
   CANNOT.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M60040: AAA68883.1: -.
DR EMBL: M59253: AAA37004.1: -.
DR EMBL: M17897: AAA37006.1: -.
DR PIR: A38696; DVHY1C.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001140; ABCtransportr.
DR Pfam: PF00005; ABC_tran; 2.
DR Pfam: PF00664; ABC_membrane; 2.
DR PRODOM: PD00006; ABC_transportr; 2.
DR SMART: SMO0382; AAA; 2.

```

```
DR PROSITE; PS00211: ABC_TRANSPORTER; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
MW Multigene family.
FT DOMAIN 1 50 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 117 71 POTENTIAL.
FT TRANSSEM 186 137 POTENTIAL.
FT TRANSSEM 206 206 POTENTIAL.
FT TRANSSEM 213 233 POTENTIAL.
FT TRANSSEM 294 314 POTENTIAL.
FT TRANSSEM 323 343 POTENTIAL.
FT TRANSSEM 344 707 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 708 728 POTENTIAL.
FT TRANSSEM 754 774 POTENTIAL.
FT TRANSSEM 830 850 POTENTIAL.
FT TRANSSEM 851 871 POTENTIAL.
FT TRANSSEM 934 954 POTENTIAL.
FT TRANSSEM 971 991 POTENTIAL.
FT DOMAIN 992 1276 POTENTIAL.
FT NP_BIND 424 431 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 1067 1074 ATP (POTENTIAL).
FT REPEAT 1 635 ATP (POTENTIAL).
FT REPEAT 636 1276
FT CONFLICT 338 339
SQ SEQUENCE 1276 AA; 140925 MW; 44F3F92A186B4DF6 CRC64;

Query Match 1.7%; Score 8; DB 1; Length 1276;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLILLAI 427
| 11111111
Db 854 LTLILLAI 861

RESULT 21
MDR3_MOUSE STANDARD; PRT; 1276 AA.
AC P21447;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE Multidrug resistance protein 3 (P-glycoprotein 3) (MDR1A).
GN ABCB1A OR ABCB4 OR PGY3 OR PGY-3 OR MDR3 OR MDR1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90205845; Pubmed=1969610;
RA Devault A., Gros P.;
RT "Two members of the mouse mdr gene family confer multidrug resistance
with overlapping but distinct drug specificities.";
RL Mol. Cell. Biol. 10:1652-1663(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90287150; Pubmed=1972547;
RA Hsu S.I.H., Cohen D., Kirschner L.S., Lothstein L., Hartstein M.,
Horwitz S.B.;
RT "Structural analysis of the mouse mdr1a (P-glycoprotein) promoter
reveals the basis for differential transcript heterogeneity in
multidrug-resistant J774.2 cells.";
RL Mol. Cell. Biol. 10:3596-3606(1990).
RN [3]
RP SEQUENCE OF 173-1276 FROM N.A.
RC STRAIN=BALB/c;
RA MEDLINE=89308614; Pubmed=2473069;
RA Hsu S.I.H., Lothstein L., Horwitz S.B.;
RT "Differential overexpression of three mdr gene family members in
multidrug-resistant J774.2 mouse cells. Evidence that distinct P-
glycoprotein precursors are encoded by unique mdr genes.";
RL J. Biol. Chem. 264:12053-12062(1989).
RC
RT J. FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED
```

```
CC DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: IN MOUSE THE MDR GENE FAMILY INCLUDES THREE OR MORE
CC RELATED BUT DISTINCT CELLULAR GENES.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M30697; AAA39517.1; -
DR EMBL: M33581; AAA39514.1; -
DR EMBL: M33580; AAA39518.1; -
DR EMBL: M24417; AAA03243.1; -
DR PIR: A34175; DVMSIA.
DR PIR: A34786; A34786.
DR MGI: MGI:97570; Abcb1a.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR001140; ABCtransportTM.
DR Pfam: PF00005; ABC_tran; 2.
DR Pfam: PF00664; ABC_membrane; 2.
DR Prodom: PD000006; ABC_transport; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE; PS00211: ABC_TRANSPORTER; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
MW Multigene family.
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 48 71 POTENTIAL.
FT TRANSSEM 117 136 POTENTIAL.
FT TRANSSEM 186 205 POTENTIAL.
FT TRANSSEM 212 232 POTENTIAL.
FT TRANSSEM 298 318 POTENTIAL.
FT TRANSSEM 327 346 POTENTIAL.
FT TRANSSEM 347 707 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 708 728 POTENTIAL.
FT TRANSSEM 753 773 POTENTIAL.
FT TRANSSEM 829 848 POTENTIAL.
FT TRANSSEM 853 880 POTENTIAL.
FT TRANSSEM 942 961 POTENTIAL.
FT TRANSSEM 964 984 POTENTIAL.
FT TRANSSEM 985 1276 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1276 1276
FT NP_BIND 423 430 ATP (BY SIMILARITY).
FT NP_BIND 1066 1073 ATP (BY SIMILARITY).
FT REPEAT 1 632
FT REPEAT 633 1276
FT CARBOHYD 83 83
FT CARBOHYD 87 87
FT CARBOHYD 90 90
FT CONFLICT 526 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 939 939 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 939 939 OL -> HV (IN REF. 2 AND 3).
FT CONFLICT 1036 1036 F -> S (IN REF. 2 AND 3).
FT CONFLICT 1036 1036 F -> V (IN REF. 2 AND 3).
SQ SEQUENCE 1276 AA; 140754 MW; 75C71F33E1F58481 CRC64;

Query Match 1.7%; Score 8; DB 1; Length 1276;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLILLAI 427
| 11111111
Db 853 LTLILLAI 860

RESULT 22
MDRL_HUMAN STANDARD; PRT; 1280 AA.
ID MDRL_HUMAN
AC P08183; Q12755; Q14812;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

DT 15-JUN-2002 (Ref. 41, Last annotation update)
DE Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen).
GN ABCB1 OR PGY1 OR MDRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67028230; PubMed=2876781.
RA Chen C.-J., Chin J.E., Ueda K., Clark D.P., Pastan I., Gottesman M.M.,
RA Roninson I.B.;
RT "Internal duplication and homology with bacterial transport proteins
RT in the mdr1 (P-glycoprotein) gene from multidrug-resistant human
RT cells.";
RL Cell 47:381-389(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094448; PubMed=1967175;
RA Chen C.-J., Clark D.P., Ueda K., Pastan I., Gottesman M.M.,
RA Roninson I.B.;
RT "Genomic organization of the human multidrug resistance (MDR1) gene
RT and origin of P-glycoproteins.";
RL J. Biol. Chem. 265:506-514(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190336; PubMed=9038218;
RA Chen G., Duran G.E., Steger K.A., Lacey N.J., Jaffrezou J.P.,
RA Dumontet C., Slikk B.I.;
RT "Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein,
RT altered phenotype, and resistance to cyclosporins.";
RL J. Biol. Chem. 272:5974-5982(1997).
RN [4]
RP SEQUENCE OF 1-234 FROM N.A.
RA Smith A., Beck C., Gibson A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 178-215 AND 800-856 FROM N.A.
RX MEDLINE=90290529; PubMed=1972623;
RA Geleier V., Weger S., Probst H.;
RT "mdr1/P-glycoprotein gene segments analyzed from various human
RT leukemic cell lines exhibiting different multidrug resistance
RT profiles.";
RL Biochem. Biophys. Res. Commun. 169:796-802(1990).
RN [6]
RP SEQUENCE OF 1-23 FROM N.A.
RA Kioke N., Tsudota J., Kakehi Y., Komano T., Gottesman M.M.,
RA Pastan I., Ueda K.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [7]
RP VARIANTS SER-893 AND THR-893.
RX MEDLINE=21686803; PubMed=11829140;
RA Saito S., Iida A., Sekine A., Miura Y., Ogawa C., Kawachi S.,
RA Higuchi S., Nakamura Y.;
RT "Three hundred twenty-six genetic variations in genes encoding nine
RT members of ATP-binding cassette, subfamily B (ABCB/MDR/TAP), in the
RT Japanese population.";
RL J. Hum. Genet. 47:38-50(2002).
CC -1- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED
CC DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, SMALL INTESTINE
CC AND BRAIN.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -1- DATABASE: NAME=Atlas Genet. CytoGenet. Oncol. Haematol.;
CC WWW="http://www.inbio.genef.fr/services/chromocancer/Genes/PGY1D105.html".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M14758; AAA59576.1; -;
DR EMBL; M29447; AAA59576.1; -;
DR EMBL; M29447; AAA59576.1; JOINED.
DR EMBL; M29424; AAA59576.1; JOINED.
DR EMBL; M29424; AAA59576.1; JOINED.
DR EMBL; M29426; AAA59576.1; JOINED.
DR EMBL; M29426; AAA59576.1; JOINED.
DR EMBL; M29428; AAA59576.1; JOINED.
DR EMBL; M29428; AAA59576.1; JOINED.
DR EMBL; M29429; AAA59576.1; JOINED.
DR EMBL; M29429; AAA59576.1; JOINED.
DR EMBL; M29431; AAA59576.1; JOINED.
DR EMBL; M29431; AAA59576.1; JOINED.
DR EMBL; M29432; AAA59576.1; JOINED.
DR EMBL; M29432; AAA59576.1; JOINED.
DR EMBL; M29433; AAA59576.1; JOINED.
DR EMBL; M29433; AAA59576.1; JOINED.
DR EMBL; M29434; AAA59576.1; JOINED.
DR EMBL; M29435; AAA59576.1; JOINED.
DR EMBL; M29436; AAA59576.1; JOINED.
DR EMBL; M29437; AAA59576.1; JOINED.
DR EMBL; M29438; AAA59576.1; JOINED.
DR EMBL; M29439; AAA59576.1; JOINED.
DR EMBL; M29440; AAA59576.1; JOINED.
DR EMBL; M29441; AAA59576.1; JOINED.
DR EMBL; M29442; AAA59576.1; JOINED.
DR EMBL; M29443; AAA59576.1; JOINED.
DR EMBL; M29444; AAA59576.1; JOINED.
DR EMBL; M29445; AAA59576.1; JOINED.
DR EMBL; M29446; AAA59576.1; JOINED.
DR EMBL; AF016535; AAB69423.1; -;
DR EMBL; AC002457; AAC82531.1; -;
DR EMBL; M37724; AAB88047.1; -;
DR EMBL; M37725; AAB88048.1; -;
DR EMBL; X58723; CAA41558.1; -;
DR PIR; A25059; DVH01;
DR PIR; A34914; A34914.
DR Genew; HGNC:40; ABCB1.
DR MIM; 171050; -;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001140; ABCtranspfltrm.
DR Pfam; PF00005; ABC_tran; 2.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD00006; ABC_transportr; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
KW Multigene family; Polymorphism.
FT DOMAIN 1 51
FT TRANSMEM 52 72
FT TRANSMEM 120 140
FT TRANSMEM 189 209
FT TRANSMEM 216 236
FT TRANSMEM 297 317
FT TRANSMEM 326 346
FT DOMAIN 347 710
FT TRANSMEM 711 731
FT TRANSMEM 757 777
FT TRANSMEM 833 853
FT TRANSMEM 854 874
FT TRANSMEM 937 957
FT TRANSMEM 974 994
FT DOMAIN 995 1280
FT NP_BIND 427 434
FT NP_BIND 1070 1077
FT REPEAT 1 637
FT REPEAT 1280 1280
FT CARBOHYD 91 91
FT CARBOHYD 94 94
FT CARBOHYD 99 99
FT VARIANT 893 893
FT VARIANT 893 893
FT VARIANT 893 893
FT CONFLICT 23 23
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> S (IN DBSNP:2032582).
/FTId=VAR_013361.
A -> T.
/FTId=VAR_013362.
S -> R (IN REF. 6).

```
FT CONFLICT 185 185 G -> V (IN REF. 1 AND 3).
FT CONFLICT 336 336 MISSING (IN REF. 3).
FT CONFLICT 412 412 G -> A (IN REF. 3).
FT CONFLICT 438 438 0 -> S (IN REF. 3).
SQ SEQUENCE 1280 AA; 141462 MW; ABIC279531F43675 CRC64;

Query Match
Best Local Similarity 1.78; Score 8; DB 1; Length 1280;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LLLLLL 427
DB 857 LLLLLL 864

RESULT 23
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 58 AA.
AC P79876; P56922;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin H precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8407;
RN SEQUENCE FROM N.A., SEQUENCE OF 47-56, AND SYNTHESIS OF 47-56.
RC TISSUE=SKIN;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL: Y09394; CAA70563.1; -.
CC DR Interpro: IPR004275; Brevinin.
CC PFam: PF03032; Brevinin.
CC KW Amphibian skin; Amidation; Signal; Multigene family.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT PROPEP 23 44
CC FT CHAIN 47 56 TEMPORIN H.
CC FT MOD_RES 56 56 AMIDATION (G-57 PROVIDE AMIDE GROUP).
CC SQ SEQUENCE 58 AA; 6806 MW; 684AECB0451E5E81 CRC64;

Query Match
Best Local Similarity 1.58; Score 7; DB 1; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 SLLLLF 176
DB 7 SLLLLF 13

RESULT 24
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 61 AA.
AC P79874;
DT 01-NOV-1997 (Rel. 35, Created)
```

```
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin B precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8407;
RN SEQUENCE FROM N.A., SEQUENCE OF 47-59, AND SYNTHESIS OF 47-59.
RC TISSUE=SKIN;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL: Y09393; CAA70562.1; -.
CC DR Interpro: IPR004275; Brevinin.
CC PFam: PF03032; Brevinin.
CC KW Amphibian skin; Antibiotic; Amidation; Signal; Multigene family.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT PROPEP 23 44
CC FT CHAIN 47 59 TEMPORIN B.
CC FT MOD_RES 59 59 AMIDATION (G-60 PROVIDE AMIDE GROUP).
CC SQ SEQUENCE 61 AA; 7101 MW; B73F75689C300357 CRC64;

Query Match
Best Local Similarity 1.58; Score 7; DB 1; Length 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 SLLLLF 176
DB 7 SLLLLF 13

RESULT 25
TEMP_RANTE
ID TEMP_RANTE STANDARD; PRT; 61 AA.
AC P79875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Temporin G precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8407;
RN SEQUENCE FROM N.A.
RP TISSUE=SKIN;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -1- SUBCELLULAR LOCATION: Secreted.
```



```

CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: Y09395; CAA70564.1; -.
CC DR InterPro: IPR004275; Brevinin.1.
CC DR Pfam: PF03032; Brevinin.1.
CC KW Amphibian skin; Antibiotic; Amidation; Signal; Multigene family.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT PROPEP 23 44 POTENTIAL.
CC FT CHAIN 47 59 TEMPORIN G.
CC FT MOD_RES 59 59 AMIDATION (G-60 PROVIDE AMIDE GROUP).
CC SQ SEQUENCE 61 AA: 7171 MW: 87548.67 Da
CC -----
OY Query Match 1.5%; Score 7; DB 1; Length 61;
OY Best Local Similarity 100.0%; Pred. No. 16;
OY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 170 SLLLF 176
OY 7 SLLLF 13
DB 7 SLLLF 13

RESULT 26
GAES_RANRU
ID GAES_RANRU STANDARD: PRT: 65 AA.
AC P80399; Q81329;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gaegurin-5 precursor.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Park J.M., Lee J.Y., Moon H.M., Lee B.J.;
RA MEDLINE=95091844; PubMed=7999137;
RA "Antimicrobial peptides from the skin of a Korean frog, Rana
RA rugosa."
RT "Antimicrobial peptides from the skin of a Korean frog, Rana
RT rugosa."
RL Biochem. Biophys. Res. Commun. 205:948-954(1994).
CC -1- FUNCTION: HAS A NON-HEMOCLYTIC ACTIVITY. HAS A BROAD SPECTRUM OF
CC ACTIVITY AGAINST BOTH GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA,
CC FUNGI AND PROTOZOA.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SKIN.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U22393; AAA64412.1; -.

```

```

DR InterPro: IPR004275; Brevinin.1.
DR Pfam: PF03032; Brevinin.1.
DR KW Amphibian skin; Antibiotic; Signal.
DR FT SIGNAL 1 22 POTENTIAL.
DR FT PROPEP 23 39 POTENTIAL.
DR FT CHAIN 42 65 GAEGURIN-5.
DR FT DISULFID 59 65 BY SIMILARITY.
DR FT CONFLICT 58 58 F->K (IN REF. 2).
DR SQ SEQUENCE 65 AA: 7414 MW: 81240.66 Da
DR -----
OY Query Match 1.5%; Score 7; DB 1; Length 65;
OY Best Local Similarity 100.0%; Pred. No. 17;
OY Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 170 SLLLF 176
OY 7 SLLLF 13
DB 7 SLLLF 13

RESULT 27
RLXN_RANCA
ID RLXN_RANCA STANDARD: PRT: 66 AA.
AC P39084;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Ranales A.; Chavanteu A.; Roch P.; Chiche L.; Grassi G.; Calas B.;
DE Ranalexin precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 47-66.
RP MEDLINE=94193792; PubMed=8144672;
RA Clark D.P., Durrell S., Maloy W.L., Zasloff M.;
RA "Ranalexin. A novel antimicrobial peptide from bullfrog (Rana
RA catesbeiana) skin, structurally related to the bacterial antibiotic,
RA polymyxin."
RL J. Biol. Chem. 269:10849-10855(1994).
RN [2]
RP STRUCTURE BY NMR OF RANALEXIN.
RP MEDLINE=98237592; PubMed=9578480;
RA Vignal E., Chavanteu A., Roch P., Chiche L., Grassi G., Calas B.,
RA Annelas A.;
RT "Solution structure of the antimicrobial peptide ranalexin and a
RT study of its interaction with perdeuterated dodecylphosphocholine
RT micelles."
RL Eur. J. Biochem. 253:221-228(1998).
CC -1- FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST
CC S.AUREUS AND E.COLI. IT ACTS AS WELL AS A MEMBRANE-DISRUPTIVE
CC AGENT AT HIGHER CONCENTRATIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GRANULAR GLANDS OF SKIN.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION STARTS AT METAMORPHOSIS AND
CC CONTINUES INTO ADULTHOOD.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: S69903; AAB30394.1; -.
CC DR PIR: A53744; A53744.
CC DR InterPro: IPR004275; Brevinin.1.
CC DR Pfam: PF03032; Brevinin.1.
CC KW Amphibian skin; Antibiotic; Hemolysis; Signal.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT PROPEP 21 44 SMALL ACIDIC PEPTIDE.

```

```
FT PEPTIDE 47 66 RANALEXIN.
SQ DISULFID 60 66
SEQUENCE 66 AA: 7615 MW: 0968AD58A3C8513 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 SLLLEFF 176
DB 7 SLLLEFF 13

RESULT 28
ATPL_BACCA STANDARD; PRT: 72 AA.
ID ATPL_BACCA
AC P41015;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase C chain (EC 3.6.3.14) (Lipid-binding protein).
GN ATP.
OS Bacillus caldotenax.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1395;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishizuka M.;
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC
CC COMPONENT (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) = ADP + phosphate +
CC H(+)(out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- MISCELLANEOUS: DICICLOHEXYLCARBODIIMIDE (DCCD) INHIBITS ATPASE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D38057; BAA07244.1; -.
DR HSSP: P00844; 1A91.
DR InterPro: IPR002379; ATPase_Csub.
DR InterPro: IPR000454; Eub_ATPase_Csub.
DR Pfam: PF00137; ATP-synt_C; 1.
DR PRINTS: PR00124; ATPASEC.
DR TIGRFAMS: TIGR01260; ATP_synt_C; 1.
DR PROSITE: PS00605; ATPASE_C; FALSE_NEG.
KW Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding.
FT BINDING 56 56 DICICLOHEXYLCARBODIIMIDE (BY SIMILARITY).
SQ SEQUENCE 72 AA: 7249 MW: 211ED1F2A538B51 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 FSFTYLG 183
DB 65 FSFTYLG 71

RESULT 29
ATPL_BACP3 STANDARD; PRT: 72 AA.
ID ATPL_BACP3
OC P00845;


```

```
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase C chain (EC 3.6.3.14) (Lipid-binding protein).
GN ATP.
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=70306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-88163679; Pubmed-2894854;
RA Ohta S., Yohda M., Ishizuka M., Hirata H., Hamamoto T.,
RA Otawara-Hamamoto Y., Matsuda K., Kagawa Y.;
RT "Sequence and over-expression of subunits of adenosine triphosphate
RT synthase in thermophilic bacterium PS3.";
RL Biochim. Biophys. Acta 933:141-155(1988).
RN [2]
RP SEQUENCE.
RX MEDLINE-80245993; Pubmed-6447066;
RA Hoppe J., Sebald W.;
RT "Amino acid sequence of the proteolipid subunit of the proton-
RT translocating ATPase complex from the thermophilic bacterium PS-3.";
RL Eur. J. Biochem. 107:57-65(1980).
CC -1- FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC
CC COMPONENT (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) = ADP + phosphate +
CC H(+)(out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- MISCELLANEOUS: DICICLOHEXYLCARBODIIMIDE (DCCD) INHIBITS ATPASE.
CC -1- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X07804; CAA30649.1; -.
DR PIR: A01048; LMHMA3.
DR PIR: S02255; S02255.
DR HSSP: P00844; 1A91.
DR InterPro: IPR002379; ATPase_Csub.
DR InterPro: IPR000454; Eub_ATPase_Csub.
DR Pfam: PF00137; ATP-synt_C; 1.
DR PRINTS: PR00124; ATPASEC.
DR TIGRFAMS: TIGR01260; ATP_synt_C; 1.
DR PROSITE: PS00605; ATPASE_C; 1.
KW Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding;
KW Formylation.
FT MOD_RES 1 1 FORMYLATION.
FT BINDING 56 56 DICICLOHEXYLCARBODIIMIDE (BY SIMILARITY).
SQ SEQUENCE 72 AA: 7334 MW: 211ED1F2BD740FE1 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 FSFTYLG 183
DB 65 FSFTYLG 71

RESULT 30
ATPL_BACST STANDARD; PRT: 72 AA.
ID ATPL_BACST
AC P42011;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)


```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 RA ATP synthase C chain (EC 3.6.3.14) (Lipid-binding protein).
 GN ATP.
 OS Bacillus stearothermophilus.
 CC Bacteria; Firmicutes; Bacillales; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishizuka M., Kamel T.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS ONE OF THE THREE CHAINS OF THE NONENZYMATIC
 CC COMPONENT (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) = ADP + phosphate +
 CC H(+)(out).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- MISCELLANEOUS: DICYCLOHEXYLCARBODIIMIDE (DCCD) INHIBITS ATPASE.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D38059; BAA07251.1; -
 DR HSSP: P00844; IAG1.
 DR InterPro: IPR002379; ATPase_Csub.
 DR InterPro: IPR000454; Eub_ATPase_Csub.
 DR Pfam: PF00137; ATP_syn_C; 1.
 DR PRINTS: PR00124; ATPASEC.
 DR TIGRFAMs: TIGR01260; ATP_syn_C; 1.
 DR PROSITE: PS00605; ATPASE_C; 1.
 KW Hydrogen ion transport; CF(0); Transmembrane; Lipid-binding.
 FT BINDING 56 56 DICYCLOHEXYLCARBODIIMIDE (BY SIMILARITY).
 SO SEQUENCE 72 AA; 7348 MW; 21ED564661D2FE1 CRC64;

 Query Match 1.5%; Score 7; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy 177 FSEYILG 183
 |||||
 Db 65 FSEYILG 71

 RESULT 31
 YMJ0_CAEEL
 ID YMJ0_CAEEL STANDARD: PRT: 106 AA.
 AC P34485;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein F59B2.10 in Chromosome III.
 GN F59B2.10.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Cosey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinon-Sproat J.,
 RA Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z11505; CAA7587.2; -
 DR PIR: S31130; S31130.
 DR WormPep: F5982.10; CE28835.
 KW Hypothetical protein.
 FT DOMAIN 11 14 POLY-LEU.
 SO SEQUENCE 106 AA; 11599 MW; FFOCCF5EEC2777A6 CRC64;

 Query Match 1.5%; Score 7; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy 168 ISSLLLL 174
 |||||
 Db 8 ISSLLLL 14

 RESULT 32
 R22A_YEAST
 ID R22A_YEAST STANDARD: PRT: 120 AA.
 AC P05749;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 60S ribosomal protein L22-A (Yl31) (RP4).
 GN RPL22A OR YLR061W OR L2168.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andre B., Urrestazu L.A.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-51.
 RX MEDLINE=83048950; PubMed=6814480;
 RA Otake E., Higo K.-I., Osawa S.;
 RT "Isolation of seventeen proteins and amino-terminal amino acid
 RT sequences of eight proteins from cytoplasmic ribosomes of yeast.";
 RL Biochemistry 21:4545-4550(1982).
 CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L22 IN YEAST.
 CC -1- SIMILARITY: BELONGS TO THE L22E FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X94607; CAA64308.1; -

```

DR EMBL; 273233; CAA97592.1; -
DR PIR; S11582; S11582.
DR SGD; S0004051; RPL22A.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
DR ProDom; PD007306; Ribosomal_L22e; 1.
DR Ribosomal protein; Multigene family.
KW INT_MET
FT CONFLICT 48 48 N -> D (IN REF. 2).
SQ SEQUENCE 120 AA; 13562 MW; 84050FE484A56D69 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 120;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEE 72
Db 114 DEEDEE 120

RESULT 33
LSPA_CHLTR STANDARD; PRT; 167 AA.
ID LSPA_CHLTR
AC 08413;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
peptidase) (Signal peptidase II) (Spsae II).
GN LSPA OR CT408.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UM-3/CX;
RX MEDLINE=9900809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY CATALYZES THE REMOVAL OF
CC SIGNAL PEPTIDES FROM PROLIPOPROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
CC membrane proliipoproteins. Hydrolyzes Xaa-Xbb-Xcc-|-Cys, in which
CC Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc
CC is often Gly or Ala, and the Cys is alkylated on sulfur with a
CC diacylglyceryl group.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A8.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE001314; AAC68005.1; -
DR MEROPS; A08.001; -
DR InterPro; IPR001872; SigPhase_A8.
DR Pfam; PF01252; Peptidase_A8; 1.
DR PRINTS; PR00781; LITOSTIGTRASE.
DR ProDom; PD004304; SigPhase_A8; 1.
DR TIGRfams; TIGR00077; lspa; 1.
DR Hydroxylase; Aspartyl protease; Transmembrane; Complete proteome.
KW TRANSMEM
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.

```

```

FT TRANSMEM 139 159 POTENTIAL.
FT ACT_SITE 116 116 BY SIMILARITY.
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 167 AA; 18939 MW; 0B9752F830B01F12 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 167;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLILLA 426
Db 10 LTLILLA 16

RESULT 34
YF6_YEAST STANDARD; PRT; 169 AA.
ID YF6_YEAST
AC P43604;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical 18.8 kDa protein in HIS2-CDCl4 intergenic region.
GN YF026C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=96287654; PubMed=8686381;
RA Eki T., Naitou M., Hagiwara H., Abe M., Ozawa M., Sasanuma S.-I.,
RA Sasanuma M., Tsuchiya Y., Shibata T., Watanabe K., Ono A.,
RA Yamazaki M., Tashiro H., Hanaoka F., Murakami Y.;
RT "Fifteen open reading frames in a 30.8 kb region of the right arm of
RT chromosome VI from Saccharomyces cerevisiae.";
RL Yeast 12:177-190(1996).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50617; BAA09265.1; -
DR SGD; S0001922; YF026C.
KW Hypothetical protein.
SQ SEQUENCE 169 AA; 18809 MW; BBlF4943C9A6815F CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 169;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ITVALLI 202
Db 8 ITVALLI 14

RESULT 35
Y129_METUA STANDARD; PRT; 170 AA.
ID Y129_METUA

```

```

AC 057593;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M0129.
GN M0129.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota: Methanococci: Methanococcales:
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=963799; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Gilek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-F., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: STRONG. TO M.JANNASCHII M0554 AND M0587.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: 067470; AAB98118.1; -
DR TIGR: M0129; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 133 153 POTENTIAL.
SQ SEQUENCE 170 AA; 19621 MW; 4F3B62C7DDA89D9A CRC64;

Query Match 1.5%; Score 7; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 ISVIVM 146
DB 144 ISVIVM 150

RESULT 36
OLE1-ARATH STANDARD: PRT: 173 AA.
ID OLE1-ARATH
AC P29525;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Oleosin 18.5 kDa.
GN AT4G25140 OR F13W23.280.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC eustoids II: Brassicales: Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92288310; PubMed=1600152;
RX van Rooijen G.J., Terning L.I., Moloney M.M.;
RT "Nucleotide sequence of an Arabidopsis thaliana oleosin gene."
RL Plant Mol. Biol. 18:1177-1179(1992).

```

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Voickaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Ternyn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermair B., Meche R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Roben J.,
RA Van der Schueren J., Grymoprez B., Chung Y.-J., Vandenbussche F.,
RA Breken M., Meltjens I., Voet M., Bastiens I., Aert R., Delfoor E.,
RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koelter P.,
RA Bernelsier S., Hempel S., Feldpausch M., Lambrecht S., Van den Daele H.,
RA De Keyser A., Buysnaert C., Gleien J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Petlett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borikova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandjean K., Danner D., Herzl A.,
RA Neumann S., Argliou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabado G., Kuendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chiford F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA Ghibons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purrelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Belke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Haeremans K.,
RA Patnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spielgel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney J., Cloud J., Abbott K., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hofman J., Till S.,
RA Grnab S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
RN [3]
RP SEQUENCE OF 1-86 FROM N.A.
RC STRAIN=cv. Columbia;
RA Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (OCT-1992) to the EMBL/Genbank/DBP databases.
CC -1- FUNCTION: MAY HAVE A STRUCTURAL ROLE TO STABILIZE THE LIPID BODY
CC DURING DESICCATION OF THE SEED BY PREVENTING COALESCENCE OF THE
CC OIL. PROBABLY INTERACTS WITH BOTH LIPID AND PHOSPHOLIPID MOETIES
CC OF LIPID BODIES. MAY ALSO PROVIDE RECOGNITION SIGNALS FOR SPECIFIC
CC LIPASE ANCHORAGE IN LIPOLYSIS DURING SEEDLING GROWTH.
CC -1- SUBCELLULAR LOCATION: SURFACE OF OIL BODIES. OLEOSINS EXIST AT A
CC MONOLAYER LIPID/WATER INTERFACE.
CC -1- SIMILARITY: BELONGS TO THE OLEOSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X62353; CAA44225.1; -

```

```
DR EMBL: AL035523; CAB36756.1; -
DR EMBL: AL161562; CAB79423.1; -
DR EMBL: Z17738; CAA79049.1; -
DR PIR: S22143; S22143.
DR PIR: S22538; S22538.
DR InterPro: IPR00136; Oleosin.
DR Pfam: PF01277; Oleosin.1.
DR PROSITE: PS00811; OLEOSINS; 1.
KW Oil body; Multigene family.
FT DOMAIN 1 45 POLAR.
FT REPEAT 46 117 HYDROPHOBIC.
SQ SEQUENCE 173 AA; 18569 MW; 4F718BC380105F73 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 173;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ITVALLI 202
DB 90 ITVALLI 96

RESULT 37
OLE5_BRANA STANDARD; PRT; 175 AA.
ID OLE5_BRANA
AC P29109;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major oleosin Nap-II (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 43-77.
RC TISSUE=Seed;
RX MEDLINE=9111733; PubMed=1989697;
RA Murphy D.J., Keen J.N., O'Sullivan J.N., Au D.M.Y., Edwards E.-W.,
RA Jackson P.J., Cummins I., Gibbons T., Shaw C.H., Ryan A.J.;
RT "A class of amphipathic proteins associated with lipid storage bodies
RT in plants. Possible similarities with animal serum apolipoproteins.";
RL Biochim. Biophys. Acta 1088:86-94(1991).
CC -1- FUNCTION: MAY HAVE A STRUCTURAL ROLE TO STABILIZE THE LIPID BODY
CC DURING DESICCATION OF THE SEED BY PREVENTING COALESCENCE OF THE
CC OIL. PROBABLY INTERACTS WITH BOTH LIPID AND PHOSPHOLIPID MOIETIES
CC OF LIPID BODIES. MAY ALSO PROVIDE RECOGNITION SIGNALS FOR SPECIFIC
CC LIPASE ANCHORAGE IN LIPOLYSIS DURING SEEDLING GROWTH.
CC -1- SUBCELLULAR LOCATION: SURFACE OF OIL BODIES. OLEOSINS EXIST AT A
CC MONOLAYER LIPID/WATER INTERFACE.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES DURING THE DESICCATION PHASE OF
CC EMBRYO DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE OLEOSIN FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X58000; CAA41064.1; -
DR InterPro: IPR00136; Oleosin.
DR Pfam: PF01277; Oleosin.1.
DR PROSITE: PS00811; OLEOSINS; 1.
KW Seed; Oil body; Multigene family; Repeat.
FT NON_TER 1 1
FT DOMAIN 48 119 POLAR.
FT REPEAT 17 26 HYDROPHOBIC.
FT REPEAT 27 36
```

```
FT CONFLICT 49 49 V -> A (IN REF. 1; AA SEQUENCE).
FT CONFLICT 66 66 L -> A (IN REF. 1; AA SEQUENCE).
FT CONFLICT 72 72 A -> L (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 175 AA; 19349 MW; E16698E285ABC8 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 173;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ITVALLI 202
DB 92 ITVALLI 98

RESULT 38
OLE5_BRANA STANDARD; PRT; 183 AA.
ID OLE5_BRANA
AC P29109;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oleosin Bn-V (BnV) (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bienvenu;
RX MEDLINE=92379264; PubMed=1511134;
RA Keddie J., Edwards E.-W., Gibbons T., Shaw C., Murphy D.J.;
RT "Sequence of an oleosin cDNA from Brassica napus.";
RL Plant Mol. Biol. 19:1079-1083(1992).
CC -1- FUNCTION: MAY HAVE A STRUCTURAL ROLE TO STABILIZE THE LIPID BODY
CC DURING DESICCATION OF THE SEED BY PREVENTING COALESCENCE OF THE
CC OIL. PROBABLY INTERACTS WITH BOTH LIPID AND PHOSPHOLIPID MOIETIES
CC OF LIPID BODIES. MAY ALSO PROVIDE RECOGNITION SIGNALS FOR SPECIFIC
CC LIPASE ANCHORAGE IN LIPOLYSIS DURING SEEDLING GROWTH.
CC -1- SUBCELLULAR LOCATION: SURFACE OF OIL BODIES. OLEOSINS EXIST AT A
CC MONOLAYER LIPID/WATER INTERFACE.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES DURING THE DESICCATION PHASE OF
CC EMBRYO DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE OLEOSIN FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X63779; CAA45313.1; -
DR PIR: S25089; S25089.
DR InterPro: IPR00136; Oleosin.
DR Pfam: PF01277; Oleosin.1.
DR PROSITE: PS00811; OLEOSINS; 1.
KW Seed; Oil body; Multigene family; Repeat.
FT NON_TER 1 1
FT DOMAIN 48 119 POLAR.
FT REPEAT 11 20 HYDROPHOBIC.
FT REPEAT 21 30
SQ SEQUENCE 183 AA; 20286 MW; 7E791E2D4EC70A26 CRC64;

Query Match
Best Local Similarity 1.5%; Score 7; DB 1; Length 183;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ITVALLI 202
DB 92 ITVALLI 98
```

```

RESULT 39
US10_HSVSB STANDARD: PRT: 208 AA.
AC P30817;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Virion protein US10 homolog (Fragment).
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
ON NCBI_TaxID=10325;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92113572; PubMed=1309859;
RA Killen A.M., Harrington L., Wall L.V.M., Kelly D.C.;
RT "Nucleotide sequence analysis of a homologue of herpes simplex virus
RT type 1 gene US9 found in the genome of simian herpes B virus.";
RL J. Gen. Virol. 73:195-199(1992).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 US10,
CC EHV-1 66, EHV-4 ORF3, AND VZV 64/69.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S75996; AAB21003.2; -.
DR PIR: P00278; P00278.
DR ZINC-Finger.
FT ZN-FING 167 189 POTENTIAL.
FT NON_TER 1 1
SQ SEQUENCE 208 AA; 22837 MW; B8076C3AC0A25E6 CRC64;

Query Match 1.5%; Score 7; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 396 ASATASG 402
|111111|
Db 202 ASATASG 208

RESULT 40
UBC_ASPF2 STANDARD: PRT: 213 AA.
AC P25869;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ubiquitin-conjugating enzyme E2-21 kDa (EC 6.3.2.19)
DE [ubiquitin-protein ligase] (ubiquitin carrier protein).
GN ASFV-UBC.
OS African swine fever virus (isolate Malawi Lil 20/1) (ASFV).
OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
ON NCBI_TaxID=10500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92155177; PubMed=1310934;
RA Hingamp P.M., Arnold J.E., Mayer R.J., Dixon L.K.;
RT "A ubiquitin conjugating enzyme encoded by African swine fever
RT virus.";
RL EMBO J. 11:361-366(1992).
CC -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO
CC OTHER PROTEINS.
CC -1- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC diphosphate + protein N-ubiquityllysine.
CC -1- PATHWAY: Ubiquitin conjugation; second step.

```

```

CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR
CC UBIQUITIN-THIOLESTER FORMATION.
CC -1- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X62440; CAA44305.1; -.
DR EMBL: X71982; CAA50851.1; -.
DR PIR: S19158; S19158.
DR HSP; 002159; 20CZ.
DR InterPro: IPR000608; UBQ_conjugat.
DR Pfam: PF00179; UQ_con; 1.
DR ProDom: PD000461; UBQ_conjugat; 1.
DR SMART: SM00212; UBQC; 1.
DR PROSITE: PS00183; UBIQUITIN_CONJUGAT_1; 1.
DR PROSITE: PS0127; UBIQUITIN_CONJUGAT_2; 1.
DR SMART: SM00212; UBQC; 1.
KW Ub1 conjugation pathway; Ligase.
FT BINDING 85 85 UBIQUITIN (BY SIMILARITY).
FT DOMAIN 183 213 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 213 AA; 24468 MW; F9671BC7385D6DE CRC64;

Query Match 1.5%; Score 7; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 66 DEEDDEE 72
|111111|
Db 203 DEEDDEE 209

RESULT 41
RADC_SYNY3 STANDARD: PRT: 243 AA.
AC P52601;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA repair protein radc homolog.
GN RADC OR SL0766.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
ON NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64k to 92k of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RADC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D64000; BAA10123.1; -.
DR InterPro: IPR003583; HHH_1.
DR InterPro: IPR001405; RadC.
DR ProDom: PD007415; RadC; 1.
DR SMART: SM00278; Hhhl; 1.

```

```

DR  TIGRFAMS: TIGR00608; radc: 1.
DR  PROSITE: PS01302; RADC: 1.
DR  DNA repair: Complete proteome.
SQ  SEQUENCE 243 AA: 26973 MW: F0E9D51F999EF6B4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 243;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  75 LKYGAKH 81
    |||||
DB  21 LKYGAKH 27

RESULT 42
ISPE.THEMA STANDARD; PRT: 271 AA.
ID  ISPE.THEMA
AC  O9XIA3;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DE  15-JUN-2002 (Rel. 41, Last annotation update)
DE  4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148) (CMK)
DE  (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase).
GN  ISPE OR TM1383.
OS  Thermotoga maritima.
OC  Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC  Thermotogaceae; Thermotoga.
OX  NCBI_TaxID=2336;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MSB / DSM 3109;
RC  MEDLINE=99287316; PubMed=10360571;
RA  Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA  Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA  McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA  Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA  Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA  Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT  *Evidence for lateral gene transfer between Archaea and Bacteria from
RT  genome sequence of Thermotoga maritima.*;
RL  Nature 399:323-329(1999).
CC  -1- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY
CC  GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
CC  SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
CC  erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-
CC  D-erythritol.
CC  -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
CC  step.
CC  -1- SIMILARITY: BELONGS TO THE ISPE FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AE001791; AAD36453.1; -.
DR  TIGR: TM1383; -.
DR  InterPro: IPR001745; GHMPKase_ATP.
DR  InterPro: IPR004424; ISPE.
DR  Pfam: PF00288; GHMP_kinases; 1.
DR  TIGRFAMS: TIGR00154; ispe.1.
KW  transferase; kinase; isoprene biosynthesis; ATP-binding;
KW  Complete proteome.
KW  NP_BIND 97 107 ATP (POTENTIAL).
SQ  SEQUENCE 271 AA: 30056 MW: 3E9E47FDAB0F336D CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 271;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY  181 YLCEVERK 187
    |||||
DB  115 YLCEVERK 121

RESULT 43
YITL_BACSU STANDARD; PRT: 280 AA.
ID  YITL_BACSU
AC  P39803; P70946; O08139;
DT  01-FEB-1995 (Rel. 31, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Hypothetical protein yitl.
GN  YITL.
OS  Bacillus subtilis.
OC  Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=1423;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168 / DB104;
RC  MEDLINE=94042884; PubMed=8226659;
RA  Shiga Y., Yamagata H., Ueda S.;
RT  *Characterization of the gene encoding an intracellular proteinase
RT  inhibitor of Bacillus subtilis and its role in regulation of the
RT  major intracellular proteinase.*;
RL  J. Bacteriol. 175:7130-7137(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RC  MEDLINE=97177785; PubMed=9025291;
RA  Levine A., Vannier F., Roche B., Autret S., Mavel D., Seror S.J.;
RT  *A 10.3 kbp segment from nprB to argJ at the 102 degrees region of the
RT  Bacillus subtilis chromosome.*;
RL  Microbiology 143:175-177(1997).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=98015415; PubMed=9353931;
RA  Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.;
RT  *Sequencing of regions downstream of addA (98 degrees) and cItc (289
RT  degrees) in Bacillus subtilis.*;
RL  Microbiology 143:3305-3308(1997).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RC  MEDLINE=98044033; PubMed=9384377;
RA  Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA  Azevedo V., Bortner L., Bessieres P., Bolotin A., Borchert S.,
RA  Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA  Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA  Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA  Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA  Enlart K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA  Fritz C., Fujita M., Fujita Y., Funa S., Gallizzi A., Galleron N.,
RA  Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA  Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA  Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA  Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA  Kobayashi Y., Koelter P., Konigstein G., Krogh S., Kumano M.,
RA  Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA  Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA  Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA  Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA  Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA  Prieecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA  Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA  Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA  Sekiguchi Y., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA  Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA  Tanouchi M., Tamakoshi A., Tanaka T., Terpsita P., Tognoni A.,
RA  Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasseroiti A.,
RA  Viari A., Wambutt R., Wedler E., Wedler H., Weltzenegger T.,
RA  Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

```



```

RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO B.SUBTILIS YPOC AND YOFU.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D16311; BAA03818.1; -
DR EMBL: Y09476; CA070630.1; -
DR EMBL: Z79580; CAB01834.1; -
DR EMBL: Z99109; CAB12952.1; -
DR PIR: A49921; A49921.
DR Subtilist: BG10850; YLT.
DR InterPro: IPR003740; DUF161.
DR Pfam: PF02588; DUF161; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 80 100 POTENTIAL.
FT TRANSMEM 151 171 POTENTIAL.
FT CONFLICT 121 121 V -> D (IN REF. 1).
FT CONFLICT 226 226 V -> L (IN REF. 1).
FT CONFLICT 278 278 R -> T (IN REF. 1).
SQ SEQUENCE 280 AA; 30535 MW; 4BF98B12B8DA59E7 CRC64;

Query Match 1.5%; Score 7; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 LTLKYGA 79
Db 125 LTLKYGA 131

RESULT 44
MCM1_YEAST
ID MCM1_YEAST STANDARD; PRT; 286 AA.
AC P11746;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Pheromone receptor transcription factor (GRM/PRTF protein).
GN MCM1 OR FUN80 OR YMR043W OR YM9532.08.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycs.
OX NCBI_TaxID=4932;
ON [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249735; Pubmed=2159934;
RA Ammerer G.;
RT "Identification, purification, and cloning of a polypeptide
RT (PRTF/GRM) that binds to mating-specific promoter elements in
RT yeast."
RL Genes Dev. 4:299-312(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89141759; Pubmed=3066908;
RA Passmore S., Maine G.T., Elble R., Christ C., Tye B.K.;
RT "Saccharomyces cerevisiae protein involved in plasmid maintenance is
RT necessary for mating of MAT alpha cells."
RL J. Mol. Biol. 204:593-606(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88030692; Pubmed=3311883;

```

```

RA Dubois E., Bercy J., Descamps F., Messenguy F.;
RT "Characterization of two new genes essential for vegetative growth in
RT Saccharomyces cerevisiae: nucleotide sequence determination and
RT chromosome mapping."
RL Gene 55:265-275(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RA Odell C., Bowman S., Barrell B.G., Rajandream M.A.;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH MAT2.
RX MEDLINE=98140702; Pubmed=9490409;
RA Tan S., Richmond T.J.;
RT "Crystal structure of the yeast MATalpha2/MCM1/DNA ternary complex."
RL Nature 391:660-666(1998).
CC -1- FUNCTION: INTERACTS WITH THE ALPHA-2 REPRESSOR OR WITH THE
CC ALPHA-1 ACTIVATOR THEREBY REGULATING THE EXPRESSION OF MATING-
CC TYPE-SPECIFIC GENES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X52453; CAA36691.1; -
DR EMBL: X14187; CAA32389.1; -
DR EMBL: M17511; AAA34609.1; -
DR EMBL: Z48502; CAA88409.1; -
DR PIR: A34599; A34599.
DR PDB: 1MNM; 18-MAR-98.
DR TRANSFAC: T00500; -
DR TRANSFAC: T00501; -
DR SGD: S0004646; MCM1.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein; 3D-structure.
FT DOMAIN 18 72 MADS.
FT DOMAIN 98 120 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 9 9 P -> S (IN REF. 3).
FT CONFLICT 37 37 S -> F (IN REF. 3).
FT CONFLICT 136 137 GA -> AR (IN REF. 3).
FT CONFLICT 158 286 MISSING (IN REF. 3).
SQ SEQUENCE 286 AA; 32802 MW; FD75B4BF549E9E3B CRC64;

Query Match 1.5%; Score 7; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DEEDDEE 72
Db 99 DEEDDEE 105

RESULT 45
ZIPA_VIBCH
ID ZIPA_VIBCH STANDARD; PRT; 291 AA.
AC O9KTD2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell division protein zipa homolog.
RN [1]
RP ZIPA OR VC0970.

```

```

OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxId=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EI Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tetelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC -!- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC Probable receptor for the septal ring structure, may anchor it
CC to the inner-membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE004178; AAF94132.1; -
DR HSSP: P71713; 1F7X.
DR TIGR: VC0970; -.
KW Cell division; Septation; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 5 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 6 26 POTENTIAL.
FT DOMAIN 27 291 CYTOPLASMIC (POTENTIAL).
FT SEQUENCE 291 AA; 32786 MW; A7DE34AC3DE64A35 CRC64;
SO QUERY MATCH 1.58; Score 7; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 66 DEEDDE 72
1 |
DB 94 DEEDDE 100

```

```

RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
CC -!- FUNCTION: INVOLVED IN A PEPTIDE INTAKE TRANSPORT SYSTEM THAT
CC PLAYS A ROLE IN THE RESISTANCE TO ANTIMICROBIAL PEPTIDES.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. OPPBC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X97282; CAA65939.1; -
DR EMBL: AE000227; AAC74374.1; -
DR EMBL: D90767; BAA14853.1; -
DR EMBL: D90768; BAA14862.1; -
DR EMBL: D90766; BAA14845.1; -
DR EcoGene: EG20256; sapC.
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp. 1.
DR PROSITE: PS00402; BPD_TRANS_PEP_TRANSP_INN_MEMBR; FALSE_NCG.
KW Transport; Peptide transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 223 243 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
FT SEQUENCE 296 AA; 31548 MW; 57CD1F8180BF0B7C CRC64;
SO QUERY MATCH 1.58; Score 7; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 136 AAIMISV 142
271 AAIMISV 277
DB 271 AAIMISV 277

```

```

RESULT 47
NKX1_BISBI
ID NKX1_BISBI STANDARD; PRT; 300 AA.
AC O46383;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 (Na(+)/K(+) /Ca(2+) -
DE exchanger protein 1) (Retinal rod Na-Ca+K exchanger) (Fragment).
GN SLC24A1 OR NKX1.
OS Bison bison (American bison).

```

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Ovis; Bovinae; Bison.
CC NCBI_TaxID=9901;
RN RP
RN SEQUENCE FROM N.A.
RX MEDLINE=98138491; PubMed=9478004;
RA Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
RT "cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison
RT with a revised bovine sequence."
RL Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+) (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF025480; AAC13320.1; -.
KW Vision; Transport; Antiport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane.
FT NON_TER 1 1
FT TRANSMEM 259 275 POTENTIAL.
FT DOMAIN 218 242 POLY-GLU.
FT NON_TER 300 300
SQ SEQUENCE 300 AA; 31671 MW; 2BE592DA5AB9781E CRC64;

Query Match 1.5%; Score 7; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEE 72
Db 224 DEEDEE 230

RESULT 48
D7_AEDAE STANDARD; PRT; 321 AA.
AC P18153;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE D7 protein precursor (Allergen Aed a 2).
GN D7
OS Aedes aegypti (Yellowfever mosquito).
CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
CC Culicoidae; Aedes.
CC NCBI_TaxID=7159;
RN RP
RN SEQUENCE FROM N.A.
RX STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=91270277; PubMed=2052024;
RA James A.A., Blackmer K., Marinotti O., Ghosh C.R., Racioppi J.V.;
RT "Isolation and characterization of the gene expressing the major
RT salivary gland protein of the female mosquito, Aedes aegypti."
RL Mol. Biochem. Parasitol. 44:245-254(1991).
CC -1- FUNCTION: THOUGHT TO BE INVOLVED IN BLOOD-FEEDING.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: ADULT FEMALE SALIVARY GLAND.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M3156; AAA29347.1; -.
DR EMBL; M3157; AAA29348.1; -.
KW Allergen; Signal.
FT SIGNAL 1 17
FT CHAIN 18 321
FT VARIANT 4 4
FT VARIANT 10 10
FT VARIANT 19 19
FT VARIANT 30 30
FT VARIANT 43 43
FT VARIANT 115 115
FT VARIANT 159 159
FT VARIANT 169 169
FT VARIANT 192 192
FT VARIANT 221 221
FT VARIANT 223 223
FT VARIANT 226 226
FT VARIANT 234 235
FT VARIANT 259 259
FT VARIANT 301 301
SQ SEQUENCE 321 AA; 37028 MW; AA8D6328E46FBC9 CRC64;

Query Match 1.5%; Score 7; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 422 LLLAIF 428
Db 4 LLLAIF 10

RESULT 49
RAD1_SCHPO STANDARD; PRT; 323 AA.
AC P22193;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA repair protein rad1.
GN RAD1 OR SPAC1952.07.
OS Schizosaccharomyces pombe (fission yeast).
CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
CC NCBI_TaxID=4896;
RN RP
RN SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=95011649; PubMed=7926829;
RA Long K.E., Sunnerhagen P., Subramani S.;
RT "The Schizosaccharomyces pombe rad1 gene consists of three exons and
RT the cDNA sequence is partially homologous to the Ustilago maydis RECI
RT cDNA."
RL Gene 148:155-159(1994).
RN RP
RN SEQUENCE FROM N.A.
RX STRAIN=90287166; PubMed=2355921;
RX MEDLINE=90287166; PubMed=2355921;
RA Sunnerhagen P., Seaton B.L., Nasim A., Subramani S.;
RT "Cloning and analysis of a gene involved in DNA repair and
RT recombination, the rad1 gene of Schizosaccharomyces pombe."
RL Mol. Cell. Biol. 10:3750-3760(1990).
RN RP
RN REVISIONS.
RX MEDLINE=94261448; PubMed=8202381;

```

RA Zhang M.O., Marr T.G.;
RT "Fission yeast gene structure and recognition";
RL Nucleic Acids Res. 22:1750-1759(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RX MEDLINE-21848401; Pubmed-11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Squires J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Shelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tilley A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicakeert G., Aert R., Robben J., Grymoprez B.,
RA Wellens I., Vanstreets E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gebel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Beyer P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rocher M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Fersburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipkova I., G.V., Ussery D., Barrett B.G., Nurse P.;
RT The genome sequence of Schizosaccharomyces pombe.;
RL Nature 415:871-880(2002).
CC -1- FUNCTION: RECOMBINATIONAL REPAIRATION OF DNA DAMAGES INDUCED BY UV
AND GAMMA RADIATION. COULD HAVE EXONUCLEASE ACTIVITY.
CC -1- ENZYME REGULATION: INHIBITED BY CAFFEINE.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: SOME, TO HUMAN AND HAMSTER GADD45.
CC -1- SIMILARITY: SOME, YEAST RAD17 AND TO U.MAYDIS RECL.
CC -1- CAUTION: REF.2 SEQUENCE STARTED AT POSITION 130, DUE TO THE FACT
THAT TWO EXONS WERE MISSED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z28385; CA82231.1; -;
DR EMBL; M38132; AAA35329.1; -;
DR EMBL; AL109820; CAB52571.1; -;
DR PIR; A35680; A35680.
DR InterPro; IPR003021; Rad1_Recl.
DR Pfam; PF02144; Rad1; 1.
DR PRINTS; PR01245; RAD1RECL.
DR DNA damage; DNA repair; Hydrolyase; Exonuclease; Nuclear protein.
FT DOMAIN 285 294 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 285 323 GLU-RICH (ACIDIC).
FT SEQUENCE 323 AA; 36527 MW; 1A2ADDFC3A55EB6 CRC64;
SQ
Query Match 1.5%; Score 7; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID YE09_S1YN3 STANDARD; PRT; 326 AA.
AC P73594;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical WD-repeat protein slr1409.
GN SLR1409.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97061201; Pubmed-8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90907; BAA17638.1; -;
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat; Complete proteome.
FT REPEAT 47 77 WD 1.
FT REPEAT 88 118 WD 2.
FT REPEAT 129 159 WD 3.
FT REPEAT 169 199 WD 4.
FT REPEAT 210 240 WD 5.
FT REPEAT 252 282 WD 6.
FT SEQUENCE 326 AA; 35759 MW; BD83A2403DE163D CRC64;
SQ
Query Match 1.5%; Score 7; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 6, 2003, 14:19:28
Job time : 47.4398 secs

QY 66 DEEDED 72
DB 286 DEEDED 292
RESULT 50
YE09_S1YN3

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:21:16 : Search time 17.4398 Seconds
(Without alignments)
593.645 Million cell updates/sec

Title: US-09-689-159A-2

Perfect score: 467
Sequence: 1 MFELPAPLSTYFQNAQMSDN.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: OLIGO
Gapop 60.0 , Gapect 60.0

Searched: 129505 seqs, 22169297 residues

Word size : 0

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	366	78.4	467	10	US-09-754-949-4
2	366	78.4	467	10	US-09-878-454A-3
3	366	78.4	467	10	US-09-895-035-14
4	366	78.4	467	12	US-10-071-900-1
5	337	72.2	467	10	US-09-895-035-12
6	265	56.7	467	10	US-09-785-474-2
7	204	43.7	467	10	US-09-785-474-4
8	204	43.7	467	10	US-09-785-474-28
9	204	43.7	467	10	US-09-785-474-30
10	204	43.7	467	10	US-09-785-474-32
11	132	28.3	180	10	US-09-895-035-8
12	128	27.4	354	10	US-09-823-153-8
13	48	10.3	65	10	US-09-864-761-38056
14	44	9.4	101	10	US-09-925-299-1227
15	28	6.0	131	9	US-10-051-767-10
16	28	6.0	448	10	US-09-754-949-6
17	28	6.0	448	10	US-09-878-454A-1
18	28	6.0	448	12	US-10-071-900-2
19	22	4.7	74	9	US-10-051-767-9

20	4.7	74	9	US-10-051-767-15	Sequence 15, Appl
22	4.7	129	9	US-10-051-767-11	Sequence 11, Appl
21	3.9	166	9	US-10-051-767-7	Sequence 7, Appl
18	3.9	166	9	US-10-051-767-13	Sequence 13, Appl
23	3.9	166	9	US-10-051-767-13	Sequence 13, Appl
24	3.9	210	10	US-10-051-767-12	Sequence 12, Appl
25	3.4	17	10	US-09-823-153-6	Sequence 6, Appl
16	3.2	15	10	US-09-823-153-9	Sequence 9, Appl
15	3.2	16	10	US-09-823-153-5	Sequence 5, Appl
27	1.7	8	10	US-08-795-903A-9	Sequence 9, Appl
28	1.7	8	10	US-09-796-264-9	Sequence 9, Appl
29	1.7	8	10	US-09-845-226-9	Sequence 9, Appl
30	1.7	45	10	US-09-982-172-103	Sequence 103, App
31	1.7	45	10	US-09-982-172-227	Sequence 227, App
32	1.7	263	9	US-10-004-717-7	Sequence 7, Appl
33	1.7	263	9	US-10-004-717-31	Sequence 31, Appl
34	1.7	263	9	US-10-004-717-31	Sequence 31, Appl
35	1.7	1272	10	US-09-769-097-2	Sequence 2, Appl
36	1.7	1272	10	US-09-769-097-4	Sequence 4, Appl
37	1.7	1276	10	US-09-866-866A-8	Sequence 8, Appl
38	1.7	1280	9	US-10-072-621-7	Sequence 7, Appl
39	1.7	1280	9	US-10-044-671-2	Sequence 2, Appl
40	1.7	1280	9	US-09-866-866A-2	Sequence 2, Appl
41	1.7	1280	10	US-09-866-866A-4	Sequence 4, Appl
42	1.7	1280	10	US-09-796-264-6	Sequence 6, Appl
43	1.5	8	10	US-09-845-226-6	Sequence 6, Appl
44	1.5	8	10	US-09-864-761-38169	Sequence 38169, A
45	1.5	25	10	US-09-864-761-38937	Sequence 38937, A
46	1.5	55	10	US-09-764-869-1215	Sequence 1215, Ap
47	1.5	58	10	US-09-814-122-39	Sequence 39, Appl
48	1.5	64	10	US-09-864-761-47359	Sequence 47359, A
49	1.5	67	10	US-09-864-761-34902	Sequence 34902, A
50	1.5	70	10	US-09-071-838-56	Sequence 56, Appl
51	1.5	74	10	US-09-897-898-8	Sequence 8, Appl
52	1.5	118	10	US-09-992-598-165	Sequence 165, App
53	1.5	118	10	US-09-992-598-165	Sequence 165, App
54	1.5	119	9	US-09-989-2933A-165	Sequence 26, Appl
55	1.5	119	9	US-08-989-734-165	Sequence 165, App
56	1.5	119	9	US-09-990-444-165	Sequence 165, App
57	1.5	119	9	US-09-989-730-165	Sequence 165, App
58	1.5	119	9	US-09-990-436-165	Sequence 165, App
59	1.5	119	9	US-09-991-181-165	Sequence 165, App
60	1.5	119	9	US-09-993-667-165	Sequence 165, App
61	1.5	119	9	US-08-989-734-165	Sequence 165, App
62	1.5	119	9	US-09-997-653-165	Sequence 165, App
63	1.5	119	9	US-10-174-590-140	Sequence 140, App
64	1.5	119	9	US-10-176-758-140	Sequence 140, App
65	1.5	119	9	US-10-063-616-26	Sequence 26, Appl
66	1.5	119	9	US-10-175-737-140	Sequence 140, App
67	1.5	119	9	US-09-993-667-165	Sequence 165, App
68	1.5	119	9	US-10-063-616-26	Sequence 26, Appl
69	1.5	119	9	US-10-175-737-140	Sequence 140, App
70	1.5	119	9	US-10-063-616-26	Sequence 26, Appl
71	1.5	119	9	US-10-063-616-26	Sequence 26, Appl
72	1.5	119	9	US-10-063-616-26	Sequence 26, Appl
73	1.5	119	9	US-10-175-738-140	Sequence 140, App
74	1.5	119	9	US-10-175-738-140	Sequence 140, App
75	1.5	119	9	US-10-176-482-140	Sequence 140, App
76	1.5	119	9	US-10-176-757-140	Sequence 140, App
77	1.5	119	9	US-10-176-913-140	Sequence 140, App
78	1.5	119	9	US-10-180-552-140	Sequence 140, App
79	1.5	119	10	US-09-889-722-165	Sequence 165, App
80	1.5	119	10	US-09-889-722-165	Sequence 165, App
81	1.5	119	10	US-09-889-722-165	Sequence 165, App
82	1.5	119	10	US-09-889-722-165	Sequence 165, App
83	1.5	119	10	US-09-889-722-165	Sequence 165, App
84	1.5	119	10	US-09-889-731-165	Sequence 165, App
85	1.5	119	10	US-09-889-732-165	Sequence 165, App
86	1.5	119	10	US-09-891-073-165	Sequence 165, App
87	1.5	119	10	US-09-990-442-165	Sequence 165, App
88	1.5	119	10	US-09-891-163-165	Sequence 165, App
89	1.5	119	10	US-09-993-604-165	Sequence 165, App
90	1.5	119	10	US-09-990-456-165	Sequence 165, App
91	1.5	119	10	US-09-889-721-165	Sequence 165, App
92	1.5	119	12	US-10-006-867-26	Sequence 26, Appl

93	7	1.5	119	12	US-10-052-598-140	Sequence 140, App	166	7	1.5	774	10	US-09-745-763-115	Sequence 115, App
94	7	1.5	232	10	US-09-897-986-11	Sequence 11, Appl	167	7	1.5	896	9	US-09-903-170C-5	Sequence 5, Appl1
95	7	1.5	242	10	US-09-864-761-36180	Sequence 36180, A	168	7	1.5	896	10	US-09-903-180B-5	Sequence 5, Appl1
96	7	1.5	247	9	US-09-738-626-6438	Sequence 6438, Ap	169	7	1.5	896	10	US-09-903-171A-5	Sequence 5, Appl1
97	7	1.5	264	9	US-09-510-332-47	Sequence 47, Appl	170	7	1.5	896	10	US-09-903-188A-5	Sequence 5, Appl1
98	7	1.5	286	10	US-09-801-368-188	Sequence 188, App	171	7	1.5	896	10	US-09-903-323A-5	Sequence 5, Appl1
99	7	1.5	301	9	US-09-738-626-5030	Sequence 5030, Ap	172	7	1.5	896	10	US-09-903-325A-5	Sequence 5, Appl1
100	7	1.5	312	9	US-09-510-332-39	Sequence 39, Appl	173	7	1.5	906	9	US-10-060-230-19	Sequence 19, Appl1
101	7	1.5	319	9	US-09-738-626-5702	Sequence 5702, Ap	174	7	1.5	906	9	US-10-060-230-20	Sequence 20, Appl
102	7	1.5	341	9	US-09-738-626-4828	Sequence 4828, Ap	175	7	1.5	906	9	US-10-060-230-21	Sequence 21, Appl
103	7	1.5	366	10	US-09-887-569A-2	Sequence 2, Appl1	176	7	1.5	906	9	US-10-060-230-22	Sequence 22, Appl
104	7	1.5	392	10	US-09-902-684-2	Sequence 13, Appl	177	7	1.5	979	10	US-09-903-187A-5	Sequence 5, Appl1
105	7	1.5	405	10	US-09-902-684-13	Sequence 237, App	178	7	1.5	2448	10	US-09-815-242-11870	Sequence 11870, A
106	7	1.5	415	10	US-09-712-363-237	Sequence 19, Appl	179	6	1.3	17	9	US-09-981-876-221	Sequence 221, App
107	7	1.5	451	10	US-09-697-898-19	Sequence 52, Appl	180	6	1.3	18	10	US-09-864-761-38208	Sequence 38208, A
108	7	1.5	494	9	US-09-902-525-52	Sequence 2, Appl1	181	6	1.3	18	10	US-09-864-761-35295	Sequence 35295, A
109	7	1.5	527	9	US-09-962-678-2	Sequence 166, App	182	6	1.3	19	10	US-09-864-761-43691	Sequence 43691, A
110	7	1.5	527	9	US-09-981-353-166	Sequence 216, App	183	6	1.3	19	10	US-09-734-520-16	Sequence 16, App
111	7	1.5	527	9	US-09-854-133-216	Sequence 522, App	184	6	1.3	19	10	US-09-071-838-232	Sequence 232, App
112	7	1.5	527	9	US-10-174-590-522	Sequence 522, App	185	6	1.3	19	12	US-10-012-034A-16	Sequence 16, Appl
113	7	1.5	527	9	US-10-176-558-522	Sequence 522, App	186	6	1.3	20	9	US-09-736-457-1855	Sequence 1855, Ap
114	7	1.5	527	9	US-10-175-737-522	Sequence 522, App	187	6	1.3	20	9	US-09-736-457-1855	Sequence 1855, Ap
115	7	1.5	527	9	US-10-173-706-522	Sequence 522, App	188	6	1.3	20	9	US-09-902-941-1855	Sequence 1855, Ap
116	7	1.5	527	9	US-10-175-738-522	Sequence 522, App	189	6	1.3	20	9	US-09-902-941-1855	Sequence 1855, Ap
117	7	1.5	527	9	US-10-175-752-522	Sequence 522, App	190	6	1.3	20	9	US-09-902-941-1855	Sequence 1855, Ap
118	7	1.5	527	9	US-10-176-482-522	Sequence 522, App	191	6	1.3	20	9	US-09-902-941-1855	Sequence 1855, Ap
119	7	1.5	527	9	US-10-176-482-522	Sequence 522, App	192	6	1.3	20	9	US-09-849-626-1855	Sequence 1855, Ap
120	7	1.5	527	9	US-10-176-557-522	Sequence 522, App	193	6	1.3	22	10	US-09-849-626-1856	Sequence 1856, Ap
121	7	1.5	527	9	US-10-180-513-522	Sequence 522, App	194	6	1.3	25	9	US-09-789-404-28	Sequence 28, Appl
122	7	1.5	527	9	US-10-180-557-522	Sequence 522, App	195	6	1.3	25	10	US-09-912-672A-7	Sequence 7, Appl1
123	7	1.5	527	10	US-09-738-973-216	Sequence 216, App	196	6	1.3	27	9	US-09-983-802-642	Sequence 35, Appl
124	7	1.5	527	12	US-10-052-586-522	Sequence 522, App	197	6	1.3	29	10	US-09-983-802-642	Sequence 642, App
125	7	1.5	566	9	US-09-992-598-41	Sequence 522, App	198	6	1.3	33	9	US-09-917-340-31	Sequence 31, Appl
126	7	1.5	566	9	US-09-989-293A-41	Sequence 41, Appl	199	6	1.3	33	9	US-09-842-582-6	Sequence 6, Appl1
127	7	1.5	566	9	US-09-989-735-41	Sequence 41, Appl	200	6	1.3	39	10	US-09-925-299-5372	Sequence 1515, Ap
128	7	1.5	566	9	US-09-989-444-41	Sequence 41, Appl	201	6	1.3	40	9	US-09-738-626-5515	Sequence 5372, Ap
129	7	1.5	566	9	US-09-989-730-41	Sequence 41, Appl	202	6	1.3	41	10	US-09-764-878-148	Sequence 148, App
130	7	1.5	566	9	US-09-989-436-41	Sequence 41, Appl	203	6	1.3	42	10	US-09-864-761-46270	Sequence 46270, A
131	7	1.5	566	9	US-09-991-181-41	Sequence 41, Appl	204	6	1.3	42	10	US-09-764-847-656	Sequence 656, App
132	7	1.5	566	9	US-09-993-687-41	Sequence 41, Appl	205	6	1.3	44	10	US-09-864-761-41268	Sequence 41268, A
133	7	1.5	566	9	US-09-989-734-41	Sequence 41, Appl	206	6	1.3	46	9	US-09-864-761-38584	Sequence 38584, A
134	7	1.5	566	9	US-09-997-653-41	Sequence 41, Appl	207	6	1.3	48	9	US-09-983-802-278	Sequence 278, App
135	7	1.5	566	9	US-10-174-590-56	Sequence 41, Appl	208	6	1.3	50	10	US-09-864-761-33963	Sequence 234, App
136	7	1.5	566	9	US-10-176-758-56	Sequence 56, Appl	209	6	1.3	53	9	US-09-861-876-157	Sequence 39963, A
137	7	1.5	566	9	US-10-175-737-56	Sequence 56, Appl	210	6	1.3	53	10	US-09-81-876-157	Sequence 157, App
138	7	1.5	566	9	US-09-993-667-41	Sequence 56, Appl	211	6	1.3	54	10	US-09-764-877-1118	Sequence 1118, Ap
139	7	1.5	566	9	US-10-173-706-56	Sequence 56, Appl	212	6	1.3	55	10	US-09-864-761-36621	Sequence 36621, A
140	7	1.5	566	9	US-10-175-738-56	Sequence 56, Appl	213	6	1.3	55	10	US-09-774-639-181	Sequence 181, App
141	7	1.5	566	9	US-10-175-752-56	Sequence 56, Appl	214	6	1.3	55	10	US-09-864-761-38777	Sequence 38777, A
142	7	1.5	566	9	US-10-176-482-56	Sequence 56, Appl	215	6	1.3	57	10	US-09-864-761-47578	Sequence 47578, A
143	7	1.5	566	9	US-10-176-757-56	Sequence 56, Appl	216	6	1.3	58	10	US-09-864-761-44799	Sequence 44799, A
144	7	1.5	566	9	US-10-176-913-56	Sequence 56, Appl	217	6	1.3	58	10	US-09-864-761-40506	Sequence 40506, A
145	7	1.5	566	9	US-10-180-552-56	Sequence 56, Appl	218	6	1.3	63	10	US-09-867-550-692	Sequence 692, App
146	7	1.5	566	9	US-10-180-557-56	Sequence 56, Appl	219	6	1.3	65	10	US-09-796-692-1165	Sequence 1165, Ap
147	7	1.5	566	10	US-09-989-722-41	Sequence 41, Appl	220	6	1.3	65	10	US-09-864-761-46591	Sequence 46591, A
148	7	1.5	566	10	US-09-989-723-41	Sequence 41, Appl	221	6	1.3	71	10	US-09-764-878-119	Sequence 119, App
149	7	1.5	566	10	US-09-989-727-41	Sequence 41, Appl	222	6	1.3	73	9	US-09-864-761-45186	Sequence 45186, A
150	7	1.5	566	10	US-09-989-727-41	Sequence 41, Appl	223	6	1.3	73	9	US-09-864-761-37973	Sequence 37973, A
151	7	1.5	566	10	US-09-989-731-41	Sequence 41, Appl	224	6	1.3	73	10	US-09-864-761-45186	Sequence 45186, A
152	7	1.5	566	10	US-09-989-733-41	Sequence 41, Appl	225	6	1.3	73	10	US-09-864-761-35230	Sequence 35230, A
153	7	1.5	566	10	US-09-991-073-41	Sequence 41, Appl	226	6	1.3	73	12	US-10-006-867-30	Sequence 30, Appl
154	7	1.5	566	10	US-09-990-442-41	Sequence 41, Appl	227	6	1.3	76	9	US-10-101-487-36	Sequence 36, Appl
155	7	1.5	566	10	US-09-991-163-41	Sequence 41, Appl	228	6	1.3	76	10	US-09-864-761-45186	Sequence 45186, A
156	7	1.5	566	10	US-09-993-604-41	Sequence 41, Appl	229	6	1.3	78	10	US-09-864-761-37973	Sequence 37973, A
157	7	1.5	566	10	US-09-990-456-41	Sequence 41, Appl	230	6	1.3	79	10	US-09-864-761-45186	Sequence 45186, A
158	7	1.5	566	12	US-10-052-586-56	Sequence 41, Appl	231	6	1.3	79	10	US-09-864-761-48376	Sequence 48376, A
159	7	1.5	663	9	US-10-108-605-245	Sequence 56, App	232	6	1.3	80	10	US-09-903-456-9	Sequence 9, Appl1
160	7	1.5	689	10	US-09-071-838-2	Sequence 2, Appl1	233	6	1.3	83	10	US-09-864-761-48130	Sequence 48130, A
161	7	1.5	714	10	US-09-978-242-3	Sequence 3, Appl1	234	6	1.3	89	10	US-09-739-907-154	Sequence 154, App
162	7	1.5	739	9	US-09-738-626-6773	Sequence 6773, Ap	235	6	1.3	90	10	US-09-864-761-42220	Sequence 42220, A
163	7	1.5	748	10	US-09-815-242-10278	Sequence 10278, A	236	6	1.3	91	10	US-09-739-907-94	Sequence 94, Appl
164	7	1.5	748	10	US-09-815-242-13880	Sequence 13880, A	237	6	1.3	91	12	US-10-001-879-160	Sequence 160, Appl
165	7	1.5	748	10	US-09-815-242-13880	Sequence 13880, A	238	6	1.3	102	10	US-09-745-763-6	Sequence 6, Appl1

239	6	1.3	105	10	US-09-925-301-1516	Sequence 1516, Ap	312	207	9	US-09-902-941-1913	Sequence 1913, Ap
240	6	1.3	108	9	US-09-950-933A-61	Sequence 61, Appl	313	207	9	US-09-738-626-4470	Sequence 5470, Ap
241	6	1.3	109	9	US-09-796-692-2460	Sequence 2460, Ap	314	207	9	US-09-849-626-1667	Sequence 1667, Ap
242	6	1.3	111	10	US-09-764-877-1774	Sequence 1774, Ap	315	207	9	US-09-849-626-1913	Sequence 1913, Ap
243	6	1.3	112	10	US-09-925-502-581	Sequence 581, App	316	208	10	US-09-214-881A-11	Sequence 11, Appl
244	6	1.3	114	9	US-09-738-626-3516	Sequence 3516, Ap	317	209	10	US-10-001-887-86	Sequence 86, Appl
245	6	1.3	114	9	US-09-925-300-1175	Sequence 1175, Ap	318	212	9	US-10-146-474-4	Sequence 4, Appl
246	6	1.3	115	9	US-10-079-623-351	Sequence 351, App	319	213	10	US-09-828-644-62	Sequence 62, Appl
247	6	1.3	115	10	US-09-903-456-23	Sequence 23, Appl	320	213	10	US-09-811-284-239	Sequence 239, App
248	6	1.3	116	10	US-09-764-869-689	Sequence 689, App	321	214	10	US-09-214-881A-1	Sequence 1, Appl
249	6	1.3	117	10	US-09-864-761-45592	Sequence 45592, A	322	214	10	US-09-214-881A-3	Sequence 3, Appl
250	6	1.3	122	10	US-09-729-674-6	Sequence 6, Appl	323	214	10	US-09-214-881A-4	Sequence 4, Appl
251	6	1.3	122	10	US-09-893-737-286	Sequence 286, App	324	214	10	US-09-214-881A-5	Sequence 5, Appl
252	6	1.3	123	9	US-09-726-258-17	Sequence 17, Appl	325	219	10	US-09-925-299-797	Sequence 797, App
253	6	1.3	124	9	US-10-051-767-8	Sequence 8, Appl	326	219	12	US-10-016-447-13	Sequence 13, Appl
254	6	1.3	124	9	US-10-051-767-14	Sequence 14, Appl	327	223	12	US-10-005-168-2	Sequence 2, Appl
255	6	1.3	126	9	US-09-738-626-4171	Sequence 4171, Ap	328	231	9	US-10-095-449-2	Sequence 2, Appl
256	6	1.3	127	9	US-09-864-761-38973	Sequence 38973, A	329	231	10	US-09-448-378-2	Sequence 2, Appl
257	6	1.3	128	10	US-09-925-300-1757	Sequence 1757, Ap	330	231	10	US-09-864-761-37211	Sequence 37211, A
258	6	1.3	130	10	US-09-741-669-294	Sequence 294, App	331	231	10	US-09-983-806-2	Sequence 2, Appl
259	6	1.3	130	10	US-09-912-020-318	Sequence 318, App	332	234	9	US-10-001-857-176	Sequence 176, App
260	6	1.3	130	10	US-09-864-761-45365	Sequence 45365, A	333	234	9	US-10-076-765-22	Sequence 22, Appl
261	6	1.3	130	10	US-09-815-242-10345	Sequence 10345, A	334	237	9	US-09-726-258-5	Sequence 25, Appl
262	6	1.3	130	10	US-09-815-242-14104	Sequence 14104, A	335	238	9	US-09-862-802-8	Sequence 8, Appl
263	6	1.3	140	9	US-09-879-461-4	Sequence 4, Appl	336	239	10	US-09-910-071-15	Sequence 15, Appl
264	6	1.3	140	10	US-09-764-864-858	Sequence 858, App	337	239	10	US-09-801-368-300	Sequence 300, App
265	6	1.3	146	10	US-09-940-497-3	Sequence 3, Appl	338	240	9	US-09-738-626-4338	Sequence 4338, App
266	6	1.3	146	10	US-09-969-834-3	Sequence 3, Appl	339	240	9	US-09-987-755-7	Sequence 7, Appl
267	6	1.3	153	10	US-09-764-887-206	Sequence 206, Appl	340	240	10	US-09-938-885A-3	Sequence 3, Appl
268	6	1.3	154	10	US-09-939-825-24	Sequence 24, Appl	341	240	10	US-09-801-368-342	Sequence 342, App
269	6	1.3	157	10	US-09-999-699-2	Sequence 2, Appl	342	246	10	US-09-925-302-511	Sequence 511, App
270	6	1.3	157	10	US-09-999-699-6	Sequence 6, Appl	343	249	9	US-09-908-193-42	Sequence 42, Appl
271	6	1.3	159	10	US-09-814-122-54	Sequence 54, Appl	344	248	9	US-09-908-193-41	Sequence 41, Appl
272	6	1.3	160	10	US-09-731-872-294	Sequence 294, App	345	249	9	US-09-908-193-46	Sequence 46, Appl
273	6	1.3	161	10	US-09-925-297-493	Sequence 493, App	346	249	9	US-10-213-700-4	Sequence 4, Appl
274	6	1.3	161	10	US-09-747-155-243	Sequence 243, App	347	251	9	US-10-213-700-3	Sequence 3, Appl
275	6	1.3	164	10	US-09-925-300-1010	Sequence 1010, Ap	348	253	10	US-09-305-856B-16	Sequence 16, Appl
276	6	1.3	169	10	US-09-764-846-207	Sequence 207, App	349	254	10	US-09-925-301-13408	Sequence 13408, Ap
277	6	1.3	170	10	US-09-976-165-22	Sequence 22, Appl	350	255	10	US-09-815-242-11101	Sequence 11101, Ap
278	6	1.3	174	10	US-09-903-456-40	Sequence 40, Appl	351	255	10	US-09-815-242-13599	Sequence 13599, A
279	6	1.3	175	9	US-10-050-786-11	Sequence 11, Appl	352	255	10	US-09-881-752A-106	Sequence 106, App
280	6	1.3	180	10	US-09-780-717-11	Sequence 11, Appl	353	256	10	US-09-815-242-10664	Sequence 25, Appl
281	6	1.3	181	10	US-09-864-761-33314	Sequence 33314, A	354	258	9	US-09-965-529-25	Sequence 25, Appl
282	6	1.3	181	10	US-09-864-761-41658	Sequence 41658, A	355	260	9	US-09-738-626-65921	Sequence 5921, Ap
283	6	1.3	182	10	US-09-811-284-182	Sequence 182, App	356	261	10	US-09-925-301-901	Sequence 901, App
284	6	1.3	183	10	US-09-925-301-1230	Sequence 1230, Ap	357	261	12	US-10-003-759-2	Sequence 2, Appl
285	6	1.3	183	9	US-10-028-072-240	Sequence 240, App	358	265	9	US-09-981-876-175	Sequence 175, App
286	6	1.3	189	9	US-10-121-049-240	Sequence 240, App	359	266	9	US-10-131-965-9	Sequence 9, Appl
287	6	1.3	189	9	US-10-123-904-240	Sequence 240, App	360	266	9	US-10-131-965-15	Sequence 15, Appl
288	6	1.3	189	9	US-10-140-470-240	Sequence 240, App	361	267	10	US-09-822-485-8	Sequence 8, Appl
289	6	1.3	189	10	US-09-864-761-34813	Sequence 34813, A	362	267	10	US-09-425-921-13	Sequence 13, Appl
290	6	1.3	189	10	US-09-867-550-1504	Sequence 1504, Ap	363	267	12	US-10-023-992-7	Sequence 7, Appl
291	6	1.3	189	10	US-09-993-999-2	Sequence 2, Appl	364	268	9	US-10-081-347-63	Sequence 3, Appl
292	6	1.3	189	10	US-09-975-374A-2	Sequence 2, Appl	365	268	10	US-09-284-663A-10	Sequence 10, Appl
293	6	1.3	191	10	US-09-764-870-362	Sequence 362, App	366	268	10	US-09-750-963-11	Sequence 11, Appl
294	6	1.3	191	10	US-09-925-300-1565	Sequence 1565, Ap	367	268	10	US-09-902-773A-7	Sequence 7, Appl
295	6	1.3	198	10	US-09-927-738-7	Sequence 7, Appl	368	268	10	US-09-251-263-12	Sequence 12, Appl
296	6	1.3	199	9	US-10-001-054-38	Sequence 38, Appl	369	268	10	US-09-736-338A-19	Sequence 19, Appl
297	6	1.3	199	9	US-10-028-072-92	Sequence 92, Appl	370	269	9	US-09-738-626-4086	Sequence 4086, Ap
298	6	1.3	199	9	US-10-121-049-92	Sequence 92, Appl	371	270	10	US-09-350-874-59	Sequence 59, Appl
299	6	1.3	199	9	US-10-123-904-92	Sequence 92, Appl	372	271	10	US-09-795-693-36	Sequence 36, Appl
300	6	1.3	199	9	US-10-140-470-92	Sequence 92, Appl	373	272	9	US-09-738-626-4596	Sequence 4596, Ap
301	6	1.3	200	8	US-08-424-550B-395	Sequence 395, App	374	272	9	US-09-738-626-6621	Sequence 6621, Ap
302	6	1.3	200	9	US-09-736-457-324	Sequence 324, App	375	273	9	US-10-218-361-1	Sequence 1, Appl
303	6	1.3	200	9	US-09-736-457-789	Sequence 789, App	376	277	10	US-09-755-456-7	Sequence 7, Appl
304	6	1.3	200	9	US-09-902-941-324	Sequence 324, App	377	280	8	US-08-910-386A-14	Sequence 14, Appl
305	6	1.3	200	9	US-09-902-941-789	Sequence 789, App	378	280	9	US-09-712-363-283	Sequence 283, App
306	6	1.3	200	9	US-09-849-626-324	Sequence 324, App	379	280	10	US-09-983-306-1	Sequence 1, Appl
307	6	1.3	201	10	US-09-849-626-789	Sequence 789, App	380	280	10	US-09-903-456-28	Sequence 28, Appl
308	6	1.3	201	10	US-09-214-881A-10	Sequence 10, Appl	381	282	10	US-09-738-626-5111	Sequence 5111, Ap
309	6	1.3	206	10	US-09-214-881A-9	Sequence 9, Appl	382	286	10	US-09-903-456-59	Sequence 59, Appl
310	6	1.3	207	9	US-09-736-457-1667	Sequence 1667, Ap	383	289	10	US-09-903-456-21	Sequence 21, Appl
311	6	1.3	207	9	US-09-902-941-1667	Sequence 1667, Ap	384	289	10	US-09-903-456-34	Sequence 34, Appl

385	6	1.3	291	10	US-09-903-456-36	Sequence 36, App1	488	6	1.3	330	10	US-09-886-055-211	Sequence 211, App
386	6	1.3	293	10	US-09-903-456-19	Sequence 19, App1	459	6	1.3	332	9	US-09-510-332-101	Sequence 101, App
387	6	1.3	294	10	US-09-927-738-9	Sequence 9, App11	459	6	1.3	333	9	US-09-976-059-2	Sequence 2, App1
388	6	1.3	295	9	US-09-978-295A-415	Sequence 415, App	460	6	1.3	333	9	US-09-738-626-5173	Sequence 5173, App
389	6	1.3	295	9	US-09-981-876-179	Sequence 179, App	461	6	1.3	333	9	US-10-108-185-6	Sequence 6, App1
390	6	1.3	295	9	US-09-978-697-415	Sequence 415, App	462	6	1.3	333	10	US-09-771-209-71	Sequence 71, App1
391	6	1.3	295	9	US-09-999-852A-415	Sequence 415, App	463	6	1.3	333	10	US-09-825-882-2	Sequence 2, App11
392	6	1.3	295	9	US-09-978-189-415	Sequence 415, App	464	6	1.3	333	10	US-09-925-299-932	Sequence 1103, App
393	6	1.3	295	9	US-09-981-876-237	Sequence 237, App	465	6	1.3	335	9	US-09-976-059-6	Sequence 6886, App
394	6	1.3	296	9	US-09-903-456-33	Sequence 33, App1	466	6	1.3	336	9	US-10-017-736-14	Sequence 6, App11
395	6	1.3	301	10	US-09-815-242-11153	Sequence 11153, A	468	6	1.3	341	10	US-09-740-288A-8	Sequence 14, App1
396	6	1.3	302	10	US-09-738-626-6782	Sequence 6782, App	470	6	1.3	344	10	US-09-915-242-11567	Sequence 11567, A
397	6	1.3	303	10	US-09-510-332-164	Sequence 164, App	471	6	1.3	346	10	US-09-903-456-14	Sequence 14, App1
398	6	1.3	310	10	US-09-305-856B-14	Sequence 14, App1	472	6	1.3	347	10	US-09-903-456-14	Sequence 11, App1
399	6	1.3	311	10	US-09-898-416-9	Sequence 9, App11	473	6	1.3	348	10	US-09-939-821-11	Sequence 12, App1
400	6	1.3	313	9	US-09-992-598-97	Sequence 97, App1	474	6	1.3	352	9	US-09-771-209-71	Sequence 13, App1
401	6	1.3	313	9	US-09-981-876-233	Sequence 233, App	475	6	1.3	359	10	US-09-799-777-45	Sequence 45, App1
402	6	1.3	313	9	US-09-988-293A-97	Sequence 97, App1	476	6	1.3	360	10	US-09-925-301-1068	Sequence 1068, App
403	6	1.3	313	9	US-09-989-735-97	Sequence 97, App1	477	6	1.3	360	10	US-09-925-301-1068	Sequence 20, App1
404	6	1.3	313	9	US-09-990-444-97	Sequence 97, App1	478	6	1.3	365	10	US-09-908-711-100	Sequence 100, App
405	6	1.3	313	9	US-09-989-730-97	Sequence 97, App1	479	6	1.3	365	9	US-10-076-785-24	Sequence 4, App11
406	6	1.3	313	9	US-09-990-436-97	Sequence 97, App1	480	6	1.3	366	10	US-09-815-242-12345	Sequence 12345, A
407	6	1.3	313	9	US-09-991-181-97	Sequence 97, App1	481	6	1.3	366	10	US-09-815-242-12768	Sequence 12768, A
408	6	1.3	313	9	US-09-993-687-97	Sequence 97, App1	482	6	1.3	366	10	US-09-888-615-71	Sequence 71, App1
409	6	1.3	313	9	US-09-989-734-97	Sequence 97, App1	483	6	1.3	380	8	US-08-945-749-7	Sequence 7, App11
410	6	1.3	313	9	US-10-028-072-398	Sequence 398, App	484	6	1.3	380	9	US-10-017-736-12	Sequence 12, App1
411	6	1.3	313	9	US-09-997-653-97	Sequence 97, App1	485	6	1.3	381	9	US-09-738-626-3549	Sequence 3549, App
412	6	1.3	313	9	US-09-993-667-97	Sequence 97, App1	486	6	1.3	381	10	US-09-839-497A-5	Sequence 5, App11
413	6	1.3	313	9	US-10-121-049-398	Sequence 398, App	487	6	1.3	386	10	US-09-815-242-5379	Sequence 5379, App
414	6	1.3	313	9	US-10-123-904-398	Sequence 398, App	488	6	1.3	391	9	US-10-017-736-11	Sequence 11, App1
415	6	1.3	313	9	US-09-989-722-97	Sequence 97, App1	489	6	1.3	393	9	US-09-815-242-11285	Sequence 11285, A
416	6	1.3	313	10	US-09-989-723-97	Sequence 97, App1	490	6	1.3	393	10	US-09-815-242-11985	Sequence 12002, A
417	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	491	6	1.3	397	10	US-09-815-242-11985	Sequence 430, App
418	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	492	6	1.3	397	10	US-09-741-669-430	Sequence 2, App11
419	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	493	6	1.3	409	10	US-09-778-927A-80	Sequence 80, App1
420	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	494	6	1.3	411	10	US-09-749-728B-25	Sequence 25, App1
421	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	495	6	1.3	414	10	US-09-925-301-706	Sequence 706, App
422	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	496	6	1.3	414	10	US-09-927-738-8	Sequence 8, App11
423	6	1.3	313	10	US-09-989-727-97	Sequence 97, App1	497	6	1.3	416	10	US-09-741-669-384	Sequence 384, App
424	6	1.3	313	10	US-09-989-731-97	Sequence 97, App1	498	6	1.3	416	10	US-09-922-331-17	Sequence 17, App1
425	6	1.3	313	10	US-09-989-732-97	Sequence 97, App1	500	6	1.3	418	9	US-09-992-331-17	Sequence 53, App1
426	6	1.3	313	10	US-09-991-073-97	Sequence 97, App1	501	6	1.3	422	10	US-09-809-545A-53	Sequence 10467, A
427	6	1.3	313	10	US-09-990-442-97	Sequence 97, App1	502	6	1.3	425	10	US-09-815-242-10467	Sequence 6036, App
428	6	1.3	313	10	US-09-991-163-97	Sequence 97, App1	503	6	1.3	426	9	US-10-066-500-17	Sequence 17, App1
429	6	1.3	313	10	US-09-993-604-97	Sequence 97, App1	504	6	1.3	428	9	US-10-028-072-292	Sequence 292, App
430	6	1.3	313	10	US-09-990-456-97	Sequence 97, App1	505	6	1.3	428	9	US-09-992-331-15	Sequence 15, App1
431	6	1.3	314	9	US-09-989-721-97	Sequence 97, App1	506	6	1.3	428	9	US-10-121-049-292	Sequence 292, App
432	6	1.3	314	9	US-09-510-332-33	Sequence 33, App1	507	6	1.3	428	9	US-10-123-904-292	Sequence 292, App
433	6	1.3	315	9	US-09-886-055-371	Sequence 371, App	508	6	1.3	428	9	US-09-347-331-10	Sequence 13506, A
434	6	1.3	315	10	US-10-104-966-5	Sequence 5, App11	509	6	1.3	431	10	US-09-815-242-113506	Sequence 820, App
435	6	1.3	315	10	US-09-815-242-11775	Sequence 11775, A	510	6	1.3	434	10	US-09-778-927A-79	Sequence 79, App1
436	6	1.3	315	10	US-09-898-416-8	Sequence 8, App11	511	6	1.3	436	9	US-09-738-626-5887	Sequence 5887, App
437	6	1.3	315	10	US-09-983-306-3	Sequence 3, App11	512	6	1.3	436	10	US-09-815-242-11399	Sequence 11399, A
438	6	1.3	315	10	US-09-983-306-6	Sequence 6, App11	513	6	1.3	440	10	US-09-738-626-5934	Sequence 5934, App
439	6	1.3	315	10	US-09-929-955-5	Sequence 5, App11	514	6	1.3	441	10	US-09-950-071-2	Sequence 2, App11
440	6	1.3	316	10	US-09-886-055-197	Sequence 197, App	515	6	1.3	441	10	US-10-063-547-76	Sequence 76, App1
441	6	1.3	317	10	US-09-305-856B-12	Sequence 12, App1	516	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
442	6	1.3	317	10	US-09-903-456-13	Sequence 13, App1	517	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
443	6	1.3	318	9	US-09-903-170C-3	Sequence 3, App11	518	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
444	6	1.3	318	10	US-09-957-156-2	Sequence 2, App11	519	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
445	6	1.3	318	10	US-09-739-907-76	Sequence 76, App1	520	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
446	6	1.3	318	10	US-09-903-180B-3	Sequence 3, App11	521	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
447	6	1.3	318	10	US-09-903-187A-3	Sequence 3, App11	522	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
448	6	1.3	318	10	US-09-903-171A-3	Sequence 3, App11	523	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
449	6	1.3	318	10	US-09-903-188A-3	Sequence 3, App11	524	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
450	6	1.3	318	10	US-09-903-323A-3	Sequence 3, App11	525	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
451	6	1.3	318	10	US-09-903-325A-3	Sequence 3, App11	526	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
452	6	1.3	318	10	US-09-903-325A-3	Sequence 3, App11	527	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
453	6	1.3	319	9	US-09-966-455A-11	Sequence 11, App1	528	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
454	6	1.3	321	10	US-09-815-242-4990	Sequence 4990, App	529	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
455	6	1.3	321	10	US-09-815-242-10635	Sequence 10635, A	530	6	1.3	442	9	US-10-063-616-76	Sequence 76, App1
456	6	1.3	323	9	US-09-791-932-119	Sequence 119, App							
457	6	1.3	324	9	US-09-738-626-6547	Sequence 6547, App							
			329	10	US-09-925-301-904	Sequence 904, App1							

531	6	1.3	466	10	US-09-778-927A-78	Sequence 78, Appl	604	6	1.3	604	9	US-09-738-626-3886	Sequence 3886, Ap
532	6	1.3	466	10	US-09-778-927A-81	Sequence 81, Appl	605	6	1.3	604	10	US-09-920-581-3	Sequence 3, Appl
533	6	1.3	468	10	US-09-860-232A-8	Sequence 8, Appl	606	6	1.3	608	9	US-09-738-626-5305	Sequence 5305, Ap
534	6	1.3	471	9	US-09-900-425A-5	Sequence 5, Appl	607	6	1.3	608	10	US-09-950-294-4	Sequence 4, Appl
535	6	1.3	475	10	US-09-826-752-14	Sequence 14, Appl	608	6	1.3	614	9	US-09-331-631A-21	Sequence 21, Appl
536	6	1.3	476	10	US-09-925-300-1582	Sequence 1582, Ap	609	6	1.3	619	10	US-09-815-242-11085	Sequence 11085, A
537	6	1.3	493	10	US-09-981-947A-10	Sequence 10, Appl	610	6	1.3	621	10	US-09-799-777-17	Sequence 77, Appl
538	6	1.3	493	10	US-09-815-242-5498	Sequence 5498, Ap	611	6	1.3	632	10	US-09-929-955-39	Sequence 29, Appl
539	6	1.3	494	10	US-09-815-242-12410	Sequence 12410, A	612	6	1.3	633	12	US-10-001-882-5	Sequence 5, Appl
540	6	1.3	500	10	US-09-323-998D-59	Sequence 59, Appl	613	6	1.3	650	9	US-09-738-626-4040	Sequence 4040, Ap
541	6	1.3	501	10	US-09-934-868-56	Sequence 56, Appl	614	6	1.3	656	9	US-09-991-496-6	Sequence 6, Appl
542	6	1.3	504	9	US-09-903-376-2	Sequence 2, Appl	615	6	1.3	661	10	US-09-874-923-6	Sequence 10, Appl
543	6	1.3	505	9	US-09-742-580-8	Sequence 8, Appl	616	6	1.3	661	9	US-10-114-893-10	Sequence 80, Appl
544	6	1.3	505	9	US-09-742-581-8	Sequence 8, Appl	617	6	1.3	662	9	US-10-047-542-80	Sequence 10, Appl
545	6	1.3	505	10	US-09-742-582-8	Sequence 90, Appl	618	6	1.3	680	10	US-09-996-184-10	Sequence 10, Appl
546	6	1.3	506	10	US-09-801-368-90	Sequence 90, Appl	619	6	1.3	686	9	US-09-881-239-3	Sequence 3, Appl
547	6	1.3	508	10	US-09-016-159-5	Sequence 5, Appl	620	6	1.3	686	10	US-09-929-955-17	Sequence 17, Appl
548	6	1.3	511	9	US-09-738-626-4770	Sequence 4770, Ap	621	6	1.3	686	10	US-09-929-955-31	Sequence 31, Appl
549	6	1.3	520	9	US-09-738-626-4493	Sequence 4493, Ap	622	6	1.3	686	10	US-09-929-955-32	Sequence 32, Appl
550	6	1.3	521	10	US-09-795-483-2	Sequence 2, Appl	623	6	1.3	686	10	US-09-929-955-43	Sequence 43, Appl
551	6	1.3	527	9	US-09-738-626-4803	Sequence 4803, Ap	624	6	1.3	686	10	US-09-929-955-44	Sequence 44, Appl
552	6	1.3	529	9	US-09-258-031B-16	Sequence 16, Appl	625	6	1.3	686	10	US-09-929-955-45	Sequence 45, Appl
553	6	1.3	529	9	US-09-258-031B-20	Sequence 20, Appl	626	6	1.3	686	10	US-09-929-955-46	Sequence 46, Appl
554	6	1.3	530	10	US-09-835-082-2	Sequence 2, Appl	627	6	1.3	686	10	US-09-929-955-47	Sequence 47, Appl
555	6	1.3	530	10	US-09-835-082-4	Sequence 4, Appl	628	6	1.3	686	10	US-09-929-955-48	Sequence 48, Appl
556	6	1.3	533	10	US-09-431-226-5	Sequence 5, Appl	629	6	1.3	686	10	US-09-929-955-49	Sequence 49, Appl
557	6	1.3	539	9	US-10-028-072-140	Sequence 140, App	630	6	1.3	686	10	US-09-881-654-2	Sequence 2, Appl
558	6	1.3	539	9	US-10-121-049-140	Sequence 140, App	631	6	1.3	697	10	US-09-881-752A-76	Sequence 76, Appl
559	6	1.3	539	9	US-10-123-904-140	Sequence 140, App	632	6	1.3	702	10	US-09-815-242-10117	Sequence 10117, A
560	6	1.3	539	9	US-10-140-470-140	Sequence 140, App	633	6	1.3	702	10	US-09-815-242-14005	Sequence 14005, A
561	6	1.3	542	9	US-10-028-072-188	Sequence 188, App	634	6	1.3	705	9	US-09-854-133-186	Sequence 186, App
562	6	1.3	542	9	US-10-174-5590-398	Sequence 398, App	635	6	1.3	705	10	US-09-925-302-531	Sequence 531, App
563	6	1.3	542	9	US-10-175-758-398	Sequence 398, App	636	6	1.3	705	10	US-09-738-973-186	Sequence 186, App
564	6	1.3	542	9	US-10-175-757-398	Sequence 398, App	637	6	1.3	709	9	US-10-118-328-4	Sequence 4, Appl
565	6	1.3	542	9	US-10-121-049-188	Sequence 188, App	638	6	1.3	717	10	US-09-817-913-9	Sequence 9, Appl
566	6	1.3	542	9	US-10-123-904-188	Sequence 188, App	639	6	1.3	717	10	US-09-817-913-9	Sequence 9, Appl
567	6	1.3	542	9	US-10-140-470-188	Sequence 140, App	640	6	1.3	724	9	US-09-908-193-25	Sequence 25, Appl
568	6	1.3	542	9	US-10-173-706-398	Sequence 398, App	641	6	1.3	728	9	US-09-881-620-351	Sequence 1, Appl
569	6	1.3	542	9	US-10-175-738-398	Sequence 398, App	642	6	1.3	729	9	US-10-108-605-251	Sequence 251, App
570	6	1.3	542	9	US-10-175-752-398	Sequence 398, App	643	6	1.3	731	9	US-09-361-630-3	Sequence 3, Appl
571	6	1.3	542	9	US-10-176-482-398	Sequence 398, App	644	6	1.3	731	9	US-10-086-464-17	Sequence 17, Appl
572	6	1.3	542	9	US-10-176-757-398	Sequence 398, App	645	6	1.3	734	9	US-09-738-626-4227	Sequence 4227, Ap
573	6	1.3	542	9	US-10-176-913-398	Sequence 398, App	646	6	1.3	746	9	US-09-981-353-30	Sequence 30, Appl
574	6	1.3	542	9	US-10-180-552-398	Sequence 398, App	647	6	1.3	746	9	US-09-982-107-4	Sequence 4, Appl
575	6	1.3	542	9	US-10-180-557-398	Sequence 398, App	648	6	1.3	747	9	US-09-974-143A-2	Sequence 2, Appl
576	6	1.3	542	12	US-10-052-586-398	Sequence 398, App	649	6	1.3	747	10	US-09-431-226-7	Sequence 7, Appl
577	6	1.3	544	10	US-09-967-624-6	Sequence 6, Appl	650	6	1.3	749	10	US-09-828-313-37	Sequence 27, Appl
578	6	1.3	546	10	US-09-746-359A-37	Sequence 37, Appl	651	6	1.3	757	10	US-09-928-175-34	Sequence 24, Appl
579	6	1.3	548	10	US-09-869-877-4	Sequence 4, Appl	652	6	1.3	763	9	US-10-081-408-2	Sequence 2, Appl
580	6	1.3	548	10	US-09-732-350-4	Sequence 4, Appl	653	6	1.3	764	9	US-09-981-353-59	Sequence 59, Appl
581	6	1.3	553	10	US-09-746-359A-11	Sequence 11, Appl	654	6	1.3	764	9	US-09-989-915-134	Sequence 124, Appl
582	6	1.3	553	10	US-09-949-192-7	Sequence 7, Appl	655	6	1.3	764	10	US-09-818-247-1	Sequence 1, Appl
583	6	1.3	560	9	US-09-912-672A-5	Sequence 5, Appl	656	6	1.3	769	9	US-09-815-242-10575	Sequence 10575, A
584	6	1.3	561	10	US-09-764-864-1539	Sequence 1539, Ap	657	6	1.3	772	10	US-09-738-626-6661	Sequence 6661, Ap
585	6	1.3	566	10	US-09-925-299-813	Sequence 813, App	658	6	1.3	772	10	US-09-935-799A-5	Sequence 2, Appl
586	6	1.3	571	10	US-09-815-242-10619	Sequence 10619, A	659	6	1.3	772	10	US-09-935-799A-5	Sequence 5, Appl
587	6	1.3	571	10	US-09-764-864-1028	Sequence 1028, Ap	660	6	1.3	775	9	US-09-992-598-326	Sequence 326, App
588	6	1.3	574	9	US-09-912-672A-2	Sequence 2, Appl	661	6	1.3	775	9	US-09-989-293A-326	Sequence 326, App
589	6	1.3	574	9	US-10-063-547-164	Sequence 164, App	662	6	1.3	775	9	US-09-989-735-336	Sequence 326, App
590	6	1.3	574	9	US-10-063-616-164	Sequence 164, App	663	6	1.3	775	9	US-09-990-444-336	Sequence 326, App
591	6	1.3	574	9	US-10-063-502-164	Sequence 164, App	664	6	1.3	775	9	US-09-989-730-336	Sequence 326, App
592	6	1.3	574	10	US-09-728-911-25	Sequence 25, Appl	665	6	1.3	775	9	US-09-990-436-336	Sequence 326, App
593	6	1.3	574	10	US-09-748-657-2	Sequence 2, Appl	666	6	1.3	775	9	US-09-991-181-336	Sequence 326, App
594	6	1.3	574	10	US-08-870-574-4	Sequence 4, Appl	667	6	1.3	775	9	US-09-993-687-336	Sequence 326, App
595	6	1.3	574	12	US-10-006-867-164	Sequence 164, App	668	6	1.3	775	9	US-09-989-734-336	Sequence 326, App
596	6	1.3	578	10	US-09-052-753-7	Sequence 7, Appl	669	6	1.3	775	9	US-09-997-653-336	Sequence 326, App
597	6	1.3	584	10	US-09-815-242-12501	Sequence 12501, A	670	6	1.3	775	9	US-09-993-667-336	Sequence 326, App
598	6	1.3	584	9	US-10-050-786-7	Sequence 7, Appl	671	6	1.3	775	10	US-09-989-723-326	Sequence 326, App
599	6	1.3	599	9	US-09-331-631A-8	Sequence 8, Appl	672	6	1.3	775	10	US-09-988-723-326	Sequence 326, App
600	6	1.3	599	10	US-09-952-013A-4	Sequence 4, Appl	673	6	1.3	775	10	US-09-989-279-326	Sequence 326, App
601	6	1.3	600	10	US-09-801-368-158	Sequence 158, App	674	6	1.3	775	10	US-09-989-727-326	Sequence 326, App
602	6	1.3	602	9	US-10-047-542-51	Sequence 51, Appl	675	6	1.3	775	10	US-09-989-731-326	Sequence 326, App
603	6	1.3	604	9	US-10-045-170A-1	Sequence 1, Appl	676	6	1.3	775	10	US-09-989-732-326	Sequence 326, App

677	6	1.3	775	10	US-09-991-073-326	Sequence 326, App	750	6	1.3	1332	9	US-10-041-856-5	Sequence 5, Appli
678	6	1.3	775	10	US-09-990-442-326	Sequence 326, App	751	6	1.3	1332	10	US-09-982-091A-4	Sequence 4, Appli
679	6	1.3	775	10	US-09-991-163-326	Sequence 326, App	752	6	1.3	1420	10	US-09-801-368-356	Sequence 326, App
680	6	1.3	775	10	US-09-993-604-326	Sequence 326, App	753	6	1.3	1427	9	US-09-991-496-97	Sequence 97, Appli
681	6	1.3	775	10	US-09-993-604-326	Sequence 326, App	754	6	1.3	1427	10	US-09-874-923-97	Sequence 97, Appli
682	6	1.3	775	10	US-09-989-721-326	Sequence 326, App	755	6	1.3	1464	9	US-09-842-777-10	Sequence 10, Appli
683	6	1.3	781	10	US-09-766-387-2	Sequence 2, Appli	756	6	1.3	1504	9	US-09-932-145-7	Sequence 7, Appli
684	6	1.3	781	10	US-09-766-387-4	Sequence 4, Appli	757	6	1.3	1507	9	US-10-017-216-6	Sequence 6, Appli
685	6	1.3	782	10	US-09-815-242-4893	Sequence 4893, Ap	758	6	1.3	1602	10	US-09-778-927A-59	Sequence 59, Appli
686	6	1.3	790	10	US-09-966-147-9	Sequence 9, Appli	759	6	1.3	1641	9	US-10-017-216-5	Sequence 5, Appli
687	6	1.3	794	10	US-09-789-404-2	Sequence 2, Appli	760	6	1.3	1641	9	US-09-991-466-96	Sequence 96, Appli
688	6	1.3	796	10	US-09-738-626-3660	Sequence 3660, Ap	761	6	1.3	1641	10	US-09-874-923-96	Sequence 96, Appli
689	6	1.3	811	10	US-09-815-242-11875	Sequence 11875, A	762	6	1.3	1643	10	US-09-738-626-6894	Sequence 6894, Ap
690	6	1.3	816	9	US-09-796-720B-2	Sequence 2, Appli	763	6	1.3	1736	10	US-09-919-497-98	Sequence 98, Appli
691	6	1.3	819	9	US-09-796-720B-4	Sequence 4, Appli	764	6	1.3	1809	10	US-09-919-497-98	Sequence 98, Appli
692	6	1.3	824	9	US-09-932-145-3	Sequence 3, Appli	765	6	1.3	1924	9	US-09-822-635-2	Sequence 2, Appli
693	6	1.3	829	9	US-09-881-239-5	Sequence 5, Appli	766	6	1.3	1958	12	US-10-028-946-4	Sequence 4, Appli
694	6	1.3	833	9	US-09-470-276-54	Sequence 54, Appli	767	6	1.3	2012	9	US-09-808-602-68	Sequence 68, Appli
695	6	1.3	847	9	US-09-870-759-52	Sequence 52, Appli	768	6	1.3	2053	9	US-10-017-216-2	Sequence 2, Appli
696	6	1.3	849	10	US-09-752-639-152	Sequence 152, App	769	6	1.3	2054	12	US-10-028-946-2	Sequence 2, Appli
697	6	1.3	849	10	US-09-984-198-152	Sequence 152, App	770	6	1.3	2055	9	US-10-017-216-4	Sequence 4, Appli
698	6	1.3	866	10	US-09-841-132-189	Sequence 189, App	771	6	1.3	2201	9	US-10-085-476-2	Sequence 2, Appli
699	6	1.3	875	12	US-10-001-852-2	Sequence 2, Appli	772	6	1.3	2491	9	US-10-000-789-2	Sequence 2, Appli
700	6	1.3	880	10	US-09-841-132-175	Sequence 175, App	773	6	1.3	2894	10	US-09-941-611-23	Sequence 23, Appli
701	6	1.3	880	9	US-10-036-041-35	Sequence 35, Appli	774	6	1.3	3011	9	US-09-747-419-20	Sequence 20, Appli
702	6	1.3	888	9	US-10-028-072-544	Sequence 544, App	775	6	1.3	3011	9	US-10-104-966-1	Sequence 1, Appli
703	6	1.3	888	9	US-10-035-855-35	Sequence 35, Appli	776	6	1.3	3011	9	US-09-891-894-3	Sequence 3, Appli
704	6	1.3	888	9	US-10-121-049-544	Sequence 544, App	777	6	1.3	3011	10	US-09-742-659-4	Sequence 4, Appli
705	6	1.3	888	9	US-10-123-904-544	Sequence 544, App	778	6	1.3	3011	10	US-09-916-359-2	Sequence 2, Appli
706	6	1.3	888	9	US-10-140-470-544	Sequence 544, App	779	6	1.3	3011	10	US-09-238-076-20	Sequence 20, Appli
707	6	1.3	888	12	US-10-036-342-35	Sequence 35, Appli	780	6	1.3	3011	10	US-09-952-572-9	Sequence 9, Appli
708	6	1.3	890	9	US-10-060-425-8	Sequence 8, Appli	781	6	1.3	3011	10	US-09-929-955-1	Sequence 1, Appli
709	6	1.3	890	9	US-10-060-425-10	Sequence 10, Appli	782	6	1.3	3012	10	US-09-238-076-2	Sequence 2, Appli
710	6	1.3	891	12	US-10-001-852-6	Sequence 6, Appli	783	6	1.3	3472	9	US-10-027-806-4	Sequence 4, Appli
711	6	1.3	911	10	US-10-066-320-2	Sequence 2, Appli	784	6	1.3	3472	9	US-10-034-623-4	Sequence 4, Appli
712	6	1.3	913	10	US-09-223-490-4	Sequence 4, Appli	785	6	1.3	4342	10	US-09-815-242-5107	Sequence 5107, Ap
713	6	1.3	918	12	US-10-001-852-7	Sequence 7, Appli	786	6	1.3	5701	10	US-09-864-761-37319	Sequence 37319, A
714	6	1.3	927	10	US-09-804-474A-4	Sequence 4, Appli	787	6	1.3	26926	6	US-09-759-508B-2	Sequence 2, Appli
715	6	1.3	950	10	US-09-321-987B-4	Sequence 4, Appli	788	6	1.1	6	1	US-08-809-423A-28	Sequence 28, Appli
716	6	1.3	961	10	US-09-220-091-3	Sequence 3, Appli	789	5	1.1	6	10	US-09-821-380-12	Sequence 12, Appli
717	6	1.3	962	9	US-09-738-626-3800	Sequence 3800, Ap	790	5	1.1	7	10	US-09-821-380-9	Sequence 9, Appli
718	6	1.3	967	12	US-10-105-929-2	Sequence 2, Appli	791	5	1.1	7	10	US-09-821-380-11	Sequence 11, Appli
719	6	1.3	968	9	US-10-163-316-7	Sequence 7, Appli	792	5	1.1	8	1	US-08-841-656A-7	Sequence 7, Appli
720	6	1.3	981	10	US-09-991-258-13	Sequence 13, Appli	793	5	1.1	8	10	US-09-821-380-10	Sequence 10, Appli
721	6	1.3	1002	10	US-09-988-117-3	Sequence 3, Appli	794	5	1.1	8	12	US-10-007-761-13	Sequence 13, Appli
722	6	1.3	1002	10	US-09-812-471-3	Sequence 3, Appli	795	5	1.1	9	8	US-08-871-076-4	Sequence 4, Appli
723	6	1.3	1002	10	US-09-812-633-3	Sequence 3, Appli	796	5	1.1	9	8	US-08-854-825-53	Sequence 53, Appli
724	6	1.3	1005	9	US-09-988-117-1	Sequence 1, Appli	797	5	1.1	9	9	US-09-277-074-14	Sequence 14, Appli
725	6	1.3	1005	10	US-09-812-471-1	Sequence 1, Appli	798	5	1.1	9	10	US-09-872-832-12	Sequence 12, Appli
726	6	1.3	1005	10	US-08-834-705-18	Sequence 18, Appli	799	5	1.1	9	10	US-09-791-378-541	Sequence 541, App
727	6	1.3	1019	1	US-10-027-591-2	Sequence 2, Appli	800	5	1.1	10	10	US-09-767-460-47	Sequence 47, Appli
728	6	1.3	1044	9	US-10-027-591-2	Sequence 2, Appli	801	5	1.1	10	10	US-09-821-380-3	Sequence 3, Appli
729	6	1.3	1047	10	US-09-866-582-37	Sequence 37, Appli	802	5	1.1	10	10	US-09-821-380-4	Sequence 4, Appli
730	6	1.3	1086	10	US-09-147-052-4	Sequence 4, Appli	803	5	1.1	10	10	US-09-791-378-635	Sequence 635, App
731	6	1.3	1090	10	US-09-866-510-14	Sequence 14, Appli	804	5	1.1	11	1	US-08-809-423A-5	Sequence 5, Appli
732	6	1.3	1099	9	US-09-932-145-4	Sequence 4, Appli	805	5	1.1	11	10	US-09-873-676-23	Sequence 23, Appli
733	6	1.3	1099	10	US-09-881-654-4	Sequence 4, Appli	806	5	1.1	12	10	US-09-734-520-75	Sequence 75, Appli
734	6	1.3	1106	9	US-09-955-363-2	Sequence 2, Appli	807	5	1.1	12	10	US-09-734-520-76	Sequence 76, Appli
735	6	1.3	1106	10	US-09-866-510-16	Sequence 16, Appli	808	5	1.1	12	12	US-10-012-034A-75	Sequence 75, Appli
736	6	1.3	1106	10	US-09-866-510-18	Sequence 18, Appli	809	5	1.1	12	12	US-10-012-034A-76	Sequence 76, Appli
737	6	1.3	1106	10	US-09-866-510-20	Sequence 20, Appli	810	5	1.1	13	9	US-09-851-138-156	Sequence 156, App
738	6	1.3	1106	10	US-09-866-510-22	Sequence 22, Appli	811	5	1.1	13	10	US-09-919-124-30	Sequence 30, Appli
739	6	1.3	1134	9	US-10-001-873-50	Sequence 50, Appli	812	5	1.1	13	10	US-09-821-380-2	Sequence 2, Appli
740	6	1.3	1163	10	US-09-893-348-18	Sequence 18, Appli	813	5	1.1	13	10	US-09-981-194-23	Sequence 23, Appli
741	6	1.3	1213	10	US-09-969-515-8	Sequence 8, Appli	814	5	1.1	13	10	US-09-943-692-29	Sequence 29, Appli
742	6	1.3	1224	10	US-09-969-515-2	Sequence 2, Appli	815	5	1.1	15	9	US-10-002-344A-208	Sequence 208, App
743	6	1.3	1229	10	US-09-815-242-5818	Sequence 5818, Ap	816	5	1.1	15	9	US-09-774-639-124	Sequence 124, App
744	6	1.3	1229	10	US-09-815-242-12946	Sequence 12946, A	817	5	1.1	16	9	US-09-759-130B-194	Sequence 194, App
745	6	1.3	1246	10	US-09-741-669-349	Sequence 349, App	818	5	1.1	16	10	US-09-818-954A-28	Sequence 28, Appli
746	6	1.3	1251	10	US-09-778-927A-58	Sequence 58, Appli	819	5	1.1	17	9	US-09-826-290-253	Sequence 253, App
747	6	1.3	1286	9	US-10-017-216-7	Sequence 7, Appli	820	5	1.1	17	9	US-09-826-290-255	Sequence 255, App
748	6	1.3	1332	9	US-10-041-856-3	Sequence 3, Appli	821	5	1.1	17	9	US-09-826-290-258	Sequence 258, App
749	6	1.3	1332	9	US-10-041-856-4	Sequence 4, Appli	822	5	1.1	17	9	US-09-826-290-448	Sequence 448, App

823	5	1.1	17	9	US-09-916-494A-26	Sequence 26, App1	896	5	1.1	26	9	US-09-349-755-7	Sequence 7, App1
824	5	1.1	17	9	US-09-759-130B-174	Sequence 174, App	897	5	1.1	26	9	US-09-349-755-14	Sequence 14, App1
825	5	1.1	17	9	US-09-759-130B-354	Sequence 354, App	898	5	1.1	26	9	US-09-166-334-7	Sequence 7, App1
826	5	1.1	17	10	US-09-864-761-46718	Sequence 46718, A	899	5	1.1	26	9	US-09-166-334-14	Sequence 14, App1
827	5	1.1	17	10	US-09-821-380-1	Sequence 1, App1	900	5	1.1	26	9	US-09-030-619-123	Sequence 123, App
828	5	1.1	17	10	US-09-798-116-12	Sequence 12, App1	901	5	1.1	26	10	US-09-864-761-35286	Sequence 35286, A
829	5	1.1	17	10	US-09-798-116-23	Sequence 23, App1	902	5	1.1	26	10	US-09-350-206-7	Sequence 7, App1
830	5	1.1	17	10	US-09-791-378-4	Sequence 4, App1	903	5	1.1	26	10	US-09-350-206-14	Sequence 14, App1
831	5	1.1	17	10	US-09-791-378-79	Sequence 79, App1	904	5	1.1	26	10	US-09-952-782-4	Sequence 4, App1
832	5	1.1	17	10	US-09-791-378-111	Sequence 111, App	905	5	1.1	26	10	US-09-952-782-23	Sequence 23, App1
833	5	1.1	17	10	US-09-791-378-114	Sequence 114, App	906	5	1.1	26	10	US-10-117-057-8	Sequence 8, App1
834	5	1.1	17	10	US-09-791-378-159	Sequence 159, App	907	5	1.1	27	9	US-09-966-459A-17	Sequence 17, App1
835	5	1.1	17	10	US-09-791-378-162	Sequence 162, App	908	5	1.1	27	9	US-09-983-802-921	Sequence 921, App
836	5	1.1	17	10	US-09-791-378-166	Sequence 166, App	909	5	1.1	27	10	US-09-864-761-35226	Sequence 35226, A
837	5	1.1	17	10	US-09-791-378-229	Sequence 229, App	910	5	1.1	27	10	US-09-864-761-44867	Sequence 44867, A
838	5	1.1	17	10	US-09-791-378-237	Sequence 237, App	911	5	1.1	27	10	US-09-952-782-22	Sequence 22, App1
839	5	1.1	17	10	US-09-791-378-240	Sequence 240, App	912	5	1.1	28	9	US-10-012-896-921	Sequence 921, App
840	5	1.1	17	10	US-09-791-378-242	Sequence 242, App	913	5	1.1	28	9	US-09-895-793-921	Sequence 921, App
841	5	1.1	17	10	US-09-791-378-307	Sequence 307, App	914	5	1.1	28	9	US-09-895-814-921	Sequence 921, App
842	5	1.1	17	10	US-09-791-378-308	Sequence 308, App	915	5	1.1	28	10	US-09-759-143-921	Sequence 921, App
843	5	1.1	17	10	US-09-791-378-340	Sequence 340, App	916	5	1.1	28	10	US-09-864-761-33674	Sequence 33674, A
844	5	1.1	17	10	US-09-791-378-621	Sequence 621, App	917	5	1.1	28	10	US-09-864-761-37130	Sequence 37130, A
845	5	1.1	17	10	US-09-791-378-647	Sequence 647, App	918	5	1.1	28	10	US-09-780-669-921	Sequence 921, App
846	5	1.1	18	9	US-10-074-956-20	Sequence 20, App1	919	5	1.1	28	10	US-09-822-827-921	Sequence 921, App
847	5	1.1	18	9	US-10-162-095-4	Sequence 4, App1	920	5	1.1	28	10	US-09-822-827-921	Sequence 921, App
848	5	1.1	18	10	US-09-864-761-48194	Sequence 48194, A	921	5	1.1	28	10	US-09-952-782-21	Sequence 21, App1
849	5	1.1	18	10	US-09-952-782-31	Sequence 31, App1	922	5	1.1	29	8	US-08-424-550B-486	Sequence 486, App
850	5	1.1	19	9	US-10-078-547-22	Sequence 22, App1	923	5	1.1	29	9	US-09-996-140-230	Sequence 230, App
851	5	1.1	19	10	US-09-864-761-42761	Sequence 42761, A	924	5	1.1	29	9	US-09-996-140-231	Sequence 231, App
852	5	1.1	19	10	US-09-952-782-30	Sequence 30, App1	925	5	1.1	29	9	US-09-996-140-232	Sequence 232, App
853	5	1.1	19	12	US-10-012-034A-15	Sequence 15, App1	926	5	1.1	29	9	US-10-223-047-16	Sequence 16, App1
854	5	1.1	20	9	US-10-007-270-29	Sequence 29, App1	927	5	1.1	29	10	US-09-864-761-44607	Sequence 44607, A
855	5	1.1	20	9	US-09-915-676-9	Sequence 9, App1	928	5	1.1	29	10	US-09-864-761-47524	Sequence 47524, A
856	5	1.1	20	10	US-09-812-528-18	Sequence 18, App1	929	5	1.1	29	10	US-09-917-340-30	Sequence 30, App1
857	5	1.1	20	10	US-09-466-320-6	Sequence 6, App1	930	5	1.1	30	9	US-09-852-797-79	Sequence 79, App1
858	5	1.1	20	10	US-09-952-782-29	Sequence 29, App1	931	5	1.1	30	10	US-09-864-761-34474	Sequence 34474, A
859	5	1.1	21	8	US-08-871-076-6	Sequence 6, App1	932	5	1.1	30	10	US-09-864-761-37450	Sequence 37450, A
860	5	1.1	21	9	US-09-909-460-15	Sequence 15, App1	933	5	1.1	30	10	US-09-864-761-40773	Sequence 40773, A
861	5	1.1	21	10	US-09-952-782-28	Sequence 28, App1	934	5	1.1	30	10	US-09-137-531-12	Sequence 12, App1
862	5	1.1	21	10	US-09-833-740-9	Sequence 9, App1	935	5	1.1	30	10	US-09-853-161-79	Sequence 19, App1
863	5	1.1	22	10	US-09-864-761-38066	Sequence 38066, A	936	5	1.1	31	9	US-09-852-659A-79	Sequence 79, App1
864	5	1.1	22	10	US-09-864-761-38136	Sequence 38136, A	937	5	1.1	31	10	US-10-042-431-20	Sequence 20, App1
865	5	1.1	22	10	US-09-875-494-19	Sequence 19, App1	938	5	1.1	31	9	US-09-759-130B-390	Sequence 390, App1
866	5	1.1	22	10	US-09-952-782-27	Sequence 27, App1	939	5	1.1	31	10	US-09-986-676A-112	Sequence 112, App
867	5	1.1	23	9	US-09-924-400-133	Sequence 133, App1	940	5	1.1	31	10	US-09-764-877-1239	Sequence 1239, App
868	5	1.1	23	9	US-09-969-920-171	Sequence 171, App	941	5	1.1	32	10	US-09-864-761-34495	Sequence 34495, A
869	5	1.1	23	10	US-09-746-919-41	Sequence 41, App1	942	5	1.1	32	10	US-09-864-761-41454	Sequence 41454, A
870	5	1.1	23	10	US-09-746-919-42	Sequence 42, App1	943	5	1.1	32	10	US-09-864-761-43444	Sequence 43444, A
871	5	1.1	23	10	US-09-832-336-6	Sequence 6, App1	944	5	1.1	32	10	US-09-864-761-45034	Sequence 45034, A
872	5	1.1	23	10	US-09-810-936-133	Sequence 133, App	945	5	1.1	32	10	US-09-864-761-45811	Sequence 45811, A
873	5	1.1	23	10	US-09-952-782-26	Sequence 26, App1	946	5	1.1	32	10	US-09-864-761-46737	Sequence 46737, A
874	5	1.1	23	10	US-09-429-755-133	Sequence 133, App	947	5	1.1	32	10	US-09-864-761-47019	Sequence 47019, A
875	5	1.1	24	9	US-10-002-344A-218	Sequence 218, App	948	5	1.1	33	10	US-09-737-379-7	Sequence 7, App1
876	5	1.1	24	9	US-09-759-130B-159	Sequence 159, App	949	5	1.1	33	9	US-09-983-802-236	Sequence 236, App
877	5	1.1	24	10	US-09-739-907-142	Sequence 142, App	950	5	1.1	33	10	US-09-864-761-44510	Sequence 44510, A
878	5	1.1	24	10	US-09-864-761-38460	Sequence 38460, A	951	5	1.1	33	10	US-09-864-761-44885	Sequence 44885, A
879	5	1.1	24	10	US-09-864-761-39114	Sequence 39114, A	952	5	1.1	33	10	US-09-764-869-1122	Sequence 1122, App
880	5	1.1	24	10	US-09-864-761-42315	Sequence 42315, A	953	5	1.1	34	9	US-09-759-130B-74	Sequence 74, App1
881	5	1.1	24	10	US-09-952-782-25	Sequence 25, App	954	5	1.1	34	10	US-09-864-761-38085	Sequence 38085, A
882	5	1.1	25	8	US-08-424-550B-180	Sequence 180, App	955	5	1.1	34	10	US-09-864-761-41080	Sequence 41080, A
883	5	1.1	25	9	US-09-731-449-10	Sequence 10, App1	956	5	1.1	34	10	US-09-864-761-44095	Sequence 44095, A
884	5	1.1	25	9	US-09-989-920-214	Sequence 214, App	957	5	1.1	34	10	US-09-864-761-47878	Sequence 47878, A
885	5	1.1	25	9	US-09-759-130B-77	Sequence 77, App1	958	5	1.1	34	10	US-09-938-719-13	Sequence 13, App1
886	5	1.1	25	10	US-09-729-472-3	Sequence 3, App1	959	5	1.1	34	10	US-09-938-703-13	Sequence 13, App1
887	5	1.1	25	10	US-09-821-984-31	Sequence 31, App1	960	5	1.1	35	9	US-09-774-639-223	Sequence 223, App
888	5	1.1	25	10	US-09-738-970-3	Sequence 3, App1	961	5	1.1	35	10	US-09-864-761-35975	Sequence 35975, A
889	5	1.1	25	10	US-09-864-761-36489	Sequence 36489, A	962	5	1.1	35	10	US-09-864-761-40336	Sequence 40336, A
890	5	1.1	25	10	US-09-864-761-40555	Sequence 40555, A	963	5	1.1	35	10	US-09-864-761-42239	Sequence 42239, A
891	5	1.1	25	10	US-09-729-499-3	Sequence 17, App1	964	5	1.1	35	10	US-09-864-761-46401	Sequence 46401, A
892	5	1.1	25	10	US-09-952-782-22	Sequence 24, App1	965	5	1.1	35	10	US-09-864-761-47358	Sequence 47358, A
893	5	1.1	25	10	US-09-952-782-22	Sequence 22, App1	966	5	1.1	36	9	US-09-852-797-82	Sequence 82, App1
894	5	1.1	25	10	US-09-952-782-22	Sequence 22, App1	967	5	1.1	36	9	US-09-983-802-182	Sequence 182, App
895	5	1.1	25	10	US-09-952-782-22	Sequence 22, App1	968	5	1.1	36	9	US-09-983-802-182	Sequence 182, App

969	5	1.1	36	10	US-09-864-761-37154	Sequence 37154, A
970	5	1.1	36	10	US-09-864-761-37406	Sequence 37406, A
971	5	1.1	36	10	US-09-864-761-40594	Sequence 40594, A
972	5	1.1	36	10	US-09-864-761-40624	Sequence 40624, A
973	5	1.1	36	10	US-09-864-761-41813	Sequence 41813, A
974	5	1.1	36	10	US-09-864-761-43021	Sequence 43021, A
975	5	1.1	36	10	US-09-853-161-82	Sequence 82, APPL
976	5	1.1	36	10	US-09-852-6559A-82	Sequence 82, APPL
977	5	1.1	36	10	US-09-764-860-336	Sequence 336, App
978	5	1.1	37	1	US-08-809-423A-14	Sequence 14, Appl
979	5	1.1	37	9	US-10-042-141-17	Sequence 179, App
980	5	1.1	37	9	US-10-042-141-184	Sequence 184, App
981	5	1.1	37	10	US-09-726-643-179	Sequence 179, App
982	5	1.1	37	10	US-09-726-643-184	Sequence 184, App
983	5	1.1	37	10	US-09-864-761-34464	Sequence 34464, A
984	5	1.1	37	10	US-09-864-761-44924	Sequence 34924, A
985	5	1.1	37	10	US-09-864-761-37682	Sequence 37682, A
986	5	1.1	37	10	US-09-864-761-47013	Sequence 47013, A
987	5	1.1	37	10	US-09-764-869-30	Sequence 930, App
988	5	1.1	37	10	US-09-772-719-6	Sequence 6, Appl
989	5	1.1	38	9	US-09-836-392-30	Sequence 30, Appl
990	5	1.1	38	9	US-10-042-141-167	Sequence 167, App
991	5	1.1	38	10	US-09-726-643-167	Sequence 167, App
992	5	1.1	38	10	US-09-864-761-39173	Sequence 39173, A
993	5	1.1	38	10	US-09-864-761-48776	Sequence 48776, A
994	5	1.1	39	9	US-09-774-639-274	Sequence 274, App
995	5	1.1	39	9	US-09-774-639-351	Sequence 351, App
996	5	1.1	39	10	US-09-864-761-33798	Sequence 33798, A
997	5	1.1	39	10	US-09-864-761-38738	Sequence 38738, A
998	5	1.1	39	10	US-09-864-761-38738	Sequence 38738, A
999	5	1.1	39	10	US-09-864-761-39865	Sequence 39865, A
1000	5	1.1	39	10	US-09-864-761-40246	Sequence 40246, A

ALIGNMENTS

```

1 RESULT 1
2 US-09-754-949-4
3 Sequence 4, Application US/09754949
4 Patent No. US20020015939A1
5 GENERAL INFORMATION:
6 APPLICANT: MCCARTHY, JUSTIN
7 APPLICANT: CORDELL, BARBARA
8 TITLE OF INVENTION: METHODS FOR IDENTIFYING
9 TITLE OF INVENTION: NEURONAL DEGENERATION
10 FILE REFERENCE: SCTOS.012A
11 CURRENT APPLICATION NUMBER: US/09/754,949
12 CURRENT FILING DATE: 2001-01-04
13 NUMBER OF SEQ ID NOS: 16
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 4
16 LENGTH: 467
17 TYPE: PRT
18 ORGANISM: Homo Sapien
19 US-09-754-949-4

```

Query Match	78.4%;	Score 366;	DB 10;	Length 467;
Best Local Similarity	99.8%;	Pred. NO. 0;		
Matches 466; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	MTELPAPLSYQNQMSEDNHLSNTVTSQNDNRERQEHNDRSLSGHEPPLSNRPGQNSR	60
Dp	1	MTELPAPLSYQNQMSEDNHLSNTVTSQNDNRERQEHNDRSLSGHEPPLSNRPGQNSR	60
QY	61	QVEODEDEDEELTLKGAKVIMLEVPVTLQWVVATKSVSFYTRKDGQLIYPTFE	120
Dp	61	QVEODEDEDEELTLKGAKVIMLEVPVTLQWVVATKSVSFYTRKDGQLIYPTFE	120
QY	121	DTFVVGQRAALSIINAALIMISVIVMHTLLVLEKKRYCQYVHAAMLIISSLLFFESFI	180
Dp	121	DTFVVGQRAALSIINAALIMISVIVMHTLLVLEKKRYCQYVHAAMLIISSLLFFESFI	180

Oy	181	YLGEFKYKYNAAVDYITVALLIMLGVGMSTHMKQPLRLOOAYLIMISALMAIYIKY	240
Db	181	YLGEFKYKYNAAVDYITVALLIMLGVGMSTHMKQPLRLOOAYLIMISALMAIYIKY	240
Oy	241	LPENTAMILLIAVISYVDLVAVLCPKQPLRMVLVETAOERNETLPEPALIYSTPMVLVMAE	300
Db	241	LPENTAMILLIAVISYVDLVAVLCPKQPLRMVLVETAOERNETLPEPALIYSTPMVLVMAE	300
Oy	301	GDPEORVRVNSKSYNMAESTPERESODTVAENDOGSEEMEARDSHLGRHSTPESRA	360
Db	301	GDPEORVRVNSKSYNMAESTPERESODTVAENDOGSEEMEARDSHLGRHSTPESRA	360
Oy	361	VOELSSSIIAGEDDEBERGVKLGLDLFIYSVLVGKASATASGDMNTTIACFVALILGLCL	420
Db	361	VOELSSSIIAGEDDEBERGVKLGLDLFIYSVLVGKASATASGDMNTTIACFVALILGLCL	420
Oy	421	TLLIILAIFFKRLPALPISITFGVLVEFYATDYLVOPFMDOLAFHOFTY	467
Db	421	TLLIILAIFFKRLPALPISITFGVLVEFYATDYLVOPFMDOLAFHOFTY	467

```

RESULT 2
US-09-878-454A-3
: Sequence 3, Application US/09878454A
: Patent No. US20020064828A1
: GENERAL INFORMATION:
: APPLICANT: Monteliro, et al.
: TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin
: FILE REFERENCE: 4115-161
: CURRENT APPLICATION NUMBER: US/09/878,454A
: CURRENT FILING DATE: 2001-06-11
: PRIORITY APPLICATION NUMBER: 60/210,939
: PRIORITY FILING DATE: 2000-06-11
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-878-454A-3

```

Query Match	78.48;	Score 366;	DB 10;	Length 467;
Best Local Similarity	99.88;	Pred. No. 0;		
Matches 466;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

QY	1	MTELPLAPLSTYFONAKOSEDNHLSTNTVSQSDNDREROEHNDRSLGHPEPLSLNPGQNSR	60
Db	1	MTELPLAPLSTYONAKOSEDNHLSTNTVSQSDNDREROEHNDRSLGHPEPLSLNPGQNSR	60
QY	61	QVEBODEEDELTLTKYGAKHVIMLFVPTLCAWVVATIKSVFYYRKDGOLITYPTE	120
Db	61	QVEBODEEDELTLTKYGAKHVIMLFVPTLCAWVVATIKSVFYYRKDGOLITYPTE	120
QY	121	DTEFVGORALHSILNAIMTSIVYMTLLVLYKXKRCYKVIHAMLISLLEFFESFL	180
Db	121	DTEFVGORALHSILNAIMTSIVYMTLLVLYKXKRCYKVIHAMLISLLEFFESFL	180
QY	181	YLGEVFETYNVAVDYITVALLIMNLGVYGMISIHMKGPLDQAVYLMISALMALVFIRY	240
Db	181	YLGEVFETYNVAVDYITVALLIMNLGVYGMISIHMKGPLDQAVYLMISALMALVFIRY	240
QY	241	LPEPTAMLLIATIVSYDVLAVLCPKGLRMLVETAQERNTEFLPALIYSTWVLYNMAE	300
Db	241	LPEPTAMLLIATIVSYDVLAVLCPKGLRMLVETAQERNTEFLPALIYSTWVLYNMAE	300
QY	301	GDPAPQRRVSKNSKYNMESERESQDITVAANDDGGSEEMEAQRDHLGHRSTPESRAA	360
Db	301	GDPAPQRRVSKNSKYNMESERESQDITVAANDDGGSEEMEAQRDHLGHRSTPESRAA	360
QY	361	VOELSSSTILAGEDEEBRGVKLIGDPLFTFYSVLGVKKASATSGMNTTICPAVAILLGGLL	420
Db	361	VOELSSSTILAGEDEEBRGVKLIGDPLFTFYSVLGVKKASATSGMNTTICPAVAILLGGLL	420

Oy 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVOPFMDLAHFORYI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVOPFMDLAHFORYI 467

RESULT 3

US-09-895-035-14
; Sequence 14, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:

; APPLICANT: Patterson, Chandra
; APPLICANT: Kaser, Lynn E.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN PRESENTILIN VARIANT
; FILE REFERENCE: PC-0047 CIP
; CURRENT APPLICATION NUMBER: US/09/895,035
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/116,640
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020082211A1 g1709856
US-09-895-035-14

Query Match 78.4%; Score 366; DB 10; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MTELPAPLSYFQNAQMSDNLSTVRSQNDNREROEHNDRLSLGHPPLSNGRPGNSR 60
Db 1 MTELPAPLSYFQNAQMSDNLSTVRSQNDNREROEHNDRLSLGHPPLSNGRPGNSR 60
Oy 61 OVEDEDEDEDELTKYGAHHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120
Db 61 OVEDEDEDEDELTKYGAHHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120
Oy 121 DTEYVGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Db 121 DTEYVGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Oy 181 YLGEVFKTYNNAVADYITVALLIMNIGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
Db 181 YLGEVFKTYNNAVADYITVALLIMNIGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
Oy 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNEITLFPALITYSTVWMLVNAE 300
Db 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNEITLFPALITYSTVWMLVNAE 300
Oy 301 GDPENQRRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRSHLGRHSTPESRAA 360
Db 301 GDPENQRRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRSHLGRHSTPESRAA 360
Oy 361 VOELSSSILAGDPEPERGVKLGIDFIFYSVLVGKASATASGDWMTTACFVAAILIGLCL 420
Db 361 VOELSSSILAGDPEPERGVKLGIDFIFYSVLVGKASATASGDWMTTACFVAAILIGLCL 420
Oy 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVOPFMDLAHFORYI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVOPFMDLAHFORYI 467

RESULT 4

US-10-071-900-1
; Sequence 1, Application US/10071900
; Patent No. US20020127341A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.

; APPLICANT: Rommens, Johanna
; APPLICANT: Fraser, Paul E.
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; FILE REFERENCE: 1034/1F810-US1
; CURRENT APPLICATION NUMBER: US/10/071,900
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/727,725
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-071-900-1

Query Match 78.4%; Score 366; DB 12; Length 467;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MTELPAPLSYFQNAQMSDNLSTVRSQNDNREROEHNDRLSLGHPPLSNGRPGNSR 60
Db 1 MTELPAPLSYFQNAQMSDNLSTVRSQNDNREROEHNDRLSLGHPPLSNGRPGNSR 60
Oy 61 OVEDEDEDEDELTKYGAHHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120
Db 61 OVEDEDEDEDELTKYGAHHVIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPTPE 120
Oy 121 DTEYVGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Db 121 DTEYVGOALHSILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Oy 181 YLGEVFKTYNNAVADYITVALLIMNIGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
Db 181 YLGEVFKTYNNAVADYITVALLIMNIGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
Oy 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNEITLFPALITYSTVWMLVNAE 300
Db 241 LPEWTAMILLAVISYVDLVAVLCPRGLRMVETAOERNEITLFPALITYSTVWMLVNAE 300
Oy 301 GDPENQRRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRSHLGRHSTPESRAA 360
Db 301 GDPENQRRVSKSKYNAESTERESODTVAENDDGFSEEMEAQRSHLGRHSTPESRAA 360
Oy 361 VOELSSSILAGDPEPERGVKLGIDFIFYSVLVGKASATASGDWMTTACFVAAILIGLCL 420
Db 361 VOELSSSILAGDPEPERGVKLGIDFIFYSVLVGKASATASGDWMTTACFVAAILIGLCL 420
Oy 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVOPFMDLAHFORYI 467
Db 421 TLLLLAIFKKALPALPISITFGLVFAYFDYLVOPFMDLAHFORYI 467

RESULT 5

US-09-895-035-12
; Sequence 12, Application US/09895035
; Patent No. US20020082211A1
; GENERAL INFORMATION:

; APPLICANT: Patterson, Chandra
; APPLICANT: Kaser, Lynn E.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN PRESENTILIN VARIANT
; FILE REFERENCE: PC-0047 CIP
; CURRENT APPLICATION NUMBER: US/09/895,035
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/116,640
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 463
; TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incycle ID No. US20020082211A1 g1244638
US-09-895-035-12

Query Match 72.2% Score 337; DB 10; Length 463;
Best Local Similarity 99.8%; Pred. No. 2e-304;
Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

30 NDNREORHNRRLSGHPEPLSNRPGNSROYVODEDEDELTKGAKHVMLEFPV 89
26 NDNREORHNRRLSGHPEPLSNRPGNSROYVODEDEDELTKGAKHVMLEFPV 85
90 TLCAVVAVATIKSVSFYTRKDGOLITPTEDTETVGORALHSILNAIMISVIMTIL 149
86 TLCAVVAVATIKSVSFYTRKDGOLITPTEDTETVGORALHSILNAIMISVIMTIL 145
150 LVLYKRYCYVIAHMLIISLLIFPFSFIYLGVEFKYVNAVDTITVALLINMGVYG 209
146 LVLYKRYCYVIAHMLIISLLIFPFSFIYLGVEFKYVNAVDTITVALLINMGVYG 205
210 MISIHWKPELRLQOAYLIMISALMALVFIKYLEPWTAMLLAVISYDVLAVLCPKGLR 269
206 MISIHWKPELRLQOAYLIMISALMALVFIKYLEPWTAMLLAVISYDVLAVLCPKGLR 265
270 MLVETAOENETLFPALISSTMWLVNMAEGDEPAORVSKNSKYNAESTERESODTVA 329
266 MLVETAOENETLFPALISSTMWLVNMAEGDEPAORVSKNSKYNAESTERESODTVA 325
330 ENDDGGSEEDPAORSHLGHPRSTPESRAAVOELSSSILAGEDPERGVKLGJDFIFY 389
326 ENDDGGSEEDPAORSHLGHPRSTPESRAAVOELSSSILAGEDPERGVKLGJDFIFY 385
390 SVLVGKASATASGDMNTTACFVAITLIGLCTLLLLATFEKALPLPISITFGVLEFYAT 449
386 SVLVGKASATASGDMNTTACFVAITLIGLCTLLLLATFEKALPLPISITFGVLEFYAT 445
450 DYLVOPFMDQLAFHQFYI 467
446 DYLVOPFMDQLAFHQFYI 463

RESULT 6
US-09-785-474-2
Sequence 2, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-785-474-2

Query Match 56.7% Score 265; DB 10; Length 467;
Best Local Similarity 99.6%; Pred. No. 1e-237;
Matches 465; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 MTELPAPLSYFQNMQMSDNHLSNTRSQNDNRREORHNRRLSGHPEPLSNRPGNSR 60
1 MTELPAPLSYFQNMQMSDNHLSNTRSQNDNRREORHNRRLSGHPEPLSNRPGNSR 60
61 QVDEDEDEDELTKYAKHVMLEFPVTLCAVVAVATIKSVSFYTRKDGOLITPTTE 120
61 QVDEDEDEDELTKYAKHVMLEFPVTLCAVVAVATIKSVSFYTRKDGOLITPTTE 120
121 DTEVVGORALHSILNAIMISVIVMTLLVLYKRYCYVIAHMLIISLLIFPFSFI 180
121 DTEVVGORALHSILNAIMISVIVMTLLVLYKRYCYVIAHMLIISLLIFPFSFI 180
181 YLGEVFKYVNAVDTITVALLINMGVGMISHWKPELRLQOAYLIMISALMALVFIKY 240
181 YLGEVFKYVNAVDTITVALLINMGVGMISHWKPELRLQOAYLIMISALMALVFIKY 240
241 LPEWTAMLLAVISYDVLAVLCPKGLRMLVETAOENETLFPALISSTMWLVNMAE 300
241 LPEWTAMLLAVISYDVLAVLCPKGLRMLVETAOENETLFPALISSTMWLVNMAE 300
301 GDPEAORVSKNSKYNAESTERESODTVAENDDGGFSEEDPAORSHLGHPRSTPESRAA 360
301 GDPEAORVSKNSKYNAESTERESODTVAENDDGGFSEEDPAORSHLGHPRSTPESRAA 360
361 VOELSSSILAGEDPERGVKLGJDFIFYSVLVGKASATASGDMNTTACFVAITLIGLCT 420
361 VOELSSSILAGEDPERGVKLGJDFIFYSVLVGKASATASGDMNTTACFVAITLIGLCT 420
421 TLLLLATFEKALPALPISITFGVLEFYATDYLVOPFMDQLAFHQFYI 467
421 TLLLLATFEKALPALPISITFGVLEFYATDYLVOPFMDQLAFHQFYI 467

RESULT 7
US-09-785-474-4
Sequence 4, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-785-474-4

Query Match 43.7%; Score 204; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTELPAFLSYFONAMSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAFLSYFONAMSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPPLSNGRPOGNSR 60
OY 61 QVVEDEDEDEELTLKYGAKHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPFT 120
DB 61 QVVEDEDEDEELTLKYGAKHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPFT 120
OY 121 DTEVGOALHSILNAAMISIVVMTILVLYKRCYKVIHAWLIISLLFFFSFI 180
DB 121 DTEVGOALHSILNAAMISIVVMTILVLYKRCYKVIHAWLIISLLFFFSFI 180
OY 181 YLGEVFKTYNAVADYITVALLIWN 204
DB 181 YLGEVFKTYNAVADYITVALLIWN 204

RESULT 8
US-09-785-474-28

; Sequence 28, Application US/09785474
; Patent No. US20010012626A1
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; MASCO, WILMA
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/785,474

FILING DATE: 20-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-785-474-28

Query Match 43.7%; Score 204; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTELPAFLSYFONAMSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPPLSNGRPOGNSR 60
DB 1 MTELPAFLSYFONAMSEDNHLSNTVRSQNDNRERQEHNDRLSLGHPPLSNGRPOGNSR 60
OY 61 QVVEDEDEDEELTLKYGAKHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPFT 120
DB 61 QVVEDEDEDEELTLKYGAKHYIMLFVPTLCMVVAVATIKSVSYTRKDGOLITPFT 120
OY 121 DTEVGOALHSILNAAMISIVVMTILVLYKRCYKVIHAWLIISLLFFFSFI 180
DB 121 DTEVGOALHSILNAAMISIVVMTILVLYKRCYKVIHAWLIISLLFFFSFI 180
OY 181 YLGEVFKTYNAVADYITVALLIWN 204
DB 181 YLGEVFKTYNAVADYITVALLIWN 204

RESULT 9

US-09-785-474-30
; Sequence 30, Application US/09785474
; Patent No. US20010012626A1
; GENERAL INFORMATION:
; APPLICANT: TANZI, RUDOLPH
; MASCO, WILMA
; TITLE OF INVENTION: Genetic Alterations Related To Familial
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/785,474
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/706,344
; FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-785-474-30

Query Match 43.7%; Score 204; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYQNAQMSDNLSTNRQNDNRQEHNDRLSLGHPPLSGRPGNSR 60
|||||
DB 1 MTELPAPLSTYQNAQMSDNLSTNRQNDNRQEHNDRLSLGHPPLSGRPGNSR 60
QY 61 QVEODEEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSYTRKDGQIITPTE 120
|||||
DB 61 QVEODEEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSYTRKDGQIITPTE 120
QY 121 DTEYVQGRALSHILNAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
|||||
DB 121 DTEYVQGRALSHILNAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIWN 204
|||||
DB 181 YLGEVFKTYNVAVDYITVALLIWN 204

RESULT 10

US-09-785-474-32
Sequence 32, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
MASCOT, WILLIAM
TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-785-474-32

Query Match 43.7%; Score 204; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYQNAQMSDNLSTNRQNDNRQEHNDRLSLGHPPLSGRPGNSR 60
|||||
DB 1 MTELPAPLSTYQNAQMSDNLSTNRQNDNRQEHNDRLSLGHPPLSGRPGNSR 60
QY 61 QVEODEEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSYTRKDGQIITPTE 120
|||||
DB 61 QVEODEEDELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSYTRKDGQIITPTE 120
QY 121 DTEYVQGRALSHILNAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
|||||
DB 121 DTEYVQGRALSHILNAIMISIVYVMTLLVLYKRCYKVIHAWLIISLLLEFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIWN 204
|||||
DB 181 YLGEVFKTYNVAVDYITVALLIWN 204

RESULT 11

US-09-895-035-1
Sequence 1, Application US/09895035
Patent No. US2002008221A1
GENERAL INFORMATION:
APPLICANT: Patterson, Chandra
Murry, Lynn E.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
FILE REFERENCE: PC-0047 CIP
CURRENT APPLICATION NUMBER: US/09/895,035
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/116,640
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US2002008221A1 1353337CD1
US-09-895-035-1

Query Match 28.3%; Score 132; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.6e-115;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 NDNREQRHNDRLSLGHPPLSGRPGNSRQVVEODEEDELTLKYGAKHYIMLFVPTV 89
|||||
DB 26 NDNREQRHNDRLSLGHPPLSGRPGNSRQVVEODEEDELTLKYGAKHYIMLFVPTV 85
QY 90 TLMVNVVAATIKSVSYTRKDGQIITPTEDETVGGRALSHILNAIMISIVYVMTLL 149
|||||
DB 86 TLMVNVVAATIKSVSYTRKDGQIITPTEDETVGGRALSHILNAIMISIVYVMTLL 145
QY 150 LVVLYKRCYKVI 161
|||||

Db 146 LVLYKRYCKYV 157

RESULT 12

US-09-823-153-8

Sequence 8, Application US/09823153

Patent No. US20020025540A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Roberts, Susan

APPLICANT: Pak, Roger

APPLICANT: Lewis, Martin

APPLICANT: Smith, David

APPLICANT: Hendrick, Joseph

APPLICANT: Vinitzky, Alexander

TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX

TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF

FILE REFERENCE: D0004

CURRENT APPLICATION NUMBER: US/09/823,153

CURRENT FILING DATE: 2001-07-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 354

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Description of Artificial Sequence: PSI PEPTIDE

US-09-823-153-8

Query Match 27.4%; Score 128; DB 10; Length 354;

Best Local Similarity 100.0%; Pred. NO. 7.3e-111;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 LFPALVYSTWVLYNNAEGPEAQRVSKNSKYNAESTERESODTVAENDDGFSSEME 341

Db 227 LFPALVYSTWVLYNNAEGPEAQRVSKNSKYNAESTERESODTVAENDDGFSSEME 286

QY 342 AQRSHLGPHTSPESRAAVLESSLAGDPDERGVKLGDFIFSVLVKASATAS 401

Db 287 AQRSHLGPHTSPESRAAVLESSLAGDPDERGVKLGDFIFSVLVKASATAS 346

QY 402 GDMNTTIA 409

Db 347 GDMNTTIA 354

RESULT 13

US-09-864-761-38056

Sequence 38056, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 38056

LENGTH: 65

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AF109907.1

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2

OTHER INFORMATION: SWISSPROT HIT: P97887, EVALU8.00e-12

OTHER INFORMATION: EST_HUMAN HIT: BE935454.1, EVALU8.1.00e-18

US-09-864-761-38056

Query Match 10.3%; Score 48; DB 10; Length 65;

Best Local Similarity 100.0%; Pred. NO. 2e-37;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 IYPTFEDTETVGGRAHLSILNAAIMISVIVMTLLVLYKRYCKYV 161

Db 1 IYPTFEDTETVGGRAHLSILNAAIMISVIVMTLLVLYKRYCKYV 48

RESULT 14

US-09-925-299-1227

Sequence 1227, Application US/09925299

Patent No. US2002005627A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1227

```

: LENGTH: 101
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (32)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1227

Query Match
Best Local Similarity 100.0%; Pred. No. 1,6e-33; Length 101;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 NETLEPALIYSTWVWLVNMAEGDEAQRVSKSKYNAESTER 322
|||||
Db 33 NETLEPALIYSTWVWLVNMAEGDEAQRVSKSKYNAESTER 76

RESULT 15
US-10-051-767-10
: Sequence 10, Application US/10051767
: Publication No. US20030022151A1
: GENERAL INFORMATION:
: APPLICANT: THINAKARAN, GOPAL
: TITLE OF INVENTION: FUNCTIONAL SCREENING
: FILE REFERENCE: ARCD:364US
: CURRENT APPLICATION NUMBER: US/10/051,767
: CURRENT FILING DATE: 2002-01-17
: PRIOR APPLICATION NUMBER: 60/262,353
: PRIOR FILING DATE: 2001-01-17
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 131
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-10-051-767-10

Query Match
Best Local Similarity 100.0%; Pred. No. 1,3e-18; Length 131;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 280
|||||
Db 10 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 37

RESULT 16
US-09-754-949-6
: Sequence 6, Application US/09754949
: Patent No. US20020015939A1
: GENERAL INFORMATION:
: APPLICANT: MCCARTHY, JUSTIN
: APPLICANT: CORDELL, BARBARA
: TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
: TITLE OF INVENTION: NEURONAL DEGENERATION
: FILE REFERENCE: SCIOS 012A
: CURRENT APPLICATION NUMBER: US/09/754,949
: CURRENT FILING DATE: 2001-01-04
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 448
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-754-949-6

Query Match
Best Local Similarity 100.0%; Pred. No. 4,2e-18; Length 448;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 253 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 280
|||||
Db 259 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 286

RESULT 17
US-09-878-454A-1
: Sequence 1, Application US/09878454A
: Patent No. US20020064828A1
: GENERAL INFORMATION:
: APPLICANT: Montelito, et al.
: TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin
: FILE REFERENCE: 4115-161
: CURRENT APPLICATION NUMBER: US/09/878,454A
: CURRENT FILING DATE: 2001-06-11
: PRIOR APPLICATION NUMBER: 60/210,939
: PRIOR FILING DATE: 2000-06-11
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 448
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-878-454A-1

Query Match
Best Local Similarity 100.0%; Pred. No. 4,2e-18; Length 448;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 280
|||||
Db 259 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 286

RESULT 18
US-10-071-900-2
: Sequence 2, Application US/10071900
: Patent No. US20020127541A1
: GENERAL INFORMATION:
: APPLICANT: St. George-Hyslop, Peter H.
: APPLICANT: Rommens, Johanna
: APPLICANT: Fraser, Paul E.
: TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
: TITLE OF INVENTION: of Use
: FILE REFERENCE: 1034/1P810-US1
: CURRENT APPLICATION NUMBER: US/10/071,900
: CURRENT FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: US/09/227,725
: PRIOR FILING DATE: 1999-01-08
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 448
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-071-900-2

Query Match
Best Local Similarity 100.0%; Pred. No. 4,2e-18; Length 448;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 280
|||||
Db 259 ISVYDLVAVLCPPKGPLRLMLVETAQERNE 286

RESULT 19
US-10-051-767-9
: Sequence 9, Application US/10051767
: Publication No. US20030022151A1
: GENERAL INFORMATION:
: APPLICANT: THINAKARAN, GOPAL
```

;; TITLE OF INVENTION: FUNCTIONAL SCREENING
;; FILE REFERENCE: ARCD:364US
;; CURRENT APPLICATION NUMBER: US/10/051,767
;; CURRENT FILING DATE: 2002-01-17
;; PRIOR APPLICATION NUMBER: 60/262,353
;; PRIOR FILING DATE: 2001-01-17
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 9
;; LENGTH: 74
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-051-767-9

Query Match 4.7%; Score 22; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 EERGVKLGIDFIYSVLVGKA 396
Db 52 EERGVKLGIDFIYSVLVGKA 73

RESULT 20
US-10-051-767-15
;; Sequence 15, Application US/10051767
;; Publication No. US20030022151A1
;; GENERAL INFORMATION:
;; APPLICANT: THINAKARAN, GOPAL
;; TITLE OF INVENTION: FUNCTIONAL SCREENING
;; FILE REFERENCE: ARCD:364US
;; CURRENT APPLICATION NUMBER: US/10/051,767
;; CURRENT FILING DATE: 2002-01-17
;; PRIOR APPLICATION NUMBER: 60/262,353
;; PRIOR FILING DATE: 2001-01-17
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 15
;; LENGTH: 74
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-051-767-15

Query Match 4.7%; Score 22; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 EERGVKLGIDFIYSVLVGKA 396
Db 52 EERGVKLGIDFIYSVLVGKA 73

RESULT 21
US-10-051-767-11
;; Sequence 11, Application US/10051767
;; Publication No. US20030022151A1
;; GENERAL INFORMATION:
;; APPLICANT: THINAKARAN, GOPAL
;; TITLE OF INVENTION: FUNCTIONAL SCREENING
;; FILE REFERENCE: ARCD:364US
;; CURRENT APPLICATION NUMBER: US/10/051,767
;; CURRENT FILING DATE: 2002-01-17
;; PRIOR APPLICATION NUMBER: 60/262,353
;; PRIOR FILING DATE: 2001-01-17
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 11

;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-051-767-11

Query Match 4.7%; Score 22; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 EERGVKLGIDFIYSVLVGKA 396
Db 105 EERGVKLGIDFIYSVLVGKA 126

RESULT 22
US-10-051-767-7
;; Sequence 7, Application US/10051767
;; Publication No. US20030022151A1
;; GENERAL INFORMATION:
;; APPLICANT: THINAKARAN, GOPAL
;; TITLE OF INVENTION: FUNCTIONAL SCREENING
;; FILE REFERENCE: ARCD:364US
;; CURRENT APPLICATION NUMBER: US/10/051,767
;; CURRENT FILING DATE: 2002-01-17
;; PRIOR APPLICATION NUMBER: 60/262,353
;; PRIOR FILING DATE: 2001-01-17
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 166
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-051-767-7

Query Match 3.9%; Score 18; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 EERGVKLGIDFIYSVL 392
Db 142 EERGVKLGIDFIYSVL 159

RESULT 23
US-10-051-767-13
;; Sequence 13, Application US/10051767
;; Publication No. US20030022151A1
;; GENERAL INFORMATION:
;; APPLICANT: THINAKARAN, GOPAL
;; TITLE OF INVENTION: FUNCTIONAL SCREENING
;; FILE REFERENCE: ARCD:364US
;; CURRENT APPLICATION NUMBER: US/10/051,767
;; CURRENT FILING DATE: 2002-01-17
;; PRIOR APPLICATION NUMBER: 60/262,353
;; PRIOR FILING DATE: 2001-01-17
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 13
;; LENGTH: 166
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-051-767-13

Query Match 3.9%; Score 18; DB 9; Length 166;

Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 375 EERGKVLGLGDFIFYSVL 392
|||||
Db 142 EERGKVLGLGDFIFYSVL 159

RESULT 24

US-10-051-767-12
; Sequence 12, Application US/10051767
; Publication No. US20030022151A1
; GENERAL INFORMATION:
; APPLICANT: THINAKARAN, GOPAL
; TITLE OF INVENTION: FUNCTIONAL SCREENING
; FILE REFERENCE: ARCD:364US
; CURRENT APPLICATION NUMBER: US/10/051,767
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/262,353
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-051-767-12

Query Match 3.9%; Score 18; DB 9; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 380 KLGLGDFIFYSVLGKAS 397
|||||
Db 191 KLGLGDFIFYSVLGKAS 208

RESULT 25

US-09-823-153-6
; Sequence 6, Application US/09823153
; Patent No. US20020025540A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitsky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: PSI PEPTIDE
US-09-823-153-6

Query Match 3.4%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 GHPEPLSNGRPGNSR 60

Db 2 GHPEPLSNGRPGNSR 17
|||||

RESULT 26

US-09-823-153-9
; Sequence 9, Application US/09823153
; Patent No. US20020025540A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitsky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPL
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: PSI PEPTIDE
US-09-823-153-9

Query Match 3.2%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 344 RDSHLGPHRSTPESR 358
|||||
Db 1 RDSHLGPHRSTPESR 15

RESULT 27

US-09-823-153-5
; Sequence 5, Application US/09823153
; Patent No. US20020025540A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitsky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPL
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: PSI PEPTIDE
US-09-823-153-5

Query Match 3.2%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 RDSHLGPHRSTPEPR 358
|||||
DB 2 RDSHLGPHRSTPEPR 16

RESULT 28

US-09-795-903A-9
; Sequence 9, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-903A-9

Query Match

Best Local Similarity 100.0%; Score 8; DB 9; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 LVNMAEGD 302
|||||

DB 1 LVNMAEGD 8

RESULT 29

US-09-796-264-9
; Sequence 9, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-796-264-9

Query Match 1.7%; Score 8; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 LVNMAEGD 302
|||||

DB 1 LVNMAEGD 8

RESULT 30

US-09-845-226-9
; Sequence 9, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Chosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-226-9

Query Match

Best Local Similarity 100.0%; Score 8; DB 10; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 LVNMAEGD 302
|||||

DB 1 LVNMAEGD 8

RESULT 31

US-09-982-172-103
; Sequence 103, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBIO
; TITLE OF INVENTION: DIRECTED THEREGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 103
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-103

Query Match 1.7%; Score 8; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLALLAI 427
| | | | |
Db 25 LTLALLAI 32

RESULT 32.
US-09-982-172-227

Sequence 227, Application US/09982172

Patent No. US20020137119A1

GENERAL INFORMATION:

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE

TITLE OF INVENTION: DIRECTED THEREGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT

TITLE OF INVENTION: UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982.172

PRIOR FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PatentIn version 3.1

SEQ ID NO 227

LENGTH: 45

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-227

Query Match 1.7%; Score 8; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLALLAI 427
| | | | |
Db 25 LTLALLAI 32

RESULT 33

US-10-004-717-7

Sequence 7, Application US/10004717

Publication No. US2002019265A1

GENERAL INFORMATION:

APPLICANT: ZOGHBI, HUDA Y.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN

TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

FILE REFERENCE: P01899US4

CURRENT APPLICATION NUMBER: US/10/004.717

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 09/585,645

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 263

TYPE: PRT

ORGANISM: Mus musculus

US-10-004-717-7

Query Match 1.7%; Score 8; DB 9; Length 263;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEDEL 73
| | | | |

Db 38 DEEDEDEL 45

RESULT 34

US-10-004-717-31

Sequence 31, Application US/10004717

Publication No. US2002019265A1

GENERAL INFORMATION:

APPLICANT: ZOGHBI, HUDA Y.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN

TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

FILE REFERENCE: P01899US4

CURRENT APPLICATION NUMBER: US/10/004.717

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 09/585,645

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 31

LENGTH: 263

TYPE: PRT

ORGANISM: Mus musculus

US-10-004-717-31

Query Match 1.7%; Score 8; DB 9; Length 263;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEDEL 73
| | | | |
Db 38 DEEDEDEL 45

RESULT 35

US-10-004-717-38

Sequence 38, Application US/10004717

Publication No. US2002019265A1

GENERAL INFORMATION:

APPLICANT: ZOGHBI, HUDA Y.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN

TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

FILE REFERENCE: P01899US4

CURRENT APPLICATION NUMBER: US/10/004.717

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 09/585,645

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 38

LENGTH: 263

TYPE: PRT

ORGANISM: Mus musculus

US-10-004-717-38

Query Match 1.7%; Score 8; DB 9; Length 263;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEDEL 73
| | | | |
Db 38 DEEDEDEL 45

RESULT 36
US-09-769-097-2
; Sequence 2, Application US/09769097
; Patent No. US20020055128A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harma Ellens
; APPLICANT: John Anthony Feld
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: GP-50009-C2
; CURRENT APPLICATION NUMBER: US/09/769,097
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/208,809
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 09/156,800
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US99/20770
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1272
; TYPE: PRT
; ORGANISM: RATTUS RATTUS
US-09-769-097-2

Query Match 1.7%: Score 8; DB 10; Length 1272;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 420 LTLALLAI 427
|||||
Db 849 LTLALLAI 856

RESULT 37
US-09-769-097-4
; Sequence 4, Application US/09769097
; Patent No. US20020055128A1
; GENERAL INFORMATION:
; APPLICANT: Kimberly Anne Brun
; APPLICANT: Richard James Chenery
; APPLICANT: Harma Ellens
; APPLICANT: John Anthony Feld
; APPLICANT: Lin Yue
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: GP-50009-C2
; CURRENT APPLICATION NUMBER: US/09/769,097
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/208,809
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 09/156,800
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US99/20770
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1272
; TYPE: PRT
; ORGANISM: RATTUS RATTUS
US-09-769-097-4

Query Match 1.7%: Score 8; DB 10; Length 1272;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTLALLAI 427
|||||
Db 849 LTLALLAI 856

RESULT 38
US-09-866-866A-8
; Sequence 8, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1276
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-866-866A-8

Query Match 1.7%: Score 8; DB 10; Length 1276;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 420 LTLALLAI 427
|||||
Db 853 LTLALLAI 860

RESULT 39
US-10-072-621-7
; Sequence 7, Application US/10072621
; Patent No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Connop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-621-7

Query Match 1.7%: Score 8; DB 9; Length 1280;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTLALLAI 427
|||||
Db 857 LTLALLAI 864

RESULT 40
US-10-044-671-2
; Sequence 2, Application US/10044671
; Patent No. US20020177147A1

```

; GENERAL INFORMATION:
; APPLICANT: Washington State University Research Foundation
; APPLICANT: Maaley, Katrina
; APPLICANT: Bentjen, Steven
; TITLE OF INVENTION: MDRI VARIANTS AND METHODS FOR THEIR USE
; FILE REFERENCE: 4630-61733
; CURRENT APPLICATION NUMBER: US/10/044,671
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/261,578
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/314,829
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-044-671-2
```

```

Query Match          1.7%; Score 8; DB 9; Length 1280;
Best Local Similarity 100.0%; Pred. No. 39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      420 LTLILLAI 427
        |||||||
Db       858 LTLILLAI 865
```

RESULT 41

```

US-09-866-866A-2
; Sequence 2, Application US/098668666A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Schuetz, John
; APPLICANT: Sorrentino, Brian
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,588
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-866A-2
```

```

Query Match          1.7%; Score 8; DB 10; Length 1280;
Best Local Similarity 100.0%; Pred. No. 39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      420 LTLILLAI 427
        |||||||
Db       857 LTLILLAI 864
```

RESULT 42

```

US-09-866-866A-4
; Sequence 4, Application US/098668666A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
```

```

; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-866A-4
```

```

Query Match          1.7%; Score 8; DB 10; Length 1280;
Best Local Similarity 100.0%; Pred. No. 39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      420 LTLILLAI 427
        |||||||
Db       857 LTLILLAI 864
```

RESULT 43

```

US-09-795-903A-6
; Sequence 6, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xianli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-795-903A-6
```

```

Query Match          1.5%; Score 7; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 11e+05;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      296 VNNAECD 302
        |||||||
Db       2 VNNAECD 8
```

RESULT 44

```

US-09-796-264-6
; Sequence 6, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
```


APPLICANT: Lin, Xinli
APPLICANT: Koelsch, Gerald
TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
TITLE OF INVENTION: of Use Thereof
FILE REFERENCE: OMRF 179
CURRENT APPLICATION NUMBER: US/09/796,264
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/604,608
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-796-264-6

Query Match 1.5%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 VNMAGSD 302
DB 2 VNMAGSD 8

RESULT 45
US-09-845-226-6
Sequence 6, Application US/09845226
Patent No. US20020115600A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Hong, Lin
APPLICANT: Chosh, Arun K.
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: OMRF 182
CURRENT APPLICATION NUMBER: US/09/845,226
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 09/603,713
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-845-226-6

Query Match 1.5%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 VNMAGSD 302
DB 2 VNMAGSD 8

RESULT 46
US-09-864-761-38169
Sequence 38169, Application US/09864761
Patent No. US20020048765A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38169
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050342.36
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
US-09-864-761-38169

Query Match 1.5%; Score 7; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 LLLPFF 177

DB 9 LLLLLFF 15

RESULT 47

US-09-864-761-38937

; Sequence 38937, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aecmca-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263,6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 38937

; LENGTH: 55

; TYPE: PRT

; ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC005848.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: EST_HUMAN HIT: BE018257.1, EVALUATE 9.00e-21

US-09-864-761-38937

Query Match 1.5%; Score 7; DB 10; Length 55;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEE 72

DB 48 DEEDEE 54

RESULT 48

US-09-764-869-1215

; Sequence 1215, Application US/09764869

; Patent No. US20020061521A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC007

; CURRENT APPLICATION NUMBER: US/09/764,869

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 2442

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1215

; LENGTH: 58

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (18)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-869-1215

Query Match 1.5%; Score 7; DB 10; Length 58;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 ISSLLL 174

DB 22 ISSLLL 28

RESULT 49

US-09-814-122-39

; Sequence 39, Application US/09814122

; Patent No. US20020058307A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen et al.

; TITLE OF INVENTION: 20 Human Secreted Proteins

; FILE REFERENCE: P2005P1

; CURRENT APPLICATION NUMBER: US/09/814,122

; CURRENT FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: US/09/166,780

; PRIOR FILING DATE: 1998-10-06

; PRIOR APPLICATION NUMBER: PCT/US98/06801

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: 60/042,726

; PRIOR FILING DATE: 1997-04-08

; PRIOR APPLICATION NUMBER: 60/042,727

; PRIOR FILING DATE: 1997-04-08

; PRIOR APPLICATION NUMBER: 60/042,728

; PRIOR FILING DATE: 1997-04-08

; PRIOR APPLICATION NUMBER: 60/042,754

; PRIOR FILING DATE: 1997-04-08

; PRIOR APPLICATION NUMBER: 60/042,825

; PRIOR FILING DATE: 1997-04-08

; PRIOR APPLICATION NUMBER: 60/048,068

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,070

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,184

; PRIOR FILING DATE: 1997-05-30

; NUMBER OF SEQ ID NOS: 86

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-814-122-39

Query Match      1.5%; Score 7; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 ISSLLL 174
DB 5 ISSLLL 11

RESULT 50
US-09-864-761-47359
; Sequence 47359, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemlica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
```

```
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47359
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005045.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P21439, EVALUATE 2.00e-27
US-09-864-761-47359

Query Match      1.5%; Score 7; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTLALLA 426
DB 30 LTLALLA 36
```

Search completed: February 6, 2003, 14:27:21
Job time : 41.4398 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 14:17:31 ; Search time 28.0975 Seconds
(without alignments)
1597.820 Million cell updates/sec

Title: US-09-689-159a-2

Perfect score: 467

Sequence: 1 MTELPAPLSTYFQNMQSEDN.....ATDYLVPFQMDLAFHQFYI 467

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	366	78.4	467	2	S58396
2	327	72.2	463	2	S63683
3	188	40.3	374	2	S63684
4	107	22.9	463	2	JC5081
5	107	22.9	467	2	JC5080
6	97	20.8	467	2	I78388
7	59	12.6	433	2	JC5390
8	28	6.0	442	2	I39174
9	28	6.0	448	2	A56993
10	27	5.8	449	2	JC5391
11	18	3.9	461	2	S60253
12	18	3.9	836	2	E89453
13	15	3.2	397	2	A84702
14	15	3.2	453	2	T00724
15	9	1.9	334	2	G90492
16	8	1.7	103	2	H65055
17	8	1.7	103	2	B91079
18	8	1.7	103	2	C85924
19	8	1.7	176	2	A49304
20	8	1.7	314	2	JC7335
21	8	1.7	317	2	AF0205
22	8	1.7	347	2	H75253
23	8	1.7	354	2	T39599
24	8	1.7	392	2	A84564
25	8	1.7	581	2	A97119
26	8	1.7	707	2	A42322
27	8	1.7	1022	2	I53078
28	8	1.7	1104	1	DVMS1A
29	8	1.7	1276	1	DVHY1C

30	8	1.7	1276	2	A34786	multidrug resistan
31	8	1.7	1280	1	DVHU1	multidrug resistan
32	8	1.7	1613	2	S39059	protein Bnc1 - hum
33	8	1.7	1726	2	A39401	metoizole surface
34	7	1.5	49	2	A56388	dopamine- and camp
35	7	1.5	65	2	S59962	antimicrobial pept
36	7	1.5	66	1	A53744	ranalexin precursor
37	7	1.5	72	1	LMHWA3	H+-transporting tw
38	7	1.5	78	2	C71978	hypothetical prote
39	7	1.5	85	2	B47354	ygdr protein - sal
40	7	1.5	86	2	C71549	hypothetical prote
41	7	1.5	103	2	AF0856	conserved hypothet
42	7	1.5	104	2	C83236	hypothetical prote
43	7	1.5	107	2	H72575	hypothetical prote
44	7	1.5	108	2	D72617	hypothetical prote
45	7	1.5	109	2	B72763	hypothetical prote
46	7	1.5	117	2	S31130	hypothetical prote
47	7	1.5	121	2	S61635	ribosomal protein
48	7	1.5	125	2	E97486	hypothetical prote
49	7	1.5	125	2	A82704	two component resp
50	7	1.5	131	2	D87491	hypothetical prote
51	7	1.5	137	2	A97989	hypothetical prote
52	7	1.5	167	2	B71518	probable signal pe
53	7	1.5	168	2	T03168	hypothetical prote
54	7	1.5	169	2	S56281	probable membrane
55	7	1.5	169	2	H72611	hypothetical prote
56	7	1.5	170	2	A64316	hypothetical prote
57	7	1.5	173	1	S22538	oleosin, 18.5K - A
58	7	1.5	175	2	S70915	major oleosin nap-
59	7	1.5	176	2	A83847	cytochrome c bioge
60	7	1.5	183	2	S25089	oleosin Bn-V - rap
61	7	1.5	184	2	T00431	hypothetical prote
62	7	1.5	188	2	T29936	hypothetical prote
63	7	1.5	194	2	F72782	hypothetical prote
64	7	1.5	208	2	P00278	hypothetical prote
65	7	1.5	210	2	S62355	high mobility grou
66	7	1.5	210	2	G83929	hypothetical prote
67	7	1.5	211	2	H90046	hypothetical prote
68	7	1.5	213	1	S19158	ubiquitin-protein
69	7	1.5	218	2	AC1253	glycine betaine/ca
70	7	1.5	218	2	A11615	membrane protein M
71	7	1.5	226	2	D49591	membrane glycoprot
72	7	1.5	226	2	S37434	probable ABC-type
73	7	1.5	226	2	PC6047	antiquitin - rat (
74	7	1.5	228	2	B54676	hypophosphatase C (E
75	7	1.5	239	2	S68257	hypothetical prote
76	7	1.5	243	2	S76271	hypothetical prote
77	7	1.5	243	2	T46461	unknown protein (I
78	7	1.5	252	2	C96556	hypothetical prote
79	7	1.5	252	2	B84609	hypothetical prote
80	7	1.5	259	2	G75186	hypothetical prote
81	7	1.5	262	2	B83827	hypothetical prote
82	7	1.5	265	2	T15486	conserved hypothet
83	7	1.5	271	2	H72261	hypothetical prote
84	7	1.5	274	2	T25404	conserved hypothet
85	7	1.5	280	2	A48921	conserved hypothet
86	7	1.5	286	2	A34599	DNA-binding protel
87	7	1.5	291	2	E82258	cell division prot
88	7	1.5	296	2	G64877	peptide transport
89	7	1.5	296	2	E90862	hypothetical prote
90	7	1.5	296	2	D85756	hypothetical prote
91	7	1.5	299	2	D84519	probable endoxylg
92	7	1.5	317	2	B98208	probable uspa prot
93	7	1.5	317	2	AG3078	hypothetical prote
94	7	1.5	318	2	T11260	NADH2 dehydrogenas
95	7	1.5	323	2	A70029	hypothetical prote
96	7	1.5	323	2	JC2578	DNA repair protein
97	7	1.5	326	2	S77304	beta transducin-ii
98	7	1.5	327	2	F87541	hypothetical prote
99	7	1.5	330	2	A86355	hypothetical prote
100	7	1.5	333	2	A99990	RNA 3' phosphate cy
101	7	1.5	339	2	S04403	geranylgeranyl-dip
102	7	1.5	340	2	G69474	conserved hypothet

103	7	1.5	341	2	AD3145	176	7	1.5	460	2	D84486	hypothetical prote
104	7	1.5	342	2	S72529	177	7	1.5	460	2	A86180	hypothetical prote
105	7	1.5	343	2	E95911	178	7	1.5	462	1	TVMSMC	transforming prote
106	7	1.5	344	2	C01628	179	7	1.5	462	1	TVMSM2	transforming prote
107	7	1.5	347	2	S47871	180	7	1.5	462	2	S20073	transforming prote
108	7	1.5	348	2	T11429	181	7	1.5	464	1	TVHWM2	transforming prote
109	7	1.5	350	2	S51494	182	7	1.5	465	2	S69038	hypothetical prote
110	7	1.5	351	1	F2KKD2	183	7	1.5	470	2	T34447	hypothetical prote
111	7	1.5	351	2	S78348	184	7	1.5	477	2	S47889	site-specific DNA-
112	7	1.5	351	2	S42646	185	7	1.5	479	2	A69036	site-specific DNA-
113	7	1.5	351	2	S73278	186	7	1.5	482	2	S12259	probable tRNA-guan
114	7	1.5	351	2	AC2342	187	7	1.5	482	2	A72471	hypothetical prote
115	7	1.5	352	2	AD2374	188	7	1.5	490	2	A96556	probable ABC trans
116	7	1.5	352	2	T07229	189	7	1.5	493	2	T18789	secreted glycoprot
117	7	1.5	352	2	JT0321	190	7	1.5	497	2	G95398	protein Y51HA.5 [
118	7	1.5	352	2	PS0097	191	7	1.5	498	2	VGBRGX	probable sugar upt
119	7	1.5	352	2	T06935	192	7	1.5	498	2	F88359	methionine-tRNA ii
120	7	1.5	353	1	F2NMD2	193	7	1.5	498	2	B95998	probable transmem
121	7	1.5	353	1	F2RMD2	194	7	1.5	512	2	S73457	hypothetical prote
122	7	1.5	353	1	F2LMD2	195	7	1.5	514	2	A95274	probable transmem
123	7	1.5	353	1	F2SPD2	196	7	1.5	517	2	T27101	hypothetical prote
124	7	1.5	353	1	F2PMD2	197	7	1.5	522	2	A75412	conserved hypotet
125	7	1.5	353	1	F2PMD2	198	7	1.5	522	2	S66087	amino acid transpo
126	7	1.5	353	2	S00929	199	7	1.5	536	1	A47190	transducer protein
127	7	1.5	353	2	S03435	200	7	1.5	536	1	E84318	HttI transducer [i
128	7	1.5	353	2	A31183	201	7	1.5	537	2	T04822	hypothetical prote
129	7	1.5	353	2	S58536	202	7	1.5	542	2	S72474	hypothetical prote
130	7	1.5	353	2	S52397	203	7	1.5	555	2	H89957	site-specific DNA-
131	7	1.5	353	2	T07549	204	7	1.5	555	1	JDVL64	formyltetrahydrofo
132	7	1.5	353	4	S52396	205	7	1.5	581	2	T16915	DNA-directed DNA p
133	7	1.5	355	2	F90391	206	7	1.5	591	2	S51303	hypothetical prote
134	7	1.5	357	2	AD2079	207	7	1.5	606	2	S70358	hypothetical prote
135	7	1.5	360	2	G98142	208	7	1.5	610	2	D84104	centromere protein
136	7	1.5	361	2	S25063	209	7	1.5	630	2	S29796	oligopeptide ABC t
137	7	1.5	367	2	A10293	210	7	1.5	632	2	T18692	hypothetical prote
138	7	1.5	368	2	T06093	211	7	1.5	632	2	T27057	hypothetical prote
139	7	1.5	370	1	D22930	212	7	1.5	665	2	S75291	cell division prot
140	7	1.5	375	2	JX0131	213	7	1.5	671	2	F51789	hypothetical prote
141	7	1.5	375	2	F71234	214	7	1.5	684	2	F86394	protein T24P13.20
142	7	1.5	376	2	AG1420	215	7	1.5	685	2	T22223	sel-1 protein - Ca
143	7	1.5	376	2	AH1795	216	7	1.5	687	1	FYFPM	white protein - fr
144	7	1.5	377	2	S30088	217	7	1.5	687	2	B70515	hypothetical prote
145	7	1.5	379	1	T29750	218	7	1.5	689	2	T52060	protein MEDA [imp
146	7	1.5	379	1	ZPBPMU	219	7	1.5	694	1	DNCHNL	nucleolin - chicle
147	7	1.5	380	2	E72768	220	7	1.5	713	2	A27441	nucleolin - Chines
148	7	1.5	380	2	S66728	221	7	1.5	721	2	S29795	hypothetical prote
149	7	1.5	385	2	E85506	222	7	1.5	726	2	B29928	hypothetical prote
150	7	1.5	392	1	A70406	223	7	1.5	731	2	B82922	phosphate transpor
151	7	1.5	396	2	I50707	224	7	1.5	731	2	T51790	hypothetical prote
152	7	1.5	397	2	T35713	225	7	1.5	740	2	T03847	hypothetical prote
153	7	1.5	397	2	S21780	226	7	1.5	746	2	S62365	Fas-binding protei
154	7	1.5	401	2	T48576	227	7	1.5	748	2	F91089	SNF1-related prote
155	7	1.5	404	2	S65991	228	7	1.5	748	2	AD0866	PTS system transcr
156	7	1.5	406	2	S59296	229	7	1.5	748	2	H85924	phosphoenolpyruvat
157	7	1.5	409	2	C87091	230	7	1.5	748	2	F65065	phosphotransferase
158	7	1.5	409	2	S26021	231	7	1.5	751	2	T48719	hypothetical prote
159	7	1.5	411	2	S58094	232	7	1.5	778	2	F97479	non-motile and pha
160	7	1.5	415	2	A70679	233	7	1.5	778	2	AF2697	two component sens
161	7	1.5	415	2	C69682	234	7	1.5	779	2	AE3037	exoribonuclease 10
162	7	1.5	417	2	T31809	235	7	1.5	790	2	T25095	hypothetical prote
163	7	1.5	421	2	T19315	236	7	1.5	809	2	AE0374	probable permealase
164	7	1.5	427	2	T50738	237	7	1.5	871	2	T28706	hypothetical prote
165	7	1.5	432	2	T33833	238	7	1.5	879	1	JDVLC	DNA-directed DNA p
166	7	1.5	438	2	AF0963	239	7	1.5	883	1	JDVLC2	chloroplast outer
167	7	1.5	440	1	B70326	240	7	1.5	884	1	JDVL7	DNA-directed DNA p
168	7	1.5	440	2	S60423	241	7	1.5	884	1	JDVLM8	DNA-directed DNA p
169	7	1.5	440	2	C82410	242	7	1.5	884	1	JDVLM59	DNA-directed DNA p
170	7	1.5	444	2	T20600	243	7	1.5	904	2	C83030	exoribonuclease RN
171	7	1.5	449	2	D87284	244	7	1.5	904	2	S32607	tfifunctional enzy
172	7	1.5	452	2	H04772	245	7	1.5	906	1	F69552	leucyl-tRNA synthet
173	7	1.5	454	2	S11511	246	7	1.5	932	2	C81730	metalloproteinase,
174	7	1.5	456	1	TVHDMC	247	7	1.5	939	2	D87326	conserved hypotet
175	7	1.5	460	2	S11558	248	7	1.5	964	2		

249	7	1.5	1051	2	S27002	322	6	1.3	83	2	JN0400	hypothetical 8.8K
250	7	1.5	1085	2	S62516	323	6	1.3	83	2	B83556	hypothetical prote
251	7	1.5	1130	2	T21134	324	6	1.3	83	2	AH3458	urease (EC 3.5.1.5
252	7	1.5	1160	2	T00272	325	6	1.3	85	2	T32664	hypothetical prote
253	7	1.5	1217	2	A43493	326	6	1.3	85	2	T17882	hypothetical prote
254	7	1.5	1234	2	S52099	327	6	1.3	86	2	S16831	Ig kappa chain V r
255	7	1.5	1234	2	I38994	328	6	1.3	86	2	D98327	cell division topo
256	7	1.5	1237	2	AE1915	329	6	1.3	86	2	A12955	cell division topo
257	7	1.5	1245	2	D71613	330	6	1.3	87	2	F45714	probable regulator
258	7	1.5	1254	2	E86160	331	6	1.3	87	2	D61547	hypothetical prote
259	7	1.5	1262	2	T33074	332	6	1.3	87	2	H96010	probable cell divi
260	7	1.5	1273	1	VDRLT	333	6	1.3	88	2	S66287	sapelin B precursor
261	7	1.5	1279	1	DHUT3	334	6	1.3	88	2	F69528	hypothetical prote
262	7	1.5	1291	1	A28334	335	6	1.3	89	2	B69094	conserved hypotet
263	7	1.5	1298	2	I54367	336	6	1.3	89	2	C86497	hypothetical prote
264	7	1.5	1302	2	A41249	337	6	1.3	89	2	B86833	hypothetical prote
265	7	1.5	1304	1	A46546	338	6	1.3	90	2	S74568	hypothetical prote
266	7	1.5	1317	2	B83346	339	6	1.3	90	2	AD3625	cell division inh1
267	7	1.5	1407	1	T00558	340	6	1.3	91	2	C87034	hypothetical prote
268	7	1.5	1410	2	T15661	341	6	1.3	91	2	D85927	partial probable t
269	7	1.5	1444	1	A30588	342	6	1.3	93	1	E64684	ribosomal protein
270	7	1.5	1568	2	T41013	343	6	1.3	96	2	T18006	hypothetical prote
271	7	1.5	1580	2	T26204	344	6	1.3	97	2	S05334	hypothetical prote
272	7	1.5	1641	2	I38614	345	6	1.3	98	2	S75343	hypothetical prote
273	7	1.5	1664	2	F84485	346	6	1.3	98	2	AE1325	probable cobalt tr
274	7	1.5	1761	2	T14289	347	6	1.3	98	2	AG1578	probable cobalt tr
275	7	1.5	2094	2	S33124	348	6	1.3	99	2	T37093	hypothetical prote
276	7	1.5	2157	2	S71461	349	6	1.3	100	2	S42602	urease (EC 3.5.1.5
277	7	1.5	2175	1	S03170	350	6	1.3	100	2	T50708	urease (EC 3.5.1.5
278	7	1.5	2276	2	T00076	351	6	1.3	100	2	AE2872	urease gamma subu
279	7	1.5	2380	2	E71604	352	6	1.3	100	2	H69534	conserved hypotet
280	7	1.5	2448	2	S53999	353	6	1.3	100	2	E43550	hypothetical prote
281	7	1.5	2647	2	A37098	354	6	1.3	101	2	S60434	probable membrane
282	7	1.5	3530	2	A39266	355	6	1.3	101	2	B97851	hypothetical prote
283	7	1.5	4128	2	JC6306	356	6	1.3	102	1	XKPO	metallicarboxypept
284	6	1.3	23	2	S31210	357	6	1.3	102	2	A32264	parathyrosin - hum
285	6	1.3	23	2	I55406	358	6	1.3	102	2	A24846	apolipoprotein A-I
286	6	1.3	29	2	B34490	359	6	1.3	102	2	S20440	bilirubin UDP-gluc
287	6	1.3	29	2	B61513	360	6	1.3	103	2	F70976	hypothetical prote
288	6	1.3	31	2	D34490	361	6	1.3	103	2	S72973	hypothetical prote
289	6	1.3	43	2	S73245	362	6	1.3	103	2	T47718	hypothetical prote
290	6	1.3	46	2	G85759	363	6	1.3	103	2	G82854	hypothetical prote
291	6	1.3	47	2	D87675	364	6	1.3	104	2	D70879	hypothetical prote
292	6	1.3	48	2	D64614	365	6	1.3	105	2	H72125	hypothetical prote
293	6	1.3	48	2	E71901	366	6	1.3	106	2	AD0408	conserved hypotet
294	6	1.3	53	2	H69359	367	6	1.3	106	2	D69447	hypothetical prote
295	6	1.3	53	2	D89989	368	6	1.3	107	2	F97648	urease gamma chain
296	6	1.3	57	2	AC2265	369	6	1.3	108	2	S69294	hypothetical prote
297	6	1.3	57	2	A82905	370	6	1.3	108	2	JC6041	agc protein precu
298	6	1.3	57	2	AC0191	371	6	1.3	108	2	AB0636	conserved hypotet
299	6	1.3	60	2	C21774	372	6	1.3	108	2	H83303	hypothetical prote
300	6	1.3	61	2	E39741	373	6	1.3	108	2	G72635	hypothetical prote
301	6	1.3	63	2	T07349	374	6	1.3	109	2	B61030	hypothetical prote
302	6	1.3	65	2	A75172	375	6	1.3	109	2	D36885	nitrogen regulator
303	6	1.3	65	2	C91082	376	6	1.3	109	2	S69307	bo-type ubiquinol
304	6	1.3	65	2	S19568	377	6	1.3	109	2	C64402	probable membrane
305	6	1.3	67	2	T07256	378	6	1.3	109	2	C82786	hypothetical prote
306	6	1.3	69	2	A87339	379	6	1.3	110	2	F75153	conserved hypotet
307	6	1.3	72	2	D97178	380	6	1.3	110	2	S70789	csng protein precu
308	6	1.3	72	2	AH0039	381	6	1.3	110	2	D68896	hypothetical prote
309	6	1.3	74	2	S54122	382	6	1.3	111	2	S65365	profilin II - bov1
310	6	1.3	75	2	T17767	383	6	1.3	111	2	G70068	hypothetical prote
311	6	1.3	76	2	T17993	384	6	1.3	111	2	T49569	hypothetical prote
312	6	1.3	76	2	A81858	385	6	1.3	112	2	T12731	hypothetical prote
313	6	1.3	77	1	XKTO	386	6	1.3	112	2	AG2539	hypothetical prote
314	6	1.3	77	1	C58652	387	6	1.3	112	2	A72695	high mobility grou
315	6	1.3	77	2	B64390	388	6	1.3	113	2	A43436	hypothetical prote
316	6	1.3	77	2	AH1279	389	6	1.3	113	2	G83978	probable lipid tra
317	6	1.3	78	2	S03763	390	6	1.3	114	1	S20862	lipid transfer pro
318	6	1.3	80	2	T11069	391	6	1.3	114	2	S29227	hypothetical prote
319	6	1.3	80	2	S34219	392	6	1.3	114	2	S32479	conserved hypotet
320	6	1.3	81	2	T47289	393	6	1.3	114	2	A64609	hypothetical prote
321	6	1.3	83	2	S15142	394	6	1.3	115	2	AH1895	hypothetical prote

395	6	1.3	115	2	H72745	hypothetical prote
396	6	1.3	116	2	A39746	NADH2 dehydrogenas
397	6	1.3	116	2	F72493	hypothetical prote
398	6	1.3	118	2	E86282	protein F10B6.28 (
399	6	1.3	119	2	H71042	probable DNA-dirc
400	6	1.3	119	2	T43514	beta-tubulin foldi
401	6	1.3	120	2	S21565	hypothetical prote
402	6	1.3	120	2	G70895	probable PE protei
403	6	1.3	121	2	E85807	unknown protein en
404	6	1.3	121	2	C90959	probable tail prot
405	6	1.3	122	2	S40314	Ig kappa chain - h
406	6	1.3	122	2	S72770	BI46_F1_2 protein
407	6	1.3	122	2	C73571	conserved hypothet
408	6	1.3	122	2	B70397	hypothetical prote
409	6	1.3	124	2	H71230	hypothetical prote
410	6	1.3	125	2	A71024	hypothetical prote
411	6	1.3	127	1	S19498	thioredoxin homolo
412	6	1.3	127	1	F57987	cytochrome c-type
413	6	1.3	127	2	A98261	cytochrome c-type
414	6	1.3	127	2	E86101	hypothetical prote
415	6	1.3	128	2	H81275	hypothetical prote
416	6	1.3	129	2	F84707	hypothetical prote
417	6	1.3	129	2	H86156	hypothetical prote
418	6	1.3	130	1	R3858	ribosomal protein
419	6	1.3	130	1	A69334	mercuric resistanc
420	6	1.3	130	1	A69894	hypothetical prote
421	6	1.3	130	2	C91150	30S ribosomal subu
422	6	1.3	130	2	G85995	30S ribosomal subu
423	6	1.3	130	2	AG1007	30S ribosomal chat
424	6	1.3	130	2	T44809	hypothetical prote
425	6	1.3	130	2	T47291	hypothetical prote
426	6	1.3	131	2	A44990	NADH2 dehydrogenas
427	6	1.3	131	2	PQ0059	T-cell receptor be
428	6	1.3	131	2	E97737	hypothetical prote
429	6	1.3	131	2	T49331	hypothetical prote
430	6	1.3	131	2	AD0744	probable membrane
431	6	1.3	131	2	B96782	unknown protein F2
432	6	1.3	132	2	S17183	interferon-induced
433	6	1.3	132	2	AB1752	hypothetical prote
434	6	1.3	132	2	AH2171	hypothetical prote
435	6	1.3	133	2	G71028	hypothetical prote
436	6	1.3	134	2	I48639	neurotoxin homolog
437	6	1.3	134	2	G82093	hypothetical prote
438	6	1.3	135	2	D71659	hypothetical prote
439	6	1.3	135	2	S74746	hypothetical prote
440	6	1.3	135	2	G72714	hypothetical prote
441	6	1.3	136	2	S36304	T-cell receptor de
442	6	1.3	136	2	S36320	T-cell receptor de
443	6	1.3	136	2	G95224	hypothetical prote
444	6	1.3	136	2	AB3058	hypothetical prote
445	6	1.3	136	2	T08787	probable testin DK
446	6	1.3	137	2	S36303	T-cell receptor de
447	6	1.3	137	2	C71118	hypothetical prote
448	6	1.3	138	2	A33334	Ig heavy chain pre
449	6	1.3	138	2	T07203	hypothetical prote
450	6	1.3	138	2	F72621	hypothetical prote
451	6	1.3	138	2	D95289	hypothetical prote
452	6	1.3	139	2	A38612	insulin-like growt
453	6	1.3	139	2	B75307	hypothetical prote
454	6	1.3	139	2	G82433	conserved hypothet
455	6	1.3	139	2	T26722	hypothetical prote
456	6	1.3	140	2	S36804	profilin II - huma
457	6	1.3	140	2	AE3007	conserved hypothet
458	6	1.3	140	2	G84608	En/Spm-like transp
459	6	1.3	141	2	S36318	T-cell receptor de
460	6	1.3	141	2	A86875	50S ribosomal prot
461	6	1.3	141	2	S54700	Pile protein - pse
462	6	1.3	141	2	E55855	lysA protein - pha
463	6	1.3	141	2	E64949	probable membrane
464	6	1.3	141	2	C90951	hypothetical prote
465	6	1.3	141	2	G85799	hypothetical prote
466	6	1.3	142	2	G82832	aspartate 1-decarb
467	6	1.3	142	2	E72571	hypothetical prote
468	6	1.3	142	2	JC7636	cystatin 1 - wheat
469	6	1.3	142	2	E84396	hypothetical prote
470	6	1.3	142	2	T47562	hypothetical prote
471	6	1.3	142	2	B72667	hypothetical prote
472	6	1.3	143	2	S36321	T-cell receptor de
473	6	1.3	143	2	T22164	hypothetical prote
474	6	1.3	143	2	H90037	hypothetical prote
475	6	1.3	144	1	PSHUYF	phospholipase A2 (
476	6	1.3	144	2	T35720	hypothetical prote
477	6	1.3	144	2	T33736	hypothetical prote
478	6	1.3	144	2	AE3266	asparagine-binding
479	6	1.3	145	1	CCR25	cytochrome c2 prec
480	6	1.3	145	2	AA1047	exoenzyme S synthe
481	6	1.3	145	2	D71868	hypothetical prote
482	6	1.3	145	2	D82105	conserved hypothet
483	6	1.3	146	1	UDHU	cystatin C precurs
484	6	1.3	146	2	G70183	chemotaxis respons
485	6	1.3	146	2	S61393	hypothetical prote
486	6	1.3	146	2	F83814	Na+/H+ antiporter
487	6	1.3	147	2	AD0953	Mioc protein (limp
488	6	1.3	147	2	D81404	hypothetical prote
489	6	1.3	147	2	B98334	hypothetical prote
490	6	1.3	147	2	AH2948	hypothetical prote
491	6	1.3	148	1	G69952	conserved hypothet
492	6	1.3	148	2	A72785	hypothetical prote
493	6	1.3	148	2	E90359	hypothetical prote
494	6	1.3	148	2	E90359	partial transposas
495	6	1.3	149	2	S41505	hypothetical prote
496	6	1.3	150	2	C86224	hypothetical prote
497	6	1.3	150	2	A64503	conserved hypothet
498	6	1.3	151	2	A81863	hypothetical prote
499	6	1.3	151	2	G90036	hypothetical prote
500	6	1.3	151	2	S73603	hypothetical prote
501	6	1.3	152	2	H83813	hypothetical prote
502	6	1.3	152	2	C97371	hypothetical prote
503	6	1.3	152	2	AC2589	conserved hypothet
504	6	1.3	153	2	G72302	hypothetical prote
505	6	1.3	153	2	AE2344	hypothetical prote
506	6	1.3	153	2	G81236	smg protein, proba
507	6	1.3	153	2	AG1021	probable acetyltra
508	6	1.3	154	2	E82112	conserved hypothet
509	6	1.3	154	2	S41029	hypothetical prote
510	6	1.3	156	2	T28997	hypothetical prote
511	6	1.3	156	2	B64036	hypothetical prote
512	6	1.3	156	2	G02355	tumor-associated m
513	6	1.3	157	2	A10583	conserved hypothet
514	6	1.3	157	2	B47130	high mobility grou
515	6	1.3	157	2	G82273	conserved hypothet
516	6	1.3	157	2	F70918	probable regulator
517	6	1.3	158	2	AG2207	hypothetical prote
518	6	1.3	159	2	F69428	hypothetical prote
519	6	1.3	159	2	T11139	NADH2 dehydrogenas
520	6	1.3	160	2	A96277	hypothetical prote
521	6	1.3	160	2	AC2799	conserved hypothet
522	6	1.3	160	2	G83727	phosphoribosylamin
523	6	1.3	161	2	G71407	transcription fact
524	6	1.3	161	2	S18991	high mobility grou
525	6	1.3	162	2	G70413	NADH2 dehydrogenas
526	6	1.3	162	2	C71000	hypothetical prote
527	6	1.3	162	2	E75257	conserved hypothet
528	6	1.3	163	2	G90503	nimD protein - Bac
529	6	1.3	164	2	A48465	ribosomal protein
530	6	1.3	166	2	G87610	hypothetical prote
531	6	1.3	167	2	A96654	molymphenum cotact
532	6	1.3	168	2	E75257	hypothetical prote
533	6	1.3	168	2	T03640	high mobility grou
534	6	1.3	168	2	C84014	intracellular prote
535	6	1.3	169	2	T49618	2',3'-cyclic-nucle
536	6	1.3	170	2	C70102	hypothetical prote
537	6	1.3	172	2	E72472	hypothetical prote
538	6	1.3	173	2	A48300	lens membrane prot
539	6	1.3	173	2	A49182	integral membrane
540	6	1.3	173	2		

541	6	1.3	173	2	G86905	hypothetical prote
542	6	1.3	174	1	RDSPYA	ferredoxin-chloroed
543	6	1.3	174	2	G83257	general secretion
544	6	1.3	174	2	SL2356	xcpz protein - pse
545	6	1.3	174	2	A27293	probable y chromos
546	6	1.3	175	2	JC5365	rbp-binding repres
547	6	1.3	175	2	AD1327	cell-division init
548	6	1.3	175	2	AF1698	cell-division init
549	6	1.3	176	1	A46606	platelet glycoprot
550	6	1.3	176	2	UT0616	cystatin-related p
551	6	1.3	178	2	A64399	hypothetical prote
552	6	1.3	179	2	T40442	hypothetical highl
553	6	1.3	181	2	B75430	transcription regu
554	6	1.3	181	2	D81450	amlnoacyl-tRNA hyd
555	6	1.3	181	2	T22884	hypothetical prote
556	6	1.3	182	2	H95055	conserved hypotnet
557	6	1.3	182	2	E97925	conserved hypotnet
558	6	1.3	183	2	C85439	probable cytoskele
559	6	1.3	183	2	S76453	hypothetical prote
560	6	1.3	183	2	G96018	probable methylate
561	6	1.3	184	2	S43778	phycoerythrin I be
562	6	1.3	184	2	H45045	phycoerythrin I be
563	6	1.3	184	2	E82124	cytochrome c bioge
564	6	1.3	184	2	T36644	probable transcrip
565	6	1.3	184	2	T08200	probable disease r
566	6	1.3	184	2	T08198	probable disease r
567	6	1.3	185	2	H75216	hypothetical prote
568	6	1.3	185	2	F89961	conserved hypotnet
569	6	1.3	186	2	F81689	conserved hypotnet
570	6	1.3	187	2	F81434	probable integral
571	6	1.3	189	2	S52907	virion protein j13
572	6	1.3	189	2	E84152	hypothetical prote
573	6	1.3	189	2	A83586	probable transcrip
574	6	1.3	191	2	T19026	hypothetical prote
575	6	1.3	191	2	T13536	hypothetical prote
576	6	1.3	191	2	F72277	hypothetical prote
577	6	1.3	192	2	B85040	hypothetical prote
578	6	1.3	193	1	G69347	conserved hypotnet
579	6	1.3	193	2	A10420	phnM protein (limpo
580	6	1.3	193	2	A97068	enzyme from phosph
581	6	1.3	193	2	C88039	membrane protein P
582	6	1.3	194	2	S28850	membrane protein P
583	6	1.3	194	2	E71064	hypothetical prote
584	6	1.3	194	2	E75083	hypothetical prote
585	6	1.3	195	2	S50456	pituitary adenylat
586	6	1.3	196	2	D95546	hypothetical prote
587	6	1.3	197	2	T04782	hypothetical prote
588	6	1.3	197	2	F70622	probable transcrip
589	6	1.3	199	2	T39861	m103 protein - fis
590	6	1.3	200	2	G83204	probable peroxidase
591	6	1.3	200	2	T30472	hypothetical prote
592	6	1.3	201	2	C64451	CDPdiacylglycerol-
593	6	1.3	201	2	S10254	HMG-1 - chicken
594	6	1.3	201	2	G64892	[acyl-carrier-prot
595	6	1.3	201	2	F90880	acyl carrier prote
596	6	1.3	201	2	C85738	acyl carrier prote
597	6	1.3	201	2	AH0664	P-factor mating ph
598	6	1.3	201	2	A36985	lipoprotein signal
599	6	1.3	201	2	A87059	acyl carrier prote
600	6	1.3	202	2	S22359	nonhistone chromos
601	6	1.3	202	2	C97472	nonhistone chromos
602	6	1.3	202	2	AG2690	probable membrane
603	6	1.3	202	2	A26301	lysE family transp
604	6	1.3	203	2	C64038	dopamine- and camp
605	6	1.3	203	2	G84350	hypothetical prote
606	6	1.3	203	2	S48955	hypothetical prote
607	6	1.3	203	2	S67607	probable membrane
608	6	1.3	204	2	A89199	conserved hypotnet
609	6	1.3	205	2	D84527	probable ADP-ribos
610	6	1.3	205	2	S26062	nonhistone chromos
611	6	1.3	205	2	G71891	hypothetical prote
612	6	1.3	205	2	E64621	conserved hypotnet
613	6	1.3	205	2	F87151	conserved hypotnet
614	6	1.3	205	2	T37103	hypothetical prote
615	6	1.3	205	2	T27923	hypothetical prote
616	6	1.3	205	2	S41002	hypothetical prote
617	6	1.3	205	2	C96998	phosphatidylserine
618	6	1.3	206	2	T31585	hypothetical prote
619	6	1.3	206	2	T41232	hypothetical prote
620	6	1.3	206	2	H84165	hypothetical prote
621	6	1.3	207	2	JC1129	nonhistone chromos
622	6	1.3	207	2	JC1114	nonhistone chromos
623	6	1.3	207	2	S74328	high-mobility grou
624	6	1.3	207	2	A82270	hypothetical prote
625	6	1.3	207	2	B71446	acetyltransferase-
626	6	1.3	208	2	S47687	hypothetical prote
627	6	1.3	208	2	E91168	hypothetical prote
628	6	1.3	208	2	E86014	probable enzyme [i
629	6	1.3	208	2	T27398	probable enzyme yh
630	6	1.3	208	2	E86221	hypothetical prote
631	6	1.3	209	2	H75626	DNA-binding respon
632	6	1.3	209	2	B83921	hypothetical prote
633	6	1.3	210	1	S74656	hypothetical prote
634	6	1.3	210	2	S54774	hypothetical prote
635	6	1.3	210	2	D44805	high mobility grou
636	6	1.3	210	2	C84278	hypothetical prote
637	6	1.3	210	2	C81216	hypothetical prote
638	6	1.3	210	2	G81793	conserved hypotnet
639	6	1.3	210	2	G72507	hypothetical prote
640	6	1.3	211	2	C84751	hypothetical prote
641	6	1.3	211	2	E70253	hypothetical prote
642	6	1.3	211	2	T29426	hypothetical prote
643	6	1.3	213	2	D81690	probable sodium-tr
644	6	1.3	213	2	A88042	protein F56D12.2 [
645	6	1.3	213	2	T30116	hypothetical prote
646	6	1.3	214	2	T47110	3-oxoadipate CoA-t
647	6	1.3	214	2	S76538	ubiquitin-protein
648	6	1.3	215	1	UOXFAS	ubiquitin-protein
649	6	1.3	215	1	S01947	nonhistone chromos
650	6	1.3	215	2	A28897	nonhistone chromos
651	6	1.3	215	2	S02826	nonhistone chromos
652	6	1.3	215	2	B97858	mat protein (limpor
653	6	1.3	215	2	H64924	hypothetical prote
654	6	1.3	215	2	C90926	hypothetical prote
655	6	1.3	215	2	G85774	hypothetical prote
656	6	1.3	216	2	S29857	nonhistone chromos
657	6	1.3	216	2	S21337	genome polyprotein
658	6	1.3	216	2	G70474	hypothetical prote
659	6	1.3	216	2	T35020	butyrate-acetoacet
660	6	1.3	217	2	T14621	hypothetical prote
661	6	1.3	217	2	S50818	FE65 nuclear prote
662	6	1.3	218	2	D71693	hypothetical prote
663	6	1.3	218	2	E89004	hypothetical prote
664	6	1.3	218	2	E70818	protein T24A6.12 [
665	6	1.3	218	2	AG3554	probable mercury t
666	6	1.3	219	2	T10509	multiple sugar-bin
667	6	1.3	219	2	C86229	phosphoglycolate p
668	6	1.3	219	2	F71363	hypothetical prote
669	6	1.3	219	2	A10242	probable amino aci
670	6	1.3	219	2	A13200	conserved hypotnet
671	6	1.3	220	1	TEBE12	dehydratogenase Atus
672	6	1.3	220	2	T42619	legumetin protein -
673	6	1.3	220	2	S43291	FLT3/FLK2 ligand (
674	6	1.3	220	2	S58343	flt3 ligand isoform
675	6	1.3	220	2	A95258	competence protein
676	6	1.3	220	2	T14951	hypothetical prote
677	6	1.3	220	2	A99523	hypothetical prote
678	6	1.3	221	2	AF3483	heme exporter prot
679	6	1.3	221	2	H72466	hypothetical prote
680	6	1.3	221	2	D75179	hypothetical prote
681	6	1.3	221	2	T23821	hypothetical prote
682	6	1.3	221	1	D86878	hypothetical prote
683	6	1.3	222	1	S25244	regulatory protein
684	6	1.3	222	2	H71642	mat protein (mat)
685	6	1.3	222	2	D82132	hypothetical prote
686	6	1.3	223	1	B48640	regulatory protein

687	6	1.3	223	2	S60088	nitrate reductase	760	6	1.3	246	2	C86033	probable outer mem
688	6	1.3	223	2	AH2354	nitrogen-responsiv	761	6	1.3	246	2	AB1753	Orf53 bacterioph
689	6	1.3	223	2	T05755	hypothetical prote	762	6	1.3	247	2	B64873	Probable membrane
690	6	1.3	224	2	S71749	DCL protein precur	763	6	1.3	247	2	C90848	hypothetical prote
691	6	1.3	225	1	A48640	global nitrogen re	764	6	1.3	247	2	B85706	hypothetical prote
692	6	1.3	225	2	T01175	hypothetical prote	765	6	1.3	247	2	T39909	hypothetical prote
693	6	1.3	225	2	B70150	hypothetical prote	766	6	1.3	247	2	I59334	leucine-rich acid
694	6	1.3	226	2	T35202	probable two-compo	767	6	1.3	247	2	E90127	hypothetical prote
695	6	1.3	226	2	D72769	ATP synthase F0 ch	768	6	1.3	247	2	AB2465	hypothetical prote
696	6	1.3	227	2	P90622	photosystem I chal	769	6	1.3	248	1	G64839	ymch protein - Esc
697	6	1.3	227	2	S04133	NADH dehydrogenas	770	6	1.3	248	2	E90771	hypothetical prote
698	6	1.3	228	1	QXASC	very hypothetical	771	6	1.3	248	2	A85634	surfactant protein
699	6	1.3	230	2	T37811	hypothetical prote	772	6	1.3	249	1	A35842	chymase (EC 3.4.21
700	6	1.3	231	2	D90966	hypothetical prote	773	6	1.3	249	2	S43309	probable HLA class
701	6	1.3	231	2	D85814	hypothetical prote	774	6	1.3	249	2	C75156	hypothetical prote
702	6	1.3	231	2	A49265	flt3/flk-2 ligand	775	6	1.3	249	2	F91274	hypothetical prote
703	6	1.3	232	2	A86720	conserved hypotet	776	6	1.3	249	2	F86115	hypothetical prote
704	6	1.3	232	2	E87681	conserved hypotet	777	6	1.3	249	2	S56415	hypothetical prote
705	6	1.3	232	2	B75561	conserved hypotet	778	6	1.3	249	2	AB1722	ABC transporter (A
706	6	1.3	232	2	D81274	N-acyleuraminat	779	6	1.3	250	2	AG1351	ABC transporter (A
707	6	1.3	232	2	A27503	testis-specific pr	780	6	1.3	250	2	C90449	conserved hypotet
708	6	1.3	232	2	E97347	probable transcrip	781	6	1.3	251	1	JH0147	uracil phosphoribo
709	6	1.3	232	2	AF0171	conserved hypotet	782	6	1.3	251	2	A91067	transposase of ins
710	6	1.3	233	2	T26133	hypothetical prote	783	6	1.3	251	2	S75353	hypothetical prote
711	6	1.3	233	2	S35020	nolW protein - Rhl	784	6	1.3	251	2	A85911	IS30 transposase
712	6	1.3	234	2	A28566	T-cell suppressor	785	6	1.3	252	2	T14964	phage lambda-relat
713	6	1.3	236	2	G75311	branched-chain aml	786	6	1.3	252	2	E97070	cobalamin-5-phosph
714	6	1.3	236	2	T22859	hypothetical prote	787	6	1.3	252	2	BVECCZ	probable typtoph
715	6	1.3	237	2	B70529	hypothetical prote	788	6	1.3	253	2	B71547	probable leucylph
716	6	1.3	237	2	T15389	hypothetical prote	789	6	1.3	253	2	S07264	beta-crystallin B1
717	6	1.3	237	2	E75169	hypothetical prote	790	6	1.3	253	2	E91039	required for sulfa
718	6	1.3	238	2	H64016	hypothetical prote	791	6	1.3	253	2	H85883	conserved hypotet
719	6	1.3	238	2	S48984	hypothetical prote	792	6	1.3	253	2	C83148	hypothetical prote
720	6	1.3	238	2	G87577	Mutr/nudix family	793	6	1.3	253	2	H86725	MADS-box protein
721	6	1.3	238	2	D96026	probable branched-	794	6	1.3	253	2	T10185	hypothetical prote
722	6	1.3	238	2	H89630	high-affinitly bran	795	6	1.3	254	2	H69057	dihydrodipicolinat
723	6	1.3	238	2	AC3588	hypothetical prote	796	6	1.3	254	2	A95181	cytochrome-c oxida
724	6	1.3	238	2	AD2138	hypothetical prote	797	6	1.3	255	2	E98048	hypothetical prote
725	6	1.3	239	2	S52823	pepsin inhibitor-1	798	6	1.3	255	2	S62759	flagellar biosynth
726	6	1.3	239	2	TI0075	hypothetical prote	799	6	1.3	255	2	T21686	probable flagellar
727	6	1.3	239	2	B83709	hypothetical prote	800	6	1.3	255	2	H71966	flagellar biosynth
728	6	1.3	239	2	AC2657	conserved hypotet	801	6	1.3	255	2	E64541	probable flagellar
729	6	1.3	240	2	A97531	branched-chain aml	802	6	1.3	255	2	B82107	spemidine/putresc
730	6	1.3	240	2	AB2750	hepatoma-derived g	803	6	1.3	256	2	C72261	NADH pyrophosphat
731	6	1.3	240	2	A55055	probable regulator	804	6	1.3	256	2	A82595	hypothetical prote
732	6	1.3	240	2	E45714	SNF7 protein - yea	805	6	1.3	257	1	G65206	hypothetical prote
733	6	1.3	240	2	T46180	probable transfera	806	6	1.3	257	2	D96016	conserved hypotet
734	6	1.3	240	2	S52590	hypothetical prote	807	6	1.3	257	2	G91243	probable flagellar
735	6	1.3	241	2	H70561	hypothetical prote	808	6	1.3	257	2	E86091	carboxyphosphoen
736	6	1.3	241	2	G71045	probable S-adenosy	809	6	1.3	257	2	AD0932	pancreatic elastas
737	6	1.3	241	2	C64006	PK-tax-orf II (alt	810	6	1.3	257	2	G71423	hypothetical prote
738	6	1.3	241	2	C46181	hypothetical prote	811	6	1.3	257	2	AC0087	hypothetical prote
739	6	1.3	241	2	AB1131	DNA-binding stress	812	6	1.3	258	2	S70439	bisphosphoglycerat
740	6	1.3	241	2	AB1491	uridylate kinase	813	6	1.3	258	2	D83779	bisphosphoglycerat
741	6	1.3	241	2	B75628	conserved hypotet	814	6	1.3	258	2	G71423	bisphosphoglycerat
742	6	1.3	241	2	G69899	transcription regu	815	6	1.3	259	1	PMRBBM	bisphosphoglycerat
743	6	1.3	241	2	T09769	transcription regu	816	6	1.3	259	1	PMRBBM	bisphosphoglycerat
744	6	1.3	243	2	E81080	conserved hypotet	817	6	1.3	259	1	PMRBBM	bisphosphoglycerat
745	6	1.3	243	2	B97423	transcription acti	818	6	1.3	259	1	PMRBBM	bisphosphoglycerat
746	6	1.3	243	2	AH2640	transcription regu	819	6	1.3	259	2	C95038	PTS system, ITC co
747	6	1.3	243	2	AI3227	geneC' protein lim	820	6	1.3	259	2	T43102	hypothetical prote
748	6	1.3	244	2	F64247	triose-phosphate 1	821	6	1.3	259	2	A71537	probable n-acetyl
749	6	1.3	244	2	S73539	triosephosphate is	822	6	1.3	260	2	G84714	hypothetical prote
750	6	1.3	244	2	C96796	probable heat shoc	823	6	1.3	261	2	G58892	cytochrome-c oxida
751	6	1.3	244	2	T26265	hypothetical prote	824	6	1.3	261	2	T11540	cytochrome-c oxida
752	6	1.3	245	1	KYBOA	chymotrypsin (EC 3	825	6	1.3	261	2	T11306	cytochrome-c oxida
753	6	1.3	245	2	C97006	transmembrane prot	826	6	1.3	261	2	C84776	hypothetical prote
754	6	1.3	245	2	H97438	hypothetical prote	827	6	1.3	262	2	T11883	cytochrome-c oxida
755	6	1.3	246	2	S38344	CDER-binding prote	828	6	1.3	262	2	F87498	exodeoxyribonuclea
756	6	1.3	246	2	S47805	hypothetical 27.4k	829	6	1.3	263	2	H84918	glutathione S-tran
757	6	1.3	246	2	D91186	probable outer mem	830	6	1.3	263	2	T18880	hypothetical prote
758	6	1.3	246	2	D91186	probable outer mem	831	6	1.3	263	2	D91186	hypothetical prote
759	6	1.3	246	2	D91186	probable outer mem	832	6	1.3	263	2	D91186	hypothetical prote

833	6	1.3	263	2	T02293	hypothetical prote
834	6	1.3	263	2	H86147	TiN6.7 protein - A
835	6	1.3	264	2	D81253	probable peptidase A
836	6	1.3	264	2	S78700	probable export pr
837	6	1.3	264	2	AF0753	flagellar biosynth
838	6	1.3	264	2	D71197	hypothetical prote
839	6	1.3	264	2	D85097	hypothetical prote
840	6	1.3	264	2	T00328	cellulase (EC 3.2.
841	6	1.3	264	2	T34320	hypothetical prote
842	6	1.3	265	2	A82000	phosphatidate cyti
843	6	1.3	265	2	B81229	phosphatidate cyti
844	6	1.3	265	2	C82358	glutamate racemase
845	6	1.3	265	2	A41327	chloromethane de
846	6	1.3	265	2	A75158	hypothetical prote
847	6	1.3	265	2	T46089	proline-rich prote
848	6	1.3	266	1	ELR11	pancreatic elasta
849	6	1.3	266	1	ELUG	pancreatic elasta
850	6	1.3	267	1	TVHUF5	fibroblast growth
851	6	1.3	267	2	A87404	ribosomal protein
852	6	1.3	267	2	JN0831	GlnR protein - Str
853	6	1.3	267	4	A56615	probable pancreati
854	6	1.3	268	2	D86270	F21F23.14 protein
855	6	1.3	268	2	AB1457	high-affinity zinc
856	6	1.3	268	2	AD1094	high-affinity zinc
857	6	1.3	268	2	C90566	hypothetical prote
858	6	1.3	269	2	A86889	zinc ABC transport
859	6	1.3	269	2	E87707	ABC transporter, p
860	6	1.3	269	2	AF0134	flagellar biosynth
861	6	1.3	270	2	F97433	putrescine transpo
862	6	1.3	270	2	AG2651	ABC transporter, m
863	6	1.3	270	2	T06118	hypothetical prote
864	6	1.3	270	2	E84578	probable senescenc
865	6	1.3	270	2	F84293	hypothetical prote
866	6	1.3	270	2	A75064	hypothetical prote
867	6	1.3	270	2	C88483	protein C05D11.13
868	6	1.3	271	2	D83059	phosphatidylserine
869	6	1.3	271	2	D85035	hypothetical prote
870	6	1.3	272	2	AC2431	permease protein o
871	6	1.3	272	2	JC7357	3IK proliferation
872	6	1.3	273	1	B64623	lipopolysaccharide
873	6	1.3	273	2	S39200	formimidopyrimidin
874	6	1.3	273	2	C71369	probable sugar ABC
875	6	1.3	273	2	AH3303	putrescine transpo
876	6	1.3	273	2	S00953	gag protein - frui
877	6	1.3	273	2	D70428	hypothetical prote
878	6	1.3	274	2	G95345	conserved hypotet
879	6	1.3	274	2	F90351	hypothetical prote
880	6	1.3	275	2	T22414	hypothetical prote
881	6	1.3	276	2	C83009	probable ATP-blind
882	6	1.3	276	2	T15455	hypothetical prote
883	6	1.3	276	2	E86756	prophage p12 prote
884	6	1.3	277	1	QREEST	sulfate/chitosulat
885	6	1.3	277	2	G91040	sulfate transport
886	6	1.3	277	2	B85885	hypothetical prote
887	6	1.3	277	2	AH0811	hypothetical prote
888	6	1.3	277	2	G71456	hypothetical prote
889	6	1.3	277	2	S16563	hypothetical prote
890	6	1.3	277	2	AF2404	no1g protein - Rhi
891	6	1.3	278	2	A56421	hypothetical prote
892	6	1.3	278	2	T21718	casein kinase II (
893	6	1.3	278	2	E83453	hypothetical prote
894	6	1.3	278	2	T46458	hypothetical prote
895	6	1.3	278	2	D71256	conserved hypotet
896	6	1.3	278	2	F75109	hypothetical prote
897	6	1.3	279	2	JC2106	tolB protein - Agr
898	6	1.3	279	2	S52639	hypothetical prote
899	6	1.3	280	2	C70696	probable transpo
900	6	1.3	280	2	F96768	hypothetical prote
901	6	1.3	281	2	D45313	putrescine transpo
902	6	1.3	281	2	A90746	permease of putre
903	6	1.3	281	2	E85596	putrescine transpo
904	6	1.3	281	2	A10162	putrescine transpo
905	6	1.3	281	2	AE0606	putrescine transpo
906	6	1.3	281	2	A72561	hypothetical prote
907	6	1.3	281	2	T20894	hypothetical prote
908	6	1.3	281	2	T32765	hypothetical prote
909	6	1.3	282	2	T14225	NADH2 dehydrogenas
910	6	1.3	282	2	AE1559	glycine betaine AB
911	6	1.3	282	2	AG1201	glycine betaine AB
912	6	1.3	282	2	D72721	probable bacterioc
913	6	1.3	282	2	T19594	hypothetical prote
914	6	1.3	282	2	T03906	cytochrome B561 ho
915	6	1.3	283	2	A69207	dihydrotetracycline
916	6	1.3	284	2	D81199	conserved hypotet
917	6	1.3	284	2	D81834	conserved hypotet
918	6	1.3	284	2	F89004	protein T24A6.13 (
919	6	1.3	284	2	C86477	protein F1504.21 (
920	6	1.3	284	2	E97054	sporulation proteol
921	6	1.3	285	2	B87426	rhodanese family p
922	6	1.3	285	2	G02240	UUP-glucuronosyltr
923	6	1.3	285	2	E69905	transcription regu
924	6	1.3	285	2	D95276	probable ABC trans
925	6	1.3	286	2	H89003	protein T24A6.5 (I
926	6	1.3	286	2	AG2000	hypothetical prote
927	6	1.3	286	2	AD3150	hypothetical prote
928	6	1.3	287	2	AF0679	ribonuclease bn (E
929	6	1.3	287	2	T51706	starvation sensing
930	6	1.3	287	2	E70925	formyltetrahydrofo
931	6	1.3	287	2	C98102	probable ribosomal
932	6	1.3	288	2	AD3150	hexulose-6-phospha
933	6	1.3	288	2	A84058	transcription regu
934	6	1.3	289	2	S17725	formyltetrahydrofo
935	6	1.3	289	2	A83608	H+-transporting tw
936	6	1.3	289	2	F70845	polysamine transpo
937	6	1.3	289	2	AH2602	hypothetical prote
938	6	1.3	289	2	H97384	conserved hypotet
939	6	1.3	290	2	A36134	hypothetical prote
940	6	1.3	290	2	F70458	Repa protein - Esc
941	6	1.3	290	2	AG1115	hypothetical prote
942	6	1.3	291	2	T04494	transcription regu
943	6	1.3	291	2	B81130	hypothetical prote
944	6	1.3	291	2	H81836	conserved hypotet
945	6	1.3	292	2	T40637	probable integral
946	6	1.3	292	2	G97111	40s ribosomal prot
947	6	1.3	292	2	D91229	uncharacterized st
948	6	1.3	292	2	C60076	probable aldolase
949	6	1.3	292	2	S40825	hypothetical 32k p
950	6	1.3	293	2	A84110	sugar ABC transport
951	6	1.3	293	2	A72306	conserved hypotet
952	6	1.3	293	2	AH0017	heat-shock chapero
953	6	1.3	293	2	T04450	hypothetical prote
954	6	1.3	293	2	A85817	hypothetical prote
955	6	1.3	293	2	E85718	hypothetical prote
956	6	1.3	294	2	H97655	probable tail comp
957	6	1.3	294	2	AE2879	purU-like protein
958	6	1.3	294	2	AB3558	formyltetrahydrofo
959	6	1.3	294	2	T34199	formyltetrahydrofo
960	6	1.3	294	2	T41953	G protein-coupled
961	6	1.3	294	2	AD1255	protein secretion
962	6	1.3	294	2	AI1617	protein secretion
963	6	1.3	295	2	B83587	probable polynucle
964	6	1.3	295	2	JE0174	frizzled protein-2
965	6	1.3	295	2	T43463	hypothetical prote
966	6	1.3	296	2	T06572	convallin precurs
967	6	1.3	296	2	AF1170	probable sugar ABC
968	6	1.3	296	2	AH1527	probable sugar ABC
969	6	1.3	296	2	D98345	SN-glycerol-3-phos
970	6	1.3	296	2	AC2937	hypothetical prote
971	6	1.3	296	2	T30575	hypothetical prote
972	6	1.3	296	2	F81155	conserved hypotet
973	6	1.3	296	2	H82977	4-hydroxybenzoate-
974	6	1.3	297	2	E86701	hypothetical prote
975	6	1.3	298	2	E91229	probable dehydroge
976	6	1.3	298	2	D86076	probable dehydroge
977	6	1.3	298	2	AI0947	probable oxidoredu
978	6	1.3	298	2	S40826	hypothetical 31.2K

Db 266 MLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKSKYNAESTRESQDTVA 325
Qy 330 ENDGCGFSEEHQAQDSDHLGPHRSTPESRAVQELSSSILAGEDEEGVGLGCDFTFY 389
Db 326 ENDGCGFSEEHQAQDSDHLGPHRSTPESRAVQELSSSILAGEDEEGVGLGCDFTFY 385
Qy 390 SVLVGKASATASGDMNTTIACFVALIIGLCTLLLLAIFKKALPALPISITFGVLFYFAT 449
Db 386 SVLVGKASATASGDMNTTIACFVALIIGLCTLLLLAIFKKALPALPISITFGVLFYFAT 445
Qy 450 DYLVOPEMDQLAFHQFYI 467
Db 446 DYLVOPEMDQLAFHQFYI 463
RESULT 3
presentin 1, splice form 374 - human
N:Alternate names: Alzheimer's disease protein 3
C:Species: Homo sapiens (man)
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C:Accession: S63684
R:Schara, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shirasawa, T.; M
FEBS Lett. 381, 7-11, 1996
A:Title: Identification and characterization of presentin I-467, I-463 and I-374.
A:Reference number: S63683; MUID:96193901; PMID:8641442
A:Accession: S63684
A:Status: preliminary; nucleic acid sequence not shown
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-374 <SAH>
A:Cross-references: EMBL:U40380; NID:g1244639; PIDN:AAB05895.1; PID:g1244640
C:Genetics:
A:Gene: GDB:PSEN1; AD3; FAD; S182; PS1
A:Cross-references: GDB:135682; OMIM:104311
A:Map position: 14q24.3-14q24.3
C:Superfamily: presentin
Query Match 40.3%; Score 188; DB 2; Length 374;
Best Local Similarity 99.7%; Pred. No. 4e-175;
Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 30 NDNREQHNDRSLGHEPLSNRPOGNSROVDEDEDELTKYGAKEHMLFYPV 89
Db 26 NDNREQHNDRSLGHEPLSNRPOGNSROVDEDEDELTKYGAKEHMLFYPV 85
Qy 90 TLCWVAVATIKSVSFYTRKDGQILYTPTEDETVGGRALHSLINAAIMSVYVMTL 149
Db 86 TLCWVAVATIKSVSFYTRKDGQILYTPTEDETVGGRALHSLINAAIMSVYVMTL 145
Qy 150 LVVLKVCYCYVTHAMLLISSLILFFPSFTYLGVEFTYNAVYITVALLIMLVGVG 209
Db 146 LVVLKVCYCYVTHAMLLISSLILFFPSFTYLGVEFTYNAVYITVALLIMLVGVG 205
Qy 210 MISIMKGPLRLOQAYLIMISALMALVFIKYLEPTAMLLIAVISYDLVAVLCRKPLR 269
Db 206 MISIMKGPLRLOQAYLIMISALMALVFIKYLEPTAMLLIAVISYDLVAVLCRKPLR 265
Qy 270 MLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKSKYNAE 318
Db 266 MLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKSKYNAE 314
RESULT 4
JC5081
presentin 1 protein isoform 463 - lesser mouse lemur
C:Species: Microcebus murinus (lesser mouse lemur)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C:Accession: JC5081
R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradler, L.; Petter, A.; Bons, N.; Bellis,
Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A:Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene in
A:Reference number: JC5080; MUID:97079199; PMID:8920931
A:Contents: brain

A:Accession: JC5081
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-463 <CAL>
A:Cross-references: EMBL:Z71333
C:Comment: This protein is an intermembrane protein with seven transmembrane domains.
C:Genetics:
A:Gene: ps1
A:Map position: 14
C:Superfamily: presentin
C:Keywords: transmembrane protein
F:78-96/Domain: transmembrane #status predicted <TM1>
F:129-150/Domain: transmembrane #status predicted <TM2>
F:160-181/Domain: transmembrane #status predicted <TM3>
F:191-209/Domain: transmembrane #status predicted <TM4>
F:217-234/Domain: transmembrane #status predicted <TM5>
F:240-257/Domain: transmembrane #status predicted <TM6>
F:404-424/Domain: transmembrane #status predicted <TM7>
Query Match 22.9%; Score 107; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 5.3e-96;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 206 GVGGMISIMKGPLRLOQAYLIMISALMALVFIKYLEPTAMLLIAVISYDLVAVLCRK 265
Db 202 GVGGMISIMKGPLRLOQAYLIMISALMALVFIKYLEPTAMLLIAVISYDLVAVLCRK 261
Qy 266 GPLRLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKN 312
Db 262 GPLRLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKN 308
RESULT 5
JC5080
presentin 1 protein isoform 467 - lesser mouse lemur
C:Species: Microcebus murinus (lesser mouse lemur)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
C:Accession: JC5080
R:Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradler, L.; Petter, A.; Bons, N.; Bell
Biochem. Biophys. Res. Commun. 228, 430-439, 1996
A:Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene
A:Reference number: JC5080; MUID:97079199; PMID:8920931
A:Accession: JC5080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-467 <CAL>
A:Cross-references: EMBL:Z71333; NID:g1707591; PIDN:CAA95930.1; PID:g1707592
A:Experimental source: brain
C:Comment: This protein is an intergal membrane protein with seven transmembrane dom
C:Genetics:
A:Gene: ps1
A:Map position: 14
C:Superfamily: presentin
C:Keywords: transmembrane protein
F:82-100/Domain: transmembrane #status predicted <TM1>
F:133-154/Domain: transmembrane #status predicted <TM2>
F:164-185/Domain: transmembrane #status predicted <TM3>
F:195-213/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:244-261/Domain: transmembrane #status predicted <TM6>
F:408-428/Domain: transmembrane #status predicted <TM7>
Query Match 22.9%; Score 107; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.4e-96;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 206 GVGGMISIMKGPLRLOQAYLIMISALMALVFIKYLEPTAMLLIAVISYDLVAVLCRK 265
Db 206 GVGGMISIMKGPLRLOQAYLIMISALMALVFIKYLEPTAMLLIAVISYDLVAVLCRK 265
Qy 266 GPLRLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKN 312
Db 266 GPLRLVETAOERNETLFPALITYSSTMVWLVNMAEGDPEAQRVSKN 312

RESULT 6

I78388

S182 protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999

C:Accession: I78388

R:Sherrington, R.; Rogaev, E.I.; Liang, Y.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Ch,

ero, I.; Pinessi, L.; Nea, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sanseau, P.; Poll,

E.; Rommens, J.M.; St George-Hyslop, P.H.

Nature 375, 754-760, 1995

A:Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer

A:Reference number: I58095; MUID:95319502; PMID:7596406

A:Accession: I78388

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <RES>

A:Cross-references: GB:I42177; NID:9904129; PIDN:AAC42094.1; PID:9904130

C:Superfamily: presenilin

Query Match 20.8%; Score 97; DB 2; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.1e-86;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 IHMKGPLRLOQAVLIMISALMAVFIKYPETAMLLIIVSYDVAVLCPRKPLRLMV 272

Db 213 IHMKGPLRLOQAVLIMISALMAVFIKYPETAMLLIIVSYDVAVLCPRKPLRLMV 272

QY 273 ETQOERNETLFPALIVSYSTWVWLVNMAEGDPEAQRV 309

Db 273 ETQOERNETLFPALIVSYSTWVWLVNMAEGDPEAQRV 309

RESULT 7

JC5390

presenilin-alpha - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C:Accession: JC5390

R:Tsujiyama, A.; Yasojima, K.; Hashimoto-Gotoh, T.

Biochem. Biophys. Res. Commun. 231, 392-396, 1997

A:Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential exp

A:Reference number: JC5390; MUID:97223465; PMID:9070286

A:Accession: JC5390

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-433 <RES>

A:Cross-references: DDBJ:D84427; NID:91944353; PIDN:BA19570.1; PID:91944354

A:Experimental source: brain

C:Comment: This protein plays a role in negative regulation of apoptotic cascades during

C:Superfamily: presenilin

F:48-66/Domain: transmembrane #status predicted <TM>

F:99-119/Domain: transmembrane #status predicted <TM>

F:130-149/Domain: transmembrane #status predicted <TM>

F:161-178/Domain: transmembrane #status predicted <TM>

F:187-203/Domain: transmembrane #status predicted <TM>

F:210-227/Domain: transmembrane #status predicted <TM>

F:374-394/Domain: transmembrane #status predicted <TM>

Query Match 12.6%; Score 59; DB 2; Length 433;

Best Local Similarity 100.0%; Pred. No. 3.4e-49;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 ACPVALIIGLCITLLLAIFKKAIPALPISITFGLVYFATDLYVQFMQALFHQFYI 467

Db 375 ACPVALIIGLCITLLLAIFKKAIPALPISITFGLVYFATDLYVQFMQALFHQFYI 433

RESULT 8

I39174

seven trans-membrane domain protein AD3LP/AD5 - human

C:Species: Homo sapiens (man)

C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Sep-1999

C:Accession: I39174

R:Li, J.; Ma, J.; Potter, H.

Proc. Natl. Acad. Sci. U.S.A. 92, 12180-12184, 1995

A:Title: Identification and expression analysis of a potential familial Alzheimer's d

A:Reference number: I39174; MUID:96109229; PMID:8618867

A:Accession: I39174

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-442 <RES>

A:Cross-references: EMBL:U34349; NID:91079575; PIDN:AAC50290.1; PID:91079576

C:Superfamily: presenilin

Query Match 6.0%; Score 28; DB 2; Length 442;

Best Local Similarity 100.0%; Pred. No. 6.2e-19;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISYVDVAVLCPRKGPLRLMIVETAQRNE 280

Db 259 ISYVDVAVLCPRKGPLRLMIVETAQRNE 286

RESULT 9

A56993

presenilin 2 - human

N:Alternate names: Alzheimer's disease protein 4

C:Species: Homo sapiens (man)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Nov-2000

C:Accession: A56993; I58098

R:Levy-Lahad, E.; Wasco, W.; Poorkaj, P.; Romano, D.M.; Oshima, J.; Pettingell, W.H.;

Science 269, 973-977, 1995

A:Title: Candidate gene for the chromosome 1 familial Alzheimer's disease locus.

A:Reference number: A56993; MUID:95365816; PMID:7638652

A:Accession: A56993

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-448 <RES>

A:Cross-references: GB:I43964; NID:9951202; PIDN:AAB59557.1; PID:9951203

R:Rogaev, E.I.; Sherrington, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; C

; Cohen, D.; Tanfelfeld, L.; Fraser, P.E.; Rommens, J.M.; St George-Hyslop, P.H.

Nature 376, 775-778, 1995

A:Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene o

A:Reference number: I58098; MUID:95379971; PMID:7651536

A:Accession: I58098

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-122 'P', 124-448 <RES>

A:Cross-references: GB:I44577; NID:9950347; PIDN:AAC42012.1; PID:9950348

A:Gene: GDB:PSEN2; AD4; STM2; PS2; E5-1

A:Cross-references: GDB:633044; OMIM:600759

A:Map position: 1q31-1q42

C:Superfamily: presenilin

Query Match 6.0%; Score 28; DB 2; Length 448;

Best Local Similarity 100.0%; Pred. No. 6.3e-19;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISYVDVAVLCPRKGPLRLMIVETAQRNE 280

Db 259 ISYVDVAVLCPRKGPLRLMIVETAQRNE 286

RESULT 10

JC5391

presenilin-beta - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C:Accession: JC5391

R:Tsujiyama, A.; Yasojima, K.; Hashimoto-Gotoh, T.

Biochem. Biophys. Res. Commun. 231, 392-396, 1997

A:Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential e

A:Reference number: JC5390; MUID:97223465; PMID:9070286

A:Accession: J05391
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1449 <TSU>
A:Cross-references: DDBJ:D84428; NID:g1944355; PIDN:BAI9571.1; PID:g1944356
A:Experimental source: brain
C:Comment: This protein plays a role in negative regulation of apoptotic cascades during
C:Superfamily: presenilin
F:91-109/Domain: transmembrane #status predicted <TM1>
F:142-162/Domain: transmembrane #status predicted <TM2>
F:173-192/Domain: transmembrane #status predicted <TM3>
F:204-221/Domain: transmembrane #status predicted <TM4>
F:230-246/Domain: transmembrane #status predicted <TM5>
F:252-279/Domain: transmembrane #status predicted <TM6>
F:390-410/Domain: transmembrane #status predicted <TM7>

Query Match 5.8%; Score 27; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 HVIMLFVPTLCMVVVATIKSVSYF 107
Db 90 HVIMLFVPTLCMVVVATIKSVSYF 116

RESULT 11
S60253
sel-12 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Sep-1998
C:Accession: S60253
R:Levitan, D.; Greenwald, I.
Nature 377, 351-354, 1995
A:Title: Facilitation of lin-12-mediated signalling by sel-12, a Caenorhabditis elegans
A:Reference number: S60253; MID:96032531; PMID:7566091
A:Accession: S60253
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1461 <LEV>
A:Cross-references: EMBL:U35660
C:Superfamily: Presenilin

Query Match 3.9%; Score 18; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 EERGVKLGDFIFYSVL 392
Db 354 EERGVKLGDFIFYSVL 371

RESULT 12
E89453
Protein F35H12.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C:Accession: E89453
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: E89453
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-836 <STO>
A:Cross-references: GB:chr.X; PIDN:AAA83176.1; PID:g1109863; GSPDB:GN00028; CESP:F35H12
A:Note: similar to M. musculus Sl82 protein (GB:I42177)
C:Genetics:
A:Gene: F35H12.3
A:Map position: X
A:Map position: X

Query Match 3.9%; Score 18; DB 2; Length 836;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 EERGVKLGDFIFYSVL 392
Db 354 EERGVKLGDFIFYSVL 371

RESULT 13
A84702
Probable presenilin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: A84702
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MID:20083487; PMID:10617197
A:Accession: A84702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <STO>
A:Cross-references: GB:AE002093; NID:g4567215; PIDN:AAD23630.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29900
A:Map position: 2
C:Superfamily: presenilin

Query Match 3.2%; Score 15; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 380 KLGIDGDFIFYSVLG 394
Db 313 KLGIDGDFIFYSVLG 327

RESULT 14
T00724
presenilin homolog F22013.19 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C:Accession: T00724
R:Shim, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.;
eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, April 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A:Reference number: Z14200
A:Accession: T00724
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-453 <SHI>
A:Cross-references: EMBL:AC003981; NID:g3063438; PID:g3063457; GSPDB:GN00059; ATSP:F2
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP:F22013.19
A:Map position: 1
A:Introns: 108/1
C:Superfamily: presenilin

Query Match 3.2%; Score 15; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 380 KLGIDGDFIFYSVLG 394
Db 369 KLGIDGDFIFYSVLG 383

RESULT 15

G90492
hypothetical protein SSO3092 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: G90492
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KUR>
A:Cross-references: GB:AE006641; NID:q13816512; PIDN:AAK43198.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO3092

Query Match 1.9%; Score 9; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LLLFFFSFI 180
|||||
DB 198 LLLFFFSFI 206

RESULT 16
H65055
hypothetical protein b2748 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: H65055
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H65055
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-103 <BLAT>
A:Cross-references: GB:AE000358; GB:U00096; NID:q2367156; PIDN:AACT5790.1; PID:q1789105;
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: hypothetical protein HI0673

Query Match 1.7%; Score 8; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
|||||
DB 4 LTTLLAI 11

RESULT 17
B91079
hypothetical protein ECS3602 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: B91079
R:Havshli, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno-
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B91079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <KAY>
A:Cross-references: GB:BA000007; PIDN:BA037025.1; PID:q13363073; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952

C:Genetics:
A:Gene: ECS3602
C:Superfamily: hypothetical protein HI0673

Query Match 1.7%; Score 8; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
|||||
DB 4 LTTLLAI 11

RESULT 18
C85924
hypothetical protein Z4056 [imported] - Escherichia coli (strain O157:H7, substrain E)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C85924
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May-
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lam, A.; Dimlant, E.; Potamousis, K.; Apoda-
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <STO>
A:Cross-references: GB:AE005174; NID:q12517202; PIDN:AACT57855.1; GSPDB:GN00145; UMGCP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4056
C:Superfamily: hypothetical protein HI0673

Query Match 1.7%; Score 8; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
|||||
DB 4 LTTLLAI 11

RESULT 19
A49304
ventral prostate major secretory protein, 20K - rat
N:Alternate names: 22K glycoprotein, prostatic; cystatin-related protein 1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2001
C:Accession: A49304; S29944; A32819; J0615; A34552; A49200; S38813
R:Ho, K.C.; Marschke, K.B.; Tan, J.; Power, S.G.; Wilson, E.M.; French, F.S.
J. Biol. Chem. 268, 27226-27235, 1993
A:Title: A complex response element in intron 1 of the androgen-regulated 20-kDa prot-
A:Reference number: A49304; MUID:94086539; PMID:8262963
A:Accession: A49304
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <HO1>
A:Cross-references: GB:U12454; NID:q499666; PIDN:AAA40732.1; PID:q499667
R:Peeters, B.
submitted to the EMBL Data Library, July 1992
A:Reference number: S29944
A:Accession: S29944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <PEE>
A:Cross-references: EMBL:Z13993; NID:q56965; PIDN:CAA78384.1; PID:q56966
R:Ho, K.C.; Snook, R.; Quarumby, V.; Viskochil, D.H.; Rennie, P.S.; Wilson, E.M.; Fren-
Biochemistry 28, 6367-6373, 1989
A:Title: Primary structure and androgen regulation of a 20-kilodalton protein specific
A:Reference number: A32819; MUID:90001187; PMID:2477055
A:Accession: A32819

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'MO', 25-176 <HOK>
 A:Cross-references: GB:M27901; NID:9530166; PIDN:AAA42345.1; PID:9530167
 R:Devos, A.; De Clercq, N.; Vercueren, I.; Heyns, W.; Rombaux, W.; Peeters, B.
 Gene 155, 159-167, 1993
 A:Title: Structure of rat genes encoding androgen-regulated cystatin-related proteins (C
 A:Reference number: J70615; MUID:93216117; PMID:8462870
 A:Accession: J70615
 A:Molecule type: DNA
 A:Residues: 1-156, 'V', 158-176 <DEV>
 A:Cross-references: GB:M13993
 R:Rindrickx, J.; Hemschoote, K.; De Clercq, N.; Van Dijk, P.; Peeters, B.; Rombaux, W.
 Mol. Endocrinol. 4, 657-667, 1990
 A:Title: Tissue-specific expression and androgen regulation of different genes encoding
 A:Reference number: A34552; MUID:91125374; PMID:2280780
 A:Accession: A34552
 A:Molecule type: mRNA
 A:Residues: 1-156, 'V', 158-176 <MIN>
 A:Cross-references: GB:M58167; NID:9205902; PIDN:AAA63498.1; PID:9205903
 R:Vercueren, I.; Winderickx, J.; Devos, A.; Peeters, B.; Heyns, W.
 Endocrinology 132, 2496-2502, 1993
 A:Title: An effect of androgens on the length of the poly(A)-tail and alternative splicing
 A:Reference number: A49200; MUID:93178358; PMID:7679983
 A:Note: Corrected and republished from Endocrinology 131, 2496-2502, 1992
 A:Accession: A49200
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 137-156, 'V', 158-176 <VER>
 A:Cross-references: EMBL:Z13993
 A:Experimental source: Mistar albino
 A:Note: sequence extracted from NCBI backbone (NCB1N.119368, NCB1P.119370)
 C:Genetics:
 A:Gene: Crp1
 A:Introns: 79/3; 111/3; 149/3
 C:Keywords: glycoprotein

Query Match 1.7%; Score 8; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 TLULLAIF 428
 |||||||
 Db 8 TLULLAIF 15

RESULT 20
 JC7335
 chitinase (EC 3.2.1.14) 1 - cone shell (Conus tulipa)
 C:Species: Conus tulipa (tulip cone)
 C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 15-Sep-2000
 C:Accession: JC7335
 R:Yamagami, T.; Tsutsun, K.; Ishiguro, M.
 Biosci. Biotechnol. Biochem. 64, 1394-1401, 2000
 A:Title: Cloning, sequencing, and expression of the tulip bulb chitinase-1 cDNA.
 A:Reference number: JC7335
 A:Accession: JC7335
 A:Molecule type: mRNA
 A:Residues: 1-314 <YAM>
 A:Cross-references: DDBJ:AB035668
 C:Comment: This enzyme, a member of class III plant chitinases, which catalyzes the hyd
 or protection against fungal pathogens.
 C:Genetics:
 A:Gene: tbc-1
 C:Superfamily: alcohol sulfotransferase
 C:Keywords: glycosidase; hydrolase

Query Match 1.7%; Score 8; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 169 SSLLLEFF 176
 |||||||

Db 7 SSLLLEFF 14

RESULT 21
 AF0205
 Probable exported protein YPO1686 [Imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AF0205
 R:Parikh, J.; Wren, B.W.; Thomson, N.R.; Tilhail, R.W.; Holden, M.T.G.; Prentice, M.
 deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0205
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC90506.1; PID:915979716; GSPDB:GN00175
 C:Genetics:
 A:Gene: YPO1686

Query Match 1.7%; Score 8; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 LISSLL 173
 |||||||
 Db 9 LISSLL 16

RESULT 22
 H75253
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: H75253
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 M.; Shen, M.; Yamathavan, J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: H75253
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <WHI>
 A:Cross-references: GB:AE002089; GB:AE000513; NID:96460427; PIDN:ANF12144.1; PID:9646
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2600
 A:Map position: 1

Query Match 1.7%; Score 8; DB 2; Length 347;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 RSTPESRA 359
 |||||||
 Db 274 RSTPESRA 281

RESULT 23
 T39599
 conserved hypothetical protein SPCL65.07c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
 C:Accession: T39599
 R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
 Submitted to the EMBL Data Library, May 1998
 A:Reference number: Z21866
 A:Accession: T39599

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-354 <LYN>
A:Cross-references: EMBL:AL023554; PIDN:CAA19027.1; GSPDB:GN00067; SPDB:SPBC16G5.07C
A:Experimental source: strain 972h-; cosmid c16G5
C:Genetics:
A:Gene: SPDB:SPBC16G5.07C
A:Map position: 2
A:introns: 72/2; 265/2
C:Superfamily: erythrocyte band 7 integral membrane protein

Query Match
Best Local Similarity 1.7%; Score 8; DB 2; Length 354;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 KASATASG 402
|||||||
DB 265 KASATASG 272

RESULT 24
A84564
hypothetical protein At2g18410 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84564
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <STO>
A:Cross-references: GB:AE002093; NID:g4309726; PIDN:AAD15496.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g18410
A:Map position: 2

Query Match
Best Local Similarity 1.7%; Score 8; DB 2; Length 392;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 LSSSILAG 371
|||||||
DB 44 LSSSILAG 51

RESULT 25
A97119
probable membrane protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: A97119
R:Molling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.T.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A97119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-581 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK79740.1; PID:g15024745; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1775

Query Match
Best Local Similarity 1.7%; Score 8; DB 2; Length 581;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 KTYNAVAD 194
|||||||
DB 232 KTYNAVAD 239

RESULT 26
A42322
ornithine decarboxylase (EC 4.1.1.17) - Leishmania donovani
C:Species: Leishmania donovani
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Apr-1998
C:Accession: A42322; S27821; S29187
R:Hanson, S.; Adelman, J.; Ullman, B.
J. Biol. Chem. 267, 2350-2359, 1992
A:Title: Amplification and molecular cloning of the ornithine decarboxylase gene of L
A:Reference number: A42322; MUID:92129311; PMID:1339439
A:Accession: A42322
A:Molecule type: DNA
A:Residues: 1-707 <HAN>
A:Cross-references: EMBL:M81192; NID:g159387; PID:g159388
A:Note: sequence extracted from NCBI backbone (NCBIN:78350, NCBI:P:78355)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match
Best Local Similarity 1.7%; Score 8; DB 2; Length 707;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 EVFKTYNV 191
|||||||
DB 168 EVFKTYNV 175

RESULT 27
I53078
homeotic gene regulator - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-2002
C:Accession: I53078
R:Randazzo, F.M.; Khavari, P.; Crabtree, G.; Tamkun, J.; Rosant, J.
Dev. Biol. 161, 229-242, 1994
A:Title: brg1: a putative murine homologue of the Drosophila brachy gene, a homeotic
A:Reference number: I53078; MUID:94123856; PMID:7904967
A:Accession: I53078
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1022 <RES>
A:Cross-references: GB:S68108; NID:g545017; PIDN:AAC60670.1; PID:g545018
C:Genetics:
A:Gene: brg1
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:860-915/Domain: bromodomain homology <BRO>

Query Match
Best Local Similarity 1.7%; Score 8; DB 2; Length 1022;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 EODEEDE 71
|||||||
DB 663 EODEEDE 670

RESULT 28
DVMS1A
multidrug resistance protein 1a - mouse (fragment)
N:Alternate names: P-glycoprotein 1a
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001
C:Accession: A34175
R:Hsu, S.I.H.; Lothstein, L.; Horwitz, S.B.
J. Biol. Chem. 264, 12053-12062, 1989
A:Title: Differential overexpression of three mdr gene family members in multidrug-re
A:Reference number: A34175; MUID:89308614; PMID:2473069
A:Accession: A34175

A:Molecule type: mRNA
A:Residues: 1-1104 <HSU>
A:Cross-references: GB:M24417; GB:J04839; NID:9200329; PIDN:AAA03243.1; PID:9200330
C:Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
structurally and functionally unrelated lipophilic antitumor drugs.
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology
C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane pr
F:234-428/Domain: ATP-binding cassette homology <ABC1>
F:251-258/Region: nucleotide-binding motif A (P-loop)
F:375-379/Region: nucleotide-binding motif B
F:877-1073/Domain: ATP-binding cassette homology <ABC2>
F:994-901/Region: nucleotide-binding motif A (P-loop)
F:1020-1024/Region: nucleotide-binding motif B
F:1073/Binding site: ATP (Lys) #status predicted
F:900/Binding site: ATP (Lys) #status predicted

Query Match 1.7%; Score 8; DB 1; Length 1104;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
|
Db 681 LTTLLAI 688

RESULT 29

DWHYC

Multidrug resistance protein 1 - Chinese hamster

N:Alternate names: P-glycoprotein pgp1

C:Species: Cricetus griseus (Chinese hamster)

C:Date: 31-Dec-1990 #sequence-revision 30-Sep-1992 #text-change 19-Jan-2001

C:Accession: A38696; C38696; A27126; S33768; 152823

R:Devault, S.E.; Hussain, A.; Davide, J.P.; Melera, P.W.

J. Biol. Chem. 265: 4545-4555, 1991

A:Title: Full length and alternatively spliced pgp-1 transcripts in multidrug-resistant

A:Accession: A38696

A:Molecule type: mRNA

A:Residues: 1-1276 <DEV>

A:Cross-references: GB:M59253; NID:q191154; PIDN:AAA37004.1; PID:q191155

A:Accession: C38696

A:Molecule type: mRNA

A:Residues: 108-1276 <DE1>

A:Cross-references: GB:M59254; NID:q191156; PIDN:AAA37005.1; PID:q191157

A:Experimental source: clone ADX185

A:Accession: B38696

A:Molecule type: mRNA

A:Residues: 1-32,771-1276 <DE2>

A:Cross-references: GB:M59252; NID:q191152; PIDN:AAA37003.1; PID:q191153

A:Experimental source: clone ADX124

R:Endicott, J.A.; Juranka, P.F.; Sarangi, F.; Gerlach, J.H.; Deuchars, K.L.; Ling, V.

Mol. Cell. Biol. 7, 4075-4081, 1987

A:Title: Simultaneous expression of two P-glycoprotein genes in drug-sensitive Chinese

A:Reference number: A27126; MOID:88122132; PMID:2893255

A:Accession: A27126

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 706-1276 <END>

A:Cross-references: GB:M18797; NID:q191158; PIDN:AAA37006.1; PID:q191159

R:Zastawny, R.L.; Ling, V.

Biochim. Biophys. Acta 1173, 303-313, 1993

A:Title: Structural and functional analysis of 5' flanking and intron 1 sequences of the

A:Reference number: S33768; MOID:93305724; PMID:8100449

A:Accession: S33768

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-21 <ZAS>

A:Cross-references: EMBL:L03286

R:Teeter, L.D.; Eckersberg, T.; Tsai, Y.; Kuo, M.T.

Cell Growth Differ. 2, 425-437, 1991

A:Title: Analysis of the Chinese hamster P-glycoprotein/multidrug resistance gene pgp1

A:Reference number: 152823; MOID:92008970; PMID:1661134

A:Accession: 152823

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>
A:Cross-references: GB:S81975; NID:9240862
C:Comment: This is an integral membrane protein overproduced in multidrug-resistant c
structurally and functionally unrelated lipophilic antitumor drugs.
C:Genetics: A:Gene: pgp1
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology
C:Keywords: alternative splicing; ATP; duplication; glycoprotein; nucleotide binding;
F:407-601/Domain: ATP-binding cassette homology <ABC1>
F:424-431/Region: nucleotide-binding motif A (P-loop)
F:548-552/Region: nucleotide-binding motif B
F:1050-1246/Domain: ATP-binding cassette homology <ABC2>
F:1067-1074/Region: nucleotide-binding motif A (P-loop)
F:1193-1197/Region: nucleotide-binding motif B
F:87,91,96/Binding site: carbonylate (asn) (covalent) #status predicted
F:430/Binding site: ATP (Lys) #status predicted
F:1073/Binding site: ATP (Lys) #status predicted

Query Match 1.7%; Score 8; DB 1; Length 1276;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
|
Db 854 LTTLLAI 861

RESULT 30

Multidrug resistance protein 1a - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jul-1990 #sequence-revision 13-Jul-1990 #text-change 02-Feb-2001

C:Accession: A34786; A35671

R:Devault, A.; Gros, P.

Mol. Cell. Biol. 10, 1652-1663, 1990

A:Title: Two members of the mouse mdr gene family confer multidrug resistance with ov

A:Accession: A34786

A:Molecule type: preliminary

A:Residues: 1-1276 <DEV>

A:Cross-references: GB:M30697; NID:q199111; PIDN:AAA39517.1; PID:q387429

A:Reference number: A35671; MOID:90287150; PMID:1972547

A:Accession: A35671

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-525, 'HV', 528-938, 'S', 940-1035, 'V', 1037-1276 <HSU>

A:Cross-references: GB:M33581; NID:q199104; PIDN:AAA39514.1; PID:q387427

C:Superfamily: multidrug resistance protein; ATP-binding cassette homology

C:Keywords: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; P-1

F:406-600/Domain: ATP-binding cassette homology <ABC1>

F:423-431/Region: nucleotide-binding motif A (P-loop)

F:547-551/Region: nucleotide-binding motif B

F:1049-1245/Domain: ATP-binding cassette homology <ABC2>

F:1066-1074/Region: nucleotide-binding motif A (P-loop)

F:1192-1196/Region: nucleotide-binding motif B

F:429/Binding site: ATP (Lys) #status predicted

F:1072/Binding site: ATP (Lys) #status predicted

Query Match 1.7%; Score 8; DB 2; Length 1276;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
|
Db 853 LTTLLAI 860

```

RESULT 31
|DVHUI
|multidrug resistance protein 1 - human
|N:Alternate names: P-glycoprotein 1
|C:Species: Homo sapiens (man)
|C:Date: 31-Dec-1990 #sequence_revision 18-Aug-1995 #text_change 19-Jan-2001
|C:Accession: A34914; PS0162; S15500; A25059; S43838; I52238; I65204
|R:Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.
|J. Biol. Chem. 265, 506-514, 1990
|A:Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin
|A:Reference number: A34914; MUID:90094448; PMID:1967175
|A:Accession: A34914
|A:Molecule type: DNA
|A:Residues: 1-1280 <CH2>
|A:Cross-references: GB:M29447; GB:J05168; NID:g187496; PIDN:AAA59576.1; PID:g386862
|R:Kloka, N.; Yamano, Y.; Komano, T.; Ueda, K.
|submitted to JIPID, April 1991
|A:Reference number: PS0162
|A:Accession: PS0162
|A:Molecule type: DNA
|A:Residues: 1-22 <KIO>
|R:Kloka, N.; Yamano, Y.; Komano, T.; Ueda, K.
|submitted to the EMBL Data Library, April 1991
|A:Description: Transcriptional regulation of multidrug resistance gene (MDR1) expression
|A:Reference number: S15500
|A:Accession: S15500
|A:Molecule type: DNA
|A:Residues: 1-22, 'R' <KI2>
|A:Cross-references: EMBL:X58723; NID:g34522; PIDN:CA41558.1; PID:g34523
|R:Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I.
|Cell 47, 381-389, 1986
|A:Title: Internal duplication and homology with bacterial transport proteins in the mdr1
|A:Reference number: A25059; MUID:87028230; PMID:2876781
|A:Accession: A25059
|A:Molecule type: mRNA
|A:Residues: 1-184, 'V', 186-1280 <CH2>
|A:Cross-references: GB:M14758; NID:g187468; PIDN:AAA59575.1; PID:g307180
|R:Chambers, T.C.; Pohl, J.; Glass, D.B.; Kuo, J.F.
|Biochem. J. 299, 309-315, 1994
|A:Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase of
|A:Reference number: S43838; MUID:94220047; PMID:7909431
|A:Accession: S43838
|A:Molecule type: protein
|A:Residues: 656-689 <CHA>
|R:Geckeler, V.; Weger, S.; Probst, H.
|Biochem. Biophys. Res. Commun. 169, 796-802, 1990
|A:Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell lin
|A:Reference number: I52238; MUID:90290529; PMID:1972623
|A:Accession: I52238
|A:Status: translated from GB/EMBL/DBJ
|A:Molecule type: DNA
|A:Residues: 178-215 <RES>
|A:Cross-references: GB:M37724; NID:g183537; PIDN:AAA8047.1; PID:g553314
|A:Accession: I65204
|A:Status: translated from GB/EMBL/DBJ
|A:Molecule type: DNA
|A:Residues: 800-856 <RE2>
|A:Cross-references: GB:M37725; NID:g183538; PIDN:AAA8048.1; PID:g553315
|C:Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
|structurally and functionally unrelated lipophilic antitumor drugs.
|C:Genetics:
|A:Gene: GDB:PGY1; MDR1
|A:Cross-references: GDB:120712; OMIM:171050
|A:Map position: 7q21-7q21
|C:Superfamily: multidrug resistance protein; ATP-binding cassette homology
|C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;
|F:1-658,553-1280/Region: duplication
|F:49-350/Domain: hydrophobic <HB1>
|F:351-637/Domain: hydrophilic <HL1>
|F:410-604/Domain: ATP-binding cassette homology <ABC1>
|F:427-434/Region: nucleotide-binding motif A (P-loop)
|F:551-555/Region: nucleotide-binding motif B
|F:638-708/Domain: linker <LIN>

```

```

F:709-993/Domain: hydrophobic <HB2>
F:994-1280/Domain: hydrophilic <HL2>
F:1053-1249/Domain: ATP-binding cassette homology <ABC2>
F:1070-1077/Region: nucleotide-binding motif A (P-loop)
F:1196-1200/Region: nucleotide-binding motif B
F:91,94,99/Binding site: carbonylate (Asn) (covalent) #status predicted
F:433/Binding site: ATP (Lys) #status predicted
F:661,667,671/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F:667,671,683/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #st
F:1076/Binding site: ATP (Lys) #status predicted

Query Match 1.7%; Score 8; DB 1; Length 1280;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LTTLLAI 427
DB 857 LTTLLAI 864

RESULT 32
S39059
Protein BRG1 - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 17-Nov-1995 #text_change 02-Aug-2002
C:Accession: S39059
R:Khavari, P.A.; Peterson, C.L.; Tankun, J.W.; Mendel, D.B.; Crabtree, G.R.
Nature 366, 170-174, 1993
A:Title: BRG1 contains a conserved domain of the SM12/SNF2 family necessary for norma
A:Reference number: S39059; MUID:94050144; PMID:823256
A:Accession: S39059
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1613 <KHA>
C:Superfamily: human SNF2alpha protein; bromodomain homology
F:1451-1506/Domain: bromodomain homology <BRO>

Query Match 1.7%; Score 8; DB 2; Length 1613;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 EDDDEDE 71
DB 1253 EDDDEDE 1260

RESULT 33
A39401
merozoite surface antigen 1 precursor - Plasmodium vivax
C:Species: Plasmodium vivax
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Nov-1999
C:Accession: A39401
R:del Portillo, H.A.; Longacre, S.; Khouri, E.; David, P.H.
Proc. Natl. Acad. Sci. U.S.A. 88, 4030-4034, 1991
A:Title: Primary structure of the merozoite surface antigen 1 of Plasmodium vivax rev
A:Reference number: A39401; MUID:91219506; PMID:2023952
A:Accession: A39401
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1726 <DEI>
A:Cross-references: GB:M60807
C:Superfamily: major merozoite surface antigen
C:Keywords: surface antigen

Query Match 1.7%; Score 8; DB 2; Length 1726;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 LFFFSFI 180
DB 4 LFFFSFI 11

```

RESULT 34
A56388
dopamine- and cAMP-regulated neuronal phosphoprotein DARPP-32 - rat (fragments)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: A56388
R:Desoluts, F.; Cohen, D.; Malrn, A.C.; Greengard, P.; Girault, J.A.
J. Biol. Chem. 270, 8772-8778, 1995
A:Title: Phosphorylation of DARPP-32, a dopamine- and cAMP-regulated phosphoprotein, by
A:Reference number: A56388; MUID:95238371; PMID:7721783
A:Accession: A56388
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-49 <DE>
C:Keywords: phosphoprotein
F:7,35,43/Binding site: phosphate (Ser) (covalent) (by casein kinase I) #status experimental

Query Match 1.5%; Score 7; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDEE 72
DB 26 DEEDEE 32

RESULT 35
S59962
antimicrobial peptide gaegurin 5 precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S59962; PC2304
R:Park, J.M.; Lee, J.Y.; Moon, H.M.; Lee, B.J.
Biochim. Biophys. Acta 1264, 23-25, 1995
A:Title: Molecular cloning of cDNAs encoding precursors of frog skin antimicrobial peptide
A:Reference number: S59961; MUID:96038814; PMID:7578251
A:Accession: S59962
A:Molecule type: mRNA
A:Residues: 1-65 <PAR>
A:Cross-references: EMBL:U02393; NID:9733137; PIDD:AAA64412.1; PID:9733138
A:Experimental source: skin
R:Park, J.M.; Jung, J.E.; Lee, B.J.
Biochim. Biophys. Res. Commun. 205, 948-954, 1994
A:Title: Antimicrobial peptides from the skin of a Korean frog, *Rana rugosa*.
A:Reference number: PC2300; MUID:95091844; PMID:7999137
A:Accession: PC2304
A:Molecule type: protein
A:Residues: 42-57, 'K', 59-65 <PAW>
A:Experimental source: skin
C:Comment: This peptide has antimicrobial activity.
C:Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
F:1-41/Domain: dermorphin precursor amino-terminal homology <DER>
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-41/Domain: propeptide #status predicted <PRO>
F:44-65/Product: antimicrobial peptide gaegurin 5 #status experimental <MAT>
F:59-65/Region: rana box motif

Query Match 1.5%; Score 7; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 SLTLFF 176
DB 7 SLTLFF 13

RESULT 36
A53744
ranalexin precursor - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A53744

R.Clark, D.P.; Durell, S.; Maloy, W.L.; Zasloff, M.
J. Biol. Chem. 269, 10849-10855, 1994
A:Title: Ranalexin. A novel antimicrobial peptide from bullfrog (*Rana catesbeiana*) sk
A:Reference number: A53744; MUID:94193792; PMID:8144672
A:Accession: A53744
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: protein
A:Residues: 1-66 <CLAD>
A:Cross-references: GB:S69903; NID:9546211; PIDD:AB30394.1; PID:9546212
C:Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
F:1-46/Domain: dermorphin precursor amino-terminal homology <DER>
F:47-66/Product: ranalexin #status experimental <MAT>
F:60-66/Disulfide bonds: #status experimental

Query Match 1.5%; Score 7; DB 1; Length 66;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 SLTLFF 176
DB 7 SLTLFF 13

RESULT 37
LMHMA3
H+-transporting two-sector ATPase (EC 3.6.3.14) lipid-binding protein - thermophilic
N:Alternate names: H+-transporting ATP synthase chain c; hydrogen ion-transporting At
C:Species: Thermophilic bacterium PS-3
C:Date: 31-Jul-1979 #sequence_revision 23-Oct-1981 #text_change 14-Dec-2001
C:Accession: S02255; A01048
R:Ohta, S.; Yoshida, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.;
Biochim. Biophys. Acta 933, 141-155, 1988
A:Title: Sequence and over-expression of subunits of adenosine triphosphate synthase
A:Reference number: S01397; MUID:88163679; PMID:2894854
A:Accession: S02255
A:Molecule type: DNA
A:Residues: 1-72 <OHR>
A:Cross-references: EMBL:X07804; NID:945808; PIDD:CA30649.1; PID:945811
A:Note: this sequence was confirmed by protein sequencing
R:Hoppe, J.; Sebald, W.
Eur. J. Biochem. 107, 57-65, 1980
A:Title: Amino acid sequence of the proteolipid subunit of the proton-translocating A
A:Reference number: A01048; MUID:80245993; PMID:6447066
A:Accession: A01048
A:Molecule type: protein
A:Residues: 1-72 <HOP>
C:Comment: This protein is a nonenzymatic component of ATPase.
C:Superfamily: H+-transporting ATP synthase lipid-binding protein
F:1-72/Product: H+-transporting ATP synthase lipid-binding protein #status experiment
F:2-28/Domain: transmembrane #status predicted <TM>
F:46-72/Domain: transmembrane #status predicted <TM>
F:1/Modified site: N-formylmethionine #status experimental
F:56/Active site: Glu #status predicted

Query Match 1.5%; Score 7; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 177 FSFIYLG 183
DB 65 FSFIYLG 71

RESULT 38
C71978
hypothetical protein jhp0055 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: C71978
R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MID:9910557; PMID:9923682
A:Accession: C71978
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <ARN>
A:Cross-references: GB:AE001445; GB:AE001439; NID:g4154559; PIDN:AMD0639.1; PID:g415456
A:Experimental source: strain J99
C:Genetics:
A:Gene: jnp0055

Query Match 1.5%; Score 7; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 KDGOLIV 115
|||||
Db 65 KDGOLIV 71

RESULT 39
B47354
Ygdf protein - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C:Date: 08-May-1995 #sequence_revision 12-May-1995 #text_change 08-Oct-1999
C:Accession: B47354
R:Can, K.; Gupta, S.D.; Sankaran, K.; Schmid, M.B.; Wu, H.C.
J. Biol. Chem. 268, 16544-16550, 1993
A:Title: Isolation and characterization of a temperature-sensitive mutant of Salmonella
A:Reference number: A47354; MID:93346403; PMID:8344935
A:Accession: B47354
A:Status: preliminary; translation not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-85 <GAN>
A:Cross-references: GB:L13259; NID:g295201; PIDN:AAA20895.1; PID:g511503
C:Genetics:
A:Gene: ygdf
C:Superfamily: phosphotransferase system enzyme I homology (fragment) <P11>
F:1-64/Domain: phosphotransferase system enzyme I homology (fragment) <P11>

Query Match 1.5%; Score 7; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 412 VAILIGL 418
|||||
Db 15 VAILIGL 21

RESULT 40
C71549
Hypothetical protein CT164 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: C71549
R:Stephens, R.S.; Kalam, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MID:9900809; PMID:9784136
A:Accession: C71549
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <ARN>
A:Cross-references: GB:AE001290; GB:AE001273; NID:g3328560; PIDN:AAC67755.1; PID:g332856
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT164

Query Match 1.5%; Score 7; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 ISSLLLL 174
|||||
Db 46 ISSLLLL 52

RESULT 41
AF0856
Conserved hypothetical protein SRY3056 [imported] - Salmonella enterica subsp. enteri
C:Species: Salmonella enterica subsp. enterica serovar typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF0856
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Croxin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Mole, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AF0856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06037.1; PID:g16504004; GSPDB:GN00176
C:Genetics:
A:Gene: SRY3056
C:Superfamily: hypothetical protein HI0673

Query Match 1.5%; Score 7; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 420 LTLILLA 426
|||||
Db 4 LTLILLA 10

RESULT 42
C83236
Hypothetical protein PA3284 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83236
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Van, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: AB2950; MID:20437337; PMID:10984043
A:Accession: C83236
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <STO>
A:Cross-references: GB:AE004750; GB:AE004091; NID:g9949400; PIDN:AAG06672.1; GSPDB:GN
C:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3284

Query Match 1.5%; Score 7; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 360 AVOELSS 366
|||||
Db 31 AVOELSS 37

RESULT 43
H72575
Hypothetical protein APE1888 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: H72575
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Tanaka, T.; Tanaka, T.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6: 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:9310339; PMID:10382966
A:Accession: H72575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <RAW>
A:Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BAA80893.1; PID:01044679; PID:9510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1888

Query Match 1.5%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 LSSSILA 370
|||||
Db 2 LSSSILA 8

RESULT 44
D72617
hypothetical protein APE1397 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: D72617
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6: 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:9310339; PMID:10382966
A:Accession: D72617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <RAW>
A:Cross-references: DDBJ:AP000061; NID:95104821; PIDN:BAA80394.1; PID:01044180; PID:9510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1397
C:Superfamily: Aeropyrum pernix hypothetical protein APE1397

Query Match 1.5%; Score 7; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 LSSSILA 370
|||||
Db 70 LSSSILA 76

RESULT 45
B72763
hypothetical protein APE0095 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: B72763
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6: 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:9310339; PMID:10382966
A:Accession: B72763
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <RAW>
A:Cross-references: DDBJ:AP000058; NID:95103388; PIDN:BAA79004.1; PID:01042780; PID:9510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0095

C:Superfamily: Aeropyrum pernix hypothetical protein APE0095

Query Match 1.5%; Score 7; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 TILLVVL 153
|||||
Db 43 TILLVVL 49

RESULT 46
S31130
hypothetical protein F59B2.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Mar-2000
C:Accession: S31130
R:Stilson, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.;
awkins, T.; Altschough, R.; Waterston, R.
submitted to the EMBL Data Library, November 1991
A:Description: The C. elegans sequencing project: A beginning.
A:Reference number: S31122
A:Accession: S31130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <SQL>
A:Cross-references: EMBL:211505; NID:96718; PID:96727
C:Genetics:
A:Insertions: 21/2; 74/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F59B2.10

Query Match 1.5%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 ISSLLLL 174
|||||
Db 8 ISSLLLL 14

RESULT 47
S61635
ribosomal protein L22.e.A, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L2168; protein YLR061w; ribosomal protein YL31
C:Species: Saccharomyces cerevisiae
C:Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 19-Apr-2002
C:Accession: S61635; S64889; S11582
R:Urestarazu, L.A.
submitted to the EMBL Data Library, December 1995
A:Reference number: S61618
A:Accession: S61635
A:Molecule type: DNA
A:Residues: 1-121 <URR>
A:Cross-references: EMBL:X94607; NID:91181264; PIDN:CAA64308.1; PID:91181282
R:Andre, B.; Urestarazu, L.A.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64872
A:Accession: S64889
A:Molecule type: DNA
A:Residues: 1-121 <AND>
A:Cross-references: EMBL:Z73233; NID:91360407; PIDN:CAA97592.1; PID:91370303; MIPS:YL
R:Okada, E.; Higo, K.; Osawa, S.
Biochemistry 21, 4545-4550, 1982
A:Title: Isolation of seventeen proteins and amino-terminal amino acid sequences of e
A:Reference number: S11575; MUID:83048950; PMID:6814480
A:Accession: S11582
A:Molecule type: protein
A:Residues: 2-17, 'B', 19-24, 'B', 26-28, 'B', 30-38, 'B', 40-43, 'Z', 45-48, 'B', 50-51, 'B' <OTA
C:Genetics:
A:Gene: SGD:RPL22A
A:Cross-references: SGD:S0004051
A:Map position: 12R

A: Introns: 4/3
A: Note: YLR061w
C: Superfamily: rat ribosomal protein L22
C: Keywords: cytosol; protein biosynthesis; ribosome

Query Match 1.5%; Score 7; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DEEDED 72
|||||
DB 115 DEEDED 121

RESULT 48
E97486
Hypothetical protein AGR_C_1913 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C: Species: Agrobacterium tumefaciens
C: Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C: Accession: E97486

R: Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Oucollo, B.; Goldman,
A.; Liu, F.; Hohlmeier, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A: Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A: Reference number: A97359; PMID:11743194

A: Accession: E97486

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-125 <KUR>

A: Cross-references: GB:AE007869; PIDN:AAK86846.1; PID:g15156060; GSPDB:GNO0169

C: Genetics:

A: Gene: AGR_C_1913

A: Map position: circular chromosome

Query Match 1.5%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 ROVEED 66
|||||
DB 41 ROVEED 47

RESULT 49
AE2704
Two component response regulator Atu1038 [imported] - Agrobacterium tumefaciens (strain

C: Species: Agrobacterium tumefaciens
C: Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C: Accession: AE2704

R: Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Gunthner, D.; Kutyavln, T.; Levy, R.; Li, M.; Mccllell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A: Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A: Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A: Reference number: AB2577; PMID:11743193

A: Accession: AE2704

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-125 <KUR>

A: Cross-references: GB:AE008688; PIDN:AAI42051.1; PID:g17739429; GSPDB:GNO0186

A: Experimental source: strain C58 (Dupont)

C: Genetics:

A: Gene: Atu1038

A: Map position: circular chromosome

Query Match 1.5%; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 ROVEED 66
|||||

DB 41 ROVEED 47

RESULT 50
D87491
Hypothetical protein CC1953 [imported] - Caulobacter crescentus

C: Species: Caulobacter crescentus
C: Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C: Accession: D87491

R: Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A: Title: Complete Genome Sequence of Caulobacter crescentus.

A: Reference number: A87249; PMID:11736598; PMID:11259647

A: Accession: D87491

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-131 <STO>

A: Cross-references: GB:AE005673; NID:g13423412; PIDN:AAK23928.1; GSPDB:GNO0148

C: Genetics:

A: Gene: CC1953

Query Match 1.5%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 137 AIMSVI 143
|||||
DB 52 AIMSVI 58

Search completed: February 6, 2003, 14:21:09
Job time : 62.0975 secs